



361 TTCCGCCAGATTGTGTCTGGCTGGACTTCTGCCACAGCTACTCCATCTGCCACAGAGAC 420  
1441 GCCCGCTCCACACCGCTGCGCGGCCCGCCAGGCTCCCGCGCTCTCTTGGCGGGACCCCC 1500  
361 TTCCGCCAGATTGTGTCTGGCTGGACTTCTGCCACAGCTACTCCATCTGCCACAGAGAC 420  
1501 TTGCATCTCGCTCTGCAACCGCCCGCGGCGAGTCCACCGGGACCCCGGGGACCAACCA 1560  
421 CTAAAGCCGAGAACCTGCTTTTGGATGAGAAAAACAACATCGCATTCGAGCTTCGGC 480  
1501 TTGCATCTCGCTCTGCAACCGCCCGCGGCGAGTCCACCGGGACCCCGGGGACCAACCA 1560  
421 CTAAAGCCGAGAACCTGCTTTTGGATGAGAAAAACAACATCGCATTCGAGCTTCGGC 480  
1561 CCCCCCAGCCCGCGGTGGGTGGGGAGCCGCTGGAGAGATGCTCTCAATCCATTC 1620  
481 ATGGCGTCCCTGAGGTGGGGAGACCTCTCTGGAGACAGCTGCGGGTCCCGCCATTAT 540  
1561 CCCCCCAGCCCGCGGTGGGTGGGGAGCCGCTGGAGAGATGCTCTCAATCCATTC 1620  
481 ATGGCGTCCCTGAGGTGGGGAGACCTCTCTGGAGACAGCTGCGGGTCCCGCCATTAT 540  
1561 CCCCCCAGCCCGCGGTGGGTGGGGAGCCGCTGGAGAGATGCTCTCAATCCATTC 1620  
541 GCCTGTCCAGAGTGTAAAGGGGAAAAATATGATGGCCGCGGACAGACATGTGGAGC 600  
1621 CGCAACAGCTTCTGGGCTCCCTCGCTTTCAACCGGCGAAGATGAGGTCCCTACCGCT 1680  
541 GCCTGTCCAGAGTGTAAAGGGGAAAAATATGATGGCCGCGGACAGACATGTGGAGC 600  
1681 GAGGAGATGTCCAGCTTGAACGACAGATCTCCCGGAGCTGGCAAAAGCTCTCTGGTTC 1740  
541 GCCTGTCCAGAGTGTAAAGGGGAAAAATATGATGGCCGCGGACAGACATGTGGAGC 600  
1681 GAGGAGATGTCCAGCTTGAACGACAGATCTCCCGGAGCTGGCAAAAGCTCTCTGGTTC 1740  
601 TGTGGAGTCACTCTCTCGCCCTGCTGCTGGGGGCTCTGCCCTTTGATGACGACAACTTC 660  
1741 GGGAACTTTCATCTCTCTGGACAAAGAAATAATTTCTCTGCTCTAAAGGACAACTTC 1800  
601 TGTGGAGTCACTCTCTCGCCCTGCTGCTGGGGGCTCTGCCCTTTGATGACGACAACTTC 660  
1741 GGGAACTTTCATCTCTCTGGACAAAGAAATAATTTCTCTGCTCTAAAGGACAACTTC 1800  
661 CGCCAGCTGTGAGAAAGGTGAAACGGGGGCTCTTCCAGATGCCCACTTCATTCCTCCA 720  
1801 CTCAGAGCATCAAAAGCAGACATCGTCCATGCTTCTGTCGATCCCGAGCTGAGTCAAC 1860  
661 CGCCAGCTGTGAGAAAGGTGAAACGGGGGCTCTTCCAGATGCCCACTTCATTCCTCCA 720  
1801 CTCAGAGCATCAAAAGCAGACATCGTCCATGCTTCTGTCGATCCCGAGCTGAGTCAAC 1860  
721 GATTGCCAGAGCTCTCTGAGGGGAAATGATGAGTGGAGCCCGAAAAAGGCTCAGTCTG 780  
1861 AGTGTGCTGTACAGACCAAGCTTTCAGGGCCGAGTCAAGGCCAGTGGCGGCCCTCCGTC 1920  
721 GATTGCCAGAGCTCTCTGAGGGGAAATGATGAGTGGAGCCCGAAAAAGGCTCAGTCTG 780  
1861 AGTGTGCTGTACAGACCAAGCTTTCAGGGCCGAGTCAAGGCCAGTGGCGGCCCTCCGTC 1920  
781 GAGCAAAATTCAGAAACATCTCTGTGTACTAGGGGGGAAAAACAGAGCCAGACCCGTGCTG 840  
1921 TTCCAAAAGCCCGTCCGCTTCCAGGTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCC 1980  
781 GAGCAAAATTCAGAAACATCTCTGTGTACTAGGGGGGAAAAACAGAGCCAGACCCGTGCTG 840  
1921 TTCCAAAAGCCCGTCCGCTTCCAGGTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCC 1980  
841 GAGCAGCCCTGCGCGCGGTAGCCATCGGAGCGCTGCCATCCCAACGAGAGCTGGAC 900  
1981 CGCGAGCGGAGCGGACGCGAGTGTGGCACTACTCTCGTCACTCTCACTCTCATCTCG 2040  
841 GAGCAGCCCTGCGCGCGGTAGCCATCGGAGCGCTGCCATCCCAACGAGAGCTGGAC 900  
1981 CGCGAGCGGAGCGGACGCGAGTGTGGCACTACTCTCGTCACTCTCACTCTCATCTCG 2040  
901 CCGAGCTCTCAGAGACATGCGCTCACTGGGCTCTTCAGGGACCGCGAGAGCTGCAT 960  
2041 GGTCCAGACCGCTCGGTTCAAGCGAGTGTGGAGACCATCAGGCAAGCTCTCTGAGCACT 2100  
901 CCGAGCTCTCAGAGACATGCGCTCACTGGGCTCTTCAGGGACCGCGAGAGCTGCAT 960  
2041 GGTCCAGACCGCTCGGTTCAAGCGAGTGTGGAGACCATCAGGCAAGCTCTCTGAGCACT 2100  
961 CGCGAGCTGCGCAGTGGAGAGGAGAAACAGAAAGATGATATATCTGCTTTGGAT 1020  
2101 CATGACAGCCCTCTCGTGGAGCCCTCGGAGCGGAGGAGAAAGGGGCCAGAGCCCGGCT 2160  
961 CGCGAGCTGCGCAGTGGAGAGGAGAAACAGAAAGATGATATATCTGCTTTGGAT 1020  
2101 CATGACAGCCCTCTCGTGGAGCCCTCGGAGCGGAGGAGAAAGGGGCCAGAGCCCGGCT 2160  
1021 CGGAGGAGCGGATCCAGCTGTGAGGACAGACCTGCTCCCGGAAATGATGTTGAC 1080  
2161 GCTGTGCCCGACCCCGAAGCTTCAGCGCCCGGAGCGGAGGAGGAGGAGGAGGAGGAGG 2220  
1021 CGGAGGAGCGGATCCAGCTGTGAGGACAGACCTGCTCCCGGAAATGATGTTGAC 1080  
2161 GCTGTGCCCGACCCCGAAGCTTCAGCGCCCGGAGCGGAGGAGGAGGAGGAGGAGGAGG 2220  
1081 CCCCCCGGAAAGCGTGTGGATTCTCCCATGCTGAGCCGTCAAGGAAAGCGGACCAAGAG 1140  
2221 AGCTCTCCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280  
1081 CCCCCCGGAAAGCGTGTGGATTCTCCCATGCTGAGCCGTCAAGGAAAGCGGACCAAGAG 1140  
2221 AGCTCTCCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280  
1141 CGGAAAGTCCATGGAAGTCTGAGCATCCAGATGCGGGGGTGGTGGCTCCCGCTGATACC 1200  
2281 CTGCCCCCTGA 2289  
1141 CGGAAAGTCCATGGAAGTCTGAGCATCCAGATGCGGGGGTGGTGGCTCCCGCTGATACC 1200  
2281 CTGCCCCCTGA 2289  
1201 ACCCGAGCGGCTTGGAGATGCGCCAGACAGCCAGAGATCCCGTAGCGTCACTGGAGCC 1260  
1201 ACCCGAGCGGCTTGGAGATGCGCCAGACAGCCAGAGATCCCGTAGCGTCACTGGAGCC 1260  
1261 TCCAGGGGTCTGCTCTCCAGCCCTTAAGCAGCCCAAGAGTCCGGTCTTTCTTTTCA 1320  
1261 TCCAGGGGTCTGCTCTCCAGCCCTTAAGCAGCCCAAGAGTCCGGTCTTTCTTTTCA 1320  
1321 CCGGAGCCGGGGCTGGAGATGAGCTCGAGCGGGGCTCCCGGCTTCCAAACGAG 1380  
1321 CCGGAGCCGGGGCTGGAGATGAGCTCGAGCGGGGCTCCCGGCTTCCAAACGAG 1380  
1321 CCGGAGCCGGGGCTGGAGATGAGCTCGAGCGGGGCTCCCGGCTTCCAAACGAG 1380  
1381 AGCTGCTCTCTCGGGGCCCCAGGGGTGGGGGCGCGGGGAGCAGCCCCCGCCCCAGT 1440  
1381 AGCTGCTCTCTCGGGGCCCCAGGGGTGGGGGCGCGGGGAGCAGCCCCCGCCCCAGT 1440  
1441 GCCCGCTCCACACCCCTGCGCGGCCCGCCAGGCTCCCGGCTCTCTTGGCGGGACCC 1500

RESULT 2  
US-10-116-326-5  
; Sequence 5, Application US/10116326  
; Patent No. 6777545  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fridde, Carl Johan  
; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0332-USA  
; CURRENT APPLICATION NUMBER: US/10/116,326  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/282,036

;; PRIOR FILING DATE: 2001-04-06  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 5  
;; LENGTH: 2112  
;; TYPE: DNA  
;; ORGANISM: homo sapiens  
US-10-116-326-5

Query Match 88.3%; Score 2020.2; DB 4; Length 2112;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	265	TTTAGTACCTGGTCTCGAGCAGCTCTCGGGGGTGGAGTATTCGACTACCTACCTGGTAAG	324
Db	88	TAATTGTACCTGGTCTCGAGCAGCTCTCGGGGGTGGAGTATTCGACTACCTGGTAAG	147
Qy	325	AAGGGAGAGCTGACGCCCAAGAGGCGCCGAAAGTTCTTCGCCCAGAGTTGTCTGCGCTG	384
Db	148	AAGGGAGAGCTGACGCCCAAGAGGCGCCGAAAGTTCTTCGCCCAGAGTTGTCTGCGCTG	207
Qy	385	GACTTCTGCCACAGTACTCCATCTGCCACAGACCTAAAGCCCGAGAACCTGCTTTTG	444
Db	208	GACTTCTGCCACAGTACTCCATCTGCCACAGACCTAAAGCCCGAGAACCTGCTTTTG	267
Qy	445	GATGAGAAAAACAATCCGGATTGACACTTCGGGATGGGTCCCTGCGAGTGGGGAC	504
Db	268	GATGAGAAAAACAATCCGGATTGACACTTCGGGATGGGTCCCTGCGAGTGGGGAC	327
Qy	505	AGCTCTCTGGAGACCACTCGGGTCCCGCCATTCATCGGTGTCAGAGGTGATTAAGGGG	564
Db	328	AGCTCTCTGGAGACCACTCGGGTCCCGCCATTCATCGGTGTCAGAGGTGATTAAGGGG	387
Qy	565	GAAAAATATGATGGCCCGCGGACAGATGTGGAGCTGTGGAGTCACTCTTCGCCCTG	624
Db	388	GAAAAATATGATGGCCCGCGGACAGATGTGGAGCTGTGGAGTCACTCTTCGCCCTG	447
Qy	625	CTCGTGGGGGTCTGCCCTTTGATGACGACAACTCCCGCAGAGTGTGGAGAGGTGAAA	684
Db	448	CTCGTGGGGGTCTGCCCTTTGATGACGACAACTCCCGCAGAGTGTGGAGAGGTGAAA	507
Qy	685	CGGGGCTCTTCCACATGCCCCCTTCACTTCCTCCAGATTGCCAGAGCCCTCGTGGGGG	744
Db	508	CGGGGCTCTTCCACATGCCCCCTTCACTTCCTCCAGATTGCCAGAGCCCTCGTGGGGG	567
Qy	745	ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG	804
Db	568	ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG	627
Qy	805	TACCTAGGCGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGCGGGTA	864
Db	628	TACCTAGGCGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGCGGGTA	687
Qy	865	GCCATGCGGAGCTGCCATCCAGCGGAGAGTGAACCCGACGTCCTAGAGAGATGCA	924
Db	688	GCCATGCGGAGCTGCCATCCAGCGGAGAGTGAACCCGACGTCCTAGAGAGATGCA	747
Qy	925	TCACTGGGCTGCTTCAGGGACCGGAGAGGCTGCATCGCAGCTGCGCAGTGAGAGGAG	984
Db	748	TCACTGGGCTGCTTCAGGGACCGGAGAGGCTGCATCGCAGCTGCGCAGTGAGAGGAG	807
Qy	985	AACCAAGAAAAGATGATATATATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGT	1044
Db	808	AACCAAGAAAAGATGATATATATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGT	867
Qy	1045	GAGACACAGACTGCTGCCCTCCCGAATGATTTGACCCCGCCCGGAAAGCGGTGGAATCT	1104
Db	868	GAGACACAGACTGCTGCCCTCCCGAATGATTTGACCCCGCCCGGAAAGCGGTGGAATCT	927
Qy	1105	CCCATGTGACCGCTACCGGAGCGGACCGAGCGGAGTCCATGGAAGTCTCTGAGC	1164
Db	928	CCCATGTGACCGCTACCGGAGCGGACCGAGCGGAGTCCATGGAAGTCTCTGAGC	987

Qy	1165	ATCACCGATCCCGGGGTGGTGGCTCCCTGTATCCCAACCGACGGGCTTGGAGATGGCC	1224
Db	988	ATCACCGATCCCGGGGTGGTGGCTCCCTGTATCCCAACCGACGGGCTTGGAGATGGCC	1047
Qy	1225	CAGCACAGCAGAGATCCCGTAGCGTCAGTGGAGCTTCCAGGCTCTGTCTCTCAGGCT	1284
Db	1048	CAGCACAGCAGAGATCCCGTAGCGTCAGTGGAGCTTCCAGGCTCTGTCTCTCAGGCT	1107
Qy	1285	CTAAGCAGCCCAAGGAGTCCGGTCTTTTCTTTTACCGAGCCGGGGCTGGAGATGAG	1344
Db	1108	CTAAGCAGCCCAAGGAGTCCGGTCTTTTCTTTTACCGAGCCGGGGCTGGAGATGAG	1167
Qy	1345	GCTCGAGCGCGGGGCTCCCGACTTCCAAAAGCAGACGCTGCTTCTCGGGGCCCGAGG	1404
Db	1168	GCTCGAGCGCGGGGCTCCCGACTTCCAAAAGCAGACGCTGCTTCTCGGGGCCCGAGG	1227
Qy	1405	GGTGGGGCGCGCGGGAGCAGCCCCCGCCCCCAGTCCCGCTCCACACCCCTGCCCGGC	1464
Db	1228	GGTGGGGCGCGCGGGAGCAGCCCCCGCCCCCAGTCCCGCTCCACACCCCTGCCCGGC	1287
Qy	1465	CCCCCAGGCTCCCGGCTCTCTGTGGGGAGCCCTCTTGAATCTGCTCTGCAACGCTTC	1524
Db	1288	CCCCCAGGCTCCCGGCTCTCTGTGGGGAGCCCTCTTGAATCTGCTCTGCAACGCTTC	1347
Qy	1525	CGGGCAGTCCCAACCGGGACCCCGGGGACCAACCCCGCCCCCAGTCCCGCTCCCGGTC	1584
Db	1348	CGGGCAGTCCCAACCGGGACCCCGGGGACCAACCCCGCCCCCAGTCCCGCTCCCGGTC	1407
Qy	1585	GGGGAGCCGCTGGAGAGTCTGCTCAATCCATCCGCAACAGCTTCTTGGGCTCCCT	1644
Db	1408	GGGGAGCCGCTGGAGAGTCTGCTCAATCCATCCGCAACAGCTTCTTGGGCTCCCT	1467
Qy	1645	CGCTTTACCGCGGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCCAGCTTCAACGCA	1704
Db	1468	CGCTTTACCGCGGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCCAGCTTCAACGCA	1527
Qy	1705	GAGTCTCCCGGAGCTGGCAAAACGCTCTGTTTGGGAACTTCACTCTCTTGGACAAA	1764
Db	1528	GAGTCTCCCGGAGCTGGCAAAACGCTCTGTTTGGGAACTTCACTCTCTTGGACAAA	1587
Qy	1765	GAAGAAACAATATTTCTCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC	1824
Db	1588	GAAGAAACAATATTTCTCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC	1647
Qy	1825	GTCCATGCTCTTCTGTCGATCCCGAGCTGAGTGCACAGTGTGTGTGTGTGTGTGTGT	1884
Db	1648	GTCCATGCTCTTCTGTCGATCCCGAGCTGAGTGCACAGTGTGTGTGTGTGTGTGTGT	1707
Qy	1885	AGGGCGAGTACAAAGGCAAGTGGGGCCCTCTCGTCTTCAAAAGCCGCTCGCTTCCAG	1944
Db	1708	AGGGCGAGTACAAAGGCAAGTGGGGCCCTCTCGTCTTCAAAAGCCGCTCGCTTCCAG	1767
Qy	1945	GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGT	2004
Db	1768	GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGT	1827
Qy	2005	GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCCGAGCTTCAAGCGA	2064
Db	1828	GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCCGAGCTTCAAGCGA	1887
Qy	2065	GTGGTGGAGACCATCCAGGCAAGTCTCTGAGCACTCATGACAGCTCTCGTGCAGGCT	2124
Db	1888	GTGGTGGAGACCATCCAGGCAAGTCTCTGAGCACTCATGACAGCTCTCGTGCAGGCT	1947
Qy	2125	CTGGCAGACGAGAAAGCGGGGCCAGACCCGGGCTGCTGGTGCCTCCACCCCGAGGCTG	2184
Db	1948	CTGGCAGACGAGAAAGCGGGGCCAGACCCGGGCTGCTGGTGCCTCCACCCCGAGGCTG	2007
Qy	2185	CAGCCCCCAGCGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGGAGGCCCCCCCC	2244
Db	2008	CAGCCCCCAGCGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGGAGGCCCCCCCC	2067
Qy	2245	AAGGACAAAGAGTCTCTGGGCCAACCAACGGGACCCCTCTGCTGCTGCA 2289	

```
Db 2068 AAGGACAAAGAGCTCTGGCCACCAACGGGACCCCTCTGCCCTGA 2112
|||||
RESULT 3
US-10-116-326-1
; Sequence 1, Application US/10116326
; Patent No. 6777545
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2337
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-116-326-1
Query Match 88.3%; Score 2020.2; DB 4; Length 2337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 265 TTATAGTACCTGGTTCTGAGACAGCTCTCGGGGGGTGAGTATTGCACTACCTGGTAAAG 324
Db 313 TATTTGTACCTGGTTCTGAGACAGCTCTCGGGGGGTGAGTATTGCACTACCTGGTAAAG 372
QY 325 AAGGGAGACTGACGCGCCAGAGAGGCGCGAAGTTCTTCGCGCAGATTGTTGTCGCGCTG 384
Db 373 AAGGGAGACTGACGCGCCAGAGAGGCGCGAAGTTCTTCGCGCAGATTGTTGTCGCGCTG 432
QY 385 GACTTCTGCCACAGTACTCCATCTGCGACAGAGACCTAAAGCCCGAGAACTGCTTTTG 444
Db 433 GACTTCTGCCACAGTACTCCATCTGCGACAGAGACCTAAAGCCCGAGAACTGCTTTTG 492
QY 445 GATGAGAAAAAACAATCCCGATTGAGACTTTCGGGATGCGGTCCCTGCGAGAGTGGGGAC 504
Db 493 GATGAGAAAAAACAATCCCGATTGAGACTTTCGGGATGCGGTCCCTGCGAGAGTGGGGAC 552
QY 505 AGCTCTCTGAGACCACTGCGGTCCCGCATTTATGCGGTCCAGAGGTGATTAGGGG 564
Db 553 AGCTCTCTGAGACCACTGCGGTCCCGCATTTATGCGGTCCAGAGGTGATTAGGGG 612
QY 565 GAAAAATATGATGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 624
Db 613 GAAAAATATGATGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 672
QY 625 CTGTTGGGGCTCTGCGCTTTGATGAGACAAACCTCGCGCAGCTGTGGAGAGAGTGAAA 684
Db 673 CTGTTGGGGCTCTGCGCTTTGATGAGACAAACCTCGCGCAGCTGTGGAGAGAGTGAAA 732
QY 685 CGGGGCTCTTCCACATGCCCCCACTTCACTTCCTCCAGATTGCGAGAGCTCTGAGGGGA 744
Db 733 CGGGGCTCTTCCACATGCCCCCACTTCACTTCCTCCAGATTGCGAGAGCTCTGAGGGGA 792
QY 745 ATGATCGAAGTGGAGCGCGGAAAAAGGCTCAGTCTGAGCAAAATTCAGAAACATCTTTGG 804
Db 793 ATGATCGAAGTGGAGCGCGGAAAAAGGCTCAGTCTGAGCAAAATTCAGAAACATCTTTGG 852
QY 805 TACCTAGGCGGGAACACAGACCGAGACCCGCTGCTGAGCGAGCCCTCGCGCGGGTA 864
Db 853 TACCTAGGCGGGAACACAGACCCGCTGCTGAGCGAGCCCTCGCGCGGGTA 912
QY 865 GCCATGCGGAGCCTGCTCCATCCACGGAGAGCTGACCCCGACGCTCTAGAGAGCATGCA 924
Db 913 GCCATGCGGAGCCTGCTCCATCCACGGAGAGCTGACCCCGACGCTCTAGAGAGCATGCA 972
```

```
QY 925 TCACTGGGCTGTCTTCAGGACACCGGAGAGGCTGCATCGGAGCTGCGCAGTGAAGGAG 984
Db 973 TCACTGGGCTGTCTTCAGGACACCGGAGAGGCTGCATCGGAGCTGCGCAGTGAAGGAG 1032
QY 985 AACCAAGAAAAAGATGATATATATCTGCTTTTGGATCGGAGAGCGGTATCCAGTGT 1044
Db 1033 AACCAAGAAAAAGATGATATATATCTGCTTTTGGATCGGAGAGCGGTATCCAGTGT 1092
QY 1045 GAGGACAGGACCTGCTCCCGGAATGATGTTGACCCCGCCCGGAAGCGTGTGGATTCT 1104
Db 1093 GAGGACAGGACCTGCTCCCGGAATGATGTTGACCCCGCCCGGAAGCGTGTGGATTCT 1152
QY 1105 CCATGCTGAGCGCTCAOGBGAAGCGGACACAGAGCGGAAGTTCATGGAAGTCTTGAGC 1164
Db 1153 CCATGCTGAGCGCTCAOGBGAAGCGGACACAGAGCGGAAGTTCATGGAAGTCTTGAGC 1212
QY 1165 ATCACCGATGCGGGGGTGTGCTCCCTGCTACCCACCGAGCGGCTTGGAGATGGCC 1224
Db 1213 ATCACCGATGCGGGGGTGTGCTCCCTGCTACCCACCGAGCGGCTTGGAGATGGCC 1272
QY 1225 CAGCAGACGAGAGATCCCGTAGCTCAGTGAAGCTTCCACGGGTCTGTCTCCAGCCCT 1284
Db 1273 CAGCAGACGAGAGATCCCGTAGCTCAGTGAAGCTTCCACGGGTCTGTCTCCAGCCCT 1332
QY 1285 CTAAGCAGCCCAAGGAGTCCGCTTTTCTTTTCAACCGGAGCGGGGCTGGAGATGAG 1344
Db 1333 CTAAGCAGCCCAAGGAGTCCGCTTTTCTTTTCAACCGGAGCGGGGCTGGAGATGAG 1392
QY 1345 GCTCGAGGCGGGGCTCCCGACTTCCAAACGACAGAGCTGCTTCTCGGGGCGCCAGG 1404
Db 1393 GCTCGAGGCGGGGCTCCCGACTTCCAAACGACAGAGCTGCTTCTCGGGGCGCCAGG 1452
QY 1405 GGTGGGGGCGCGGGGAGAGCGCCCGCGCCCGCAGTCCCGCTTCCACCCCTGCGCGGC 1464
Db 1453 GGTGGGGGCGCGGGGAGAGCGCCCGCGCCCGCAGTCCCGCTTCCACCCCTGCGCGGC 1512
QY 1465 CCCCCAGGCTCCCGGCTCTCTGCGGGGACCCCTTTGCACTGCGCTCTGCAACGCCCC 1524
Db 1513 CCCCCAGGCTCCCGGCTCTCTGCGGGGACCCCTTTGCACTGCGCTCTGCAACGCCCC 1572
QY 1525 CGGGCAGTCCCAACCGGGGACCCCGGGGACAAACACCCCGAGCCCGCGGCTGGCGTC 1584
Db 1573 CGGGCAGTCCCAACCGGGGACCCCGGGGACAAACACCCCGAGCCCGCGGCTGGCGTC 1632
QY 1585 GGGGAGCGGCTGAGGAGTCTCTCAATCCATCGCAACAGCTTCTGGGCTCCCT 1644
Db 1633 GGGGAGCGGCTGAGGAGTCTCTCAATCCATCGCAACAGCTTCTGGGCTCCCT 1692
QY 1645 CGCTTTCAACCGGCGAAGATGCAAGTCCCTTACCGCTGAGGAGATGTCAGCTTGAACCCA 1704
Db 1693 CGCTTTCAACCGGCGAAGATGCAAGTCCCTTACCGCTGAGGAGATGTCAGCTTGAACCCA 1752
QY 1705 GAGTCTCTCCCGAGCTGGCAAAACGCTCTGCTTGGGAACTTCACTCTCTTGGACAAA 1764
Db 1753 GAGTCTCTCCCGAGCTGGCAAAACGCTCTGCTTGGGAACTTCACTCTCTTGGACAAA 1812
QY 1765 GAAGAAACAATATTTCTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAAGCAGATC 1824
Db 1813 GAAGAAACAATATTTCTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAAGCAGATC 1872
QY 1825 GTCCATGCTCTGTCGATFCCCGAGCTGAGTCAAGTGTGTCGATGTCAGACAGCTTC 1884
Db 1873 GTCCATGCTCTGTCGATFCCCGAGCTGAGTCAAGTGTGTCGATGTCAGACAGCTTC 1932
QY 1885 AGGGCGAGTACAAAGCGAGTGGCGCCCTCTCCAAAGCCCGCTCCGCTCCAG 1944
Db 1933 AGGGCGAGTACAAAGCGAGTGGCGCCCTCTCCAAAGCCCGCTCCGCTCCAG 1992
QY 1945 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGAGT 2004
Db 1993 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGAGT 2052
```



Qy 2005 GGTGCATCTACTCGCTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGGTTCAAGCGA 2064  
Db 2053 GGTGCATCTACTCGCTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGGTTCAAGCGA 2112  
Qy 2065 GTGTGGAGACCATCCAGGCAAGCTCTGTAGCACTCATGACCAAGCCCTCGTGCAGGCC 2124  
Db 2113 GTGTGGAGACCATCCAGGCAAGCTCTGTAGCACTCATGACCAAGCCCTCGTGCAGGCC 2172  
Qy 2125 CTGCGAGACGAGAAAGCGGGCCGAGACCCCGGGCTGTGTGTCGCCACCCCGAAGCCTG 2184  
Db 2173 CTGCGAGACGAGAAAGCGGGCCGAGACCCCGGGCTGTGTGTCGCCACCCCGAAGCCTG 2232  
Qy 2185 CAGCCCCACCCCGCCGCGAGACCCAGAGCTGAGCAAGCTCTCCCGCGAGGCCCCCCC 2244  
Db 2233 CAGCCCCACCCCGCCGCGAGACCCAGAGCTGAGCAAGCTCTCCCGCGAGGCCCCCCC 2292  
Qy 2245 AAGGACAAGAGCTCTTGGCCACCAACGGGACCCCTCTGCCCTGA 2289  
Db 2293 AAGGACAAGAGCTCTTGGCCACCAACGGGACCCCTCTGCCCTGA 2337

RESULT 4  
US-10-003-690-1  
; Sequence 1, Application US/10003690  
; Patent No. 6787345  
; GENERAL INFORMATION:  
; APPLICANT: RORY A.J. CURTIS  
; TITLE OF INVENTION: 55053, A NO. 6787345el Human Eukaryotic Kinase  
; TITLE OF INVENTION: and Uses Therefor  
; FILE REFERENCE: MNI-206  
; CURRENT APPLICATION NUMBER: US/10/003,690  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/248,893  
; PRIOR FILING DATE: 2000-11-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2980  
; TYPE: DNA  
; ORGANISM: Homo.sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (86)...(2419)  
US-10-003-690-1

Query Match 88.3%; Score 2020.2; DB 4; Length 2980;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 265 TTTAGGTACTCTGGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG 324  
Db 398 TATTGTACTCTGGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG 457  
Qy 325 AAGGGGAGCTGACGCGCCAGAGGCCCGAAGTCTTCGCCAGATGTGTGCGCTG 384  
Db 458 AAGGGGAGCTGACGCGCCAGAGGCCCGAAGTCTTCGCCAGATGTGTGCGCTG 517  
Qy 385 GACTTCTGCCACAGCTACTCTCATCTGCGACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 444  
Db 518 GACTTCTGCCACAGCTACTCTCATCTGCGACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 577  
Qy 445 GATGAGAAAAAACAATCCGATTCGACAGCTTCGGCATGGCGTCCCTGCGAGGTGGGGGAC 504  
Db 578 GATGAGAAAAAACAATCCGATTCGACAGCTTCGGCATGGCGTCCCTGCGAGGTGGGGGAC 637  
Qy 505 AGCTCTCGAGACAGCTGCGGTGCCCGCCCATTTATGCGTGTCCAGAGGTGATTAAGGG 564  
Db 638 AGCTCTCGAGACAGCTGCGGTGCCCGCCCATTTATGCGTGTCCAGAGGTGATTAAGGG 697  
Qy 565 GAAAAATATGATGCGCGCGGACAGATGTGAGCTGTGAGTCACTCTTCGCGCTG 624  
Db 698 GAAAAATATGATGCGCGCGGACAGATGTGAGTCACTCTTCGCGCTG 757

Qy 625 CTGCTGGGGGCTCTGCGCTTTGATGACGACAACTCCGCGAGCTGCTGGAGAAAGGTGAAA 684  
Db 758 CTGCTGGGGGCTCTGCGCTTTGATGACGACAACTCCGCGAGCTGCTGGAGAAAGGTGAAA 817  
Qy 685 CGGGCGCTCTTCCACATGCCCCCACTTCACTTCCAGATTGCCAGAGCTCTCTCAGGGGA 744  
Db 818 CGGGCGCTCTTCCACATGCCCCCACTTCACTTCCAGATTGCCAGAGCTCTCTCAGGGGA 877  
Qy 745 ATGATCGAATGAGAGCCGGAAGGCTCAGTCTGAGCAAAATTCAGAAACATCCTTTGG 804  
Db 878 ATGATCGAATGAGAGCCGGAAGGCTCAGTCTGAGCAAAATTCAGAAACATCCTTTGG 937  
Qy 805 TACTTAGCGGGGAAAACAGAGCCGAGCCGCTGCTGAGCCAGCCCTGCGCGCGGGTA 864  
Db 938 TACTTAGCGGGGAAAACAGAGCCGAGCCGCTGCTGAGCCAGCCCTGCGCGCGGGTA 997  
Qy 865 GCATGCGGAGCCCTGCCATCAACGAGAGCTGAGACCCCGACCTCTAGAGAGCATGGCA 924  
Db 998 GCATGCGGAGCCCTGCCATCAACGAGAGCTGAGACCCCGACCTCTAGAGAGCATGGCA 1057  
Qy 925 TCACTGGGCTGCTTCAGGGACCGGAGAGCTGCATCGGAGCTGCGCAGTGTGAGAGGAG 984  
Db 1058 TCACTGGGCTGCTTCAGGGACCGGAGAGCTGCATCGGAGCTGCGCAGTGTGAGAGGAG 1117  
Qy 985 AACCAAGAAAAGATGATATATATCTCTTTTGGATCGGAGAGCGGTATCCAGCTGT 1044  
Db 1118 AACCAAGAAAAGATGATATATATCTCTTTTGGATCGGAGAGCGGTATCCAGCTGT 1177  
Qy 1045 GAGGACCAAGCACTGCTCCCGGAATGATGTTGACCCCGGAAAGCGTGTGATTTCT 1104  
Db 1178 GAGGACCAAGCACTGCTCCCGGAATGATGTTGACCCCGGAAAGCGTGTGATTTCT 1237  
Qy 1105 CCATGCTGAGCGCTCACGGGAAAGCGGCGACGAGCGGAAAGTCCATGGAAGTCTCTGAGC 1164  
Db 1238 CCATGCTGAGCGCTCACGGGAAAGCGGCGACGAGCGGAAAGTCCATGGAAGTCTCTGAGC 1297  
Qy 1165 ATCAACGATGCGGGGGTGTGCTCCCTGTATCCACCGAGCGGGCTTGGAGATGGCC 1224  
Db 1298 ATCAACGATGCGGGGGTGTGCTCCCTGTATCCACCGAGCGGGCTTGGAGATGGCC 1357  
Qy 1225 CAGCAGACGAGAGATCCCTAGGCTCAGTGGAGCTTCCAGGGTCTGCTCTCAGAGCCT 1284  
Db 1358 CAGCAGACGAGAGATCCCTAGGCTCAGTGGAGCTTCCAGGGTCTGCTCTCAGAGCCT 1417  
Qy 1285 CTAAAGAGCCCAAGAGTCTCGGCTTTTCTTTTCAACGGAGCCGGGGCTGGAGATGAG 1344  
Db 1418 CTAAAGAGCCCAAGAGTCTCGGCTTTTCTTTTCAACGGAGCCGGGGCTGGAGATGAG 1477  
Qy 1345 GCTCGAGCGGGGGCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGGCCCGAGG 1404  
Db 1478 GCTCGAGCGGGGGCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGGCCCGAGG 1537  
Qy 1405 GGTGGGGGCGCGGGGAGAGCCCGCCCGCCAGTCCCGCTCCACACCCCTGCCCGGC 1464  
Db 1538 GGTGGGGGCGCGGGGAGAGCCCGCCCGCCAGTCCCGCTCCACACCCCTGCCCGGC 1597  
Qy 1465 CCCCAGGCTCTCCCGCGCTCTCTGGCGGACCCCTTGAACCTCTGTCACACGCGCC 1524  
Db 1598 CCCCAGGCTCTCCCGCGCTCTCTGGCGGACCCCTTGAACCTCTGTCACACGCGCC 1657  
Qy 1525 CGGGCCAGTCCCAACCGGGACCCCGGGGACAAACACCCCGAGCCCGCGGTGGCGTC 1584  
Db 1658 CGGGCCAGTCCCAACCGGGACCCCGGGGACAAACACCCCGAGCCCGCGGTGGCGTC 1717  
Qy 1585 GGGGAGCCCGCTGGAGAGTCTCTCAATCCATCCGCAACAGCTTCTGGGCTCCGCT 1644  
Db 1718 GGGGAGCCCGCTGGAGAGTCTCTCAATCCATCCGCAACAGCTTCTGGGCTCCGCT 1777  
Qy 1645 CGCTTTTCCCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCCAGCTTTCAGCGCA 1704  
Db 1778 CGCTTTTCCCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCCAGCTTTCAGCGCA 1837  
Qy 1705 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTTCGGGAACTTTCATCTCTCTGGACAAA 1764

```
Db 1838 GAGTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTGGGAACCTTCATCTCTTTGGCAAA 1897
Qy 1765 GAAGAAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAAAGCAGCATC 1824
Db 1898 GAAGAAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAAAGCAGCATC 1957
Qy 1825 GTCCATGCCCTTCTGTGATCCCGAGCTCAGCTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1884
Db 1958 GTCCATGCCCTTCTGTGATCCCGAGCTCAGCTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2017
Qy 1885 AGGCCGAGTACAAAGGACAGTGGGGCCCTCTCGTCTTCAAAAGCCCGTCCGTTCCAG 1944
Db 2018 AGGCCGAGTACAAAGGACAGTGGGGCCCTCTCGTCTTCAAAAGCCCGTCCGTTCCAG 2077
Qy 1945 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGCAGCGAGGT 2004
Db 2078 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGCAGCGAGGT 2137
Qy 2005 GTGGGATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGGTTCAAGCGA 2064
Db 2138 GTGGGATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGGTTCAAGCGA 2197
Qy 2065 GTGGTGAGACCATCCAGGACAGCTCTCAGCACTCATGACCAAGCCCTCCGTCAGGCC 2124
Db 2198 GTGGTGAGACCATCCAGGACAGCTCTCAGCACTCATGACCAAGCCCTCCGTCAGGCC 2257
Qy 2125 CTGCGACAGCAAGAACGGGGCCAGACCCGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2184
Db 2258 CTGCGACAGCAAGAACGGGGCCAGACCCGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2317
Qy 2185 CAGCCCCCAGCCGGCCCGCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCGCC 2244
Db 2318 CAGCCCCCAGCCGGCCCGCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCGCC 2377
Qy 2245 AAGGACAAAGATCTCTGGGCAACAAAGGACCCCTCTGCGCTGA 2289
Db 2378 AAGGACAAAGATCTCTGGGCAACAAAGGACCCCTCTGCGCTGA 2422
```

## RESULT 5

```
US-10-003-690-3
; Sequence 3, Application US/10003690
; Patent No. 6787345
; GENERAL INFORMATION:
; APPLICANT: RORY A.J. CURTIS
; TITLE OF INVENTION: 55053, A No. 6787345el Human Eukaryotic Kinase
; FILE REFERENCE: and Uses Therefor
; CURRENT APPLICATION NUMBER: US/10/003,690
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/248,893
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2334
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2334)
US-10-003-690-3
```

```
Query Match 88.1%; Score 2017.2; DB 4; Length 2334;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 265 TTTAGGTACCTGGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 324
Db 313 TATTGTACCTGGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 372
Qy 325 AAGGGAGAGCTGACGCCCAAGAGAGGCCCGAAAGTTCTTCCGCCAGATTGTGTCTGCGCTG 384
```

```
Db 373 AAGGGAGAGCTGACGCCCAAGAGAGGCCCGAAAGTTCTTCCGCCAGATTGTGTCTGCGCTG 432
Qy 385 GACTTCTGCGCACAGCTACTCCATCTGCGCACAGAGACTTAAGCCCGAGAAACCTGCTTTTG 444
Db 433 GACTTCTGCGCACAGCTACTCCATCTGCGCACAGAGACTTAAGCCCGAGAAACCTGCTTTTG 492
Qy 445 GATGAGAAAAAACAATCCGATTCGAGACTTCGGGATGCGCTGCTGCGAGTGGGGGAC 504
Db 493 GATGAGAAAAAACAATCCGATTCGAGACTTCGGGATGCGCTGCTGCGAGTGGGGGAC 552
Qy 505 AGCTTCTGAGAGACAGCTGCGGGTCCCGCCATATGCGTGTCCAGAGGTGATTAAAGGG 564
Db 553 AGCTTCTGAGAGACAGCTGCGGGTCCCGCCATATGCGTGTCCAGAGGTGATTAAAGGG 612
Qy 565 GAAAAATATGATGCGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCCGCCCTG 624
Db 613 GAAAAATATGATGCGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCCGCCCTG 672
Qy 625 CTCGTGGGGCTCTGCCCTTTGATGACGACAACTCCGCCAGCTGTGGAAGAGGTGAAA 684
Db 673 CTCGTGGGGCTCTGCCCTTTGATGACGACAACTCCGCCAGCTGTGGAAGAGGTGAAA 732
Qy 685 CGGGGGCTCTTCCACATGCCCCCATTTCTCCAGATTGCCAGAGCTCTCTGAGGGGA 744
Db 733 CGGGGGCTCTTCCACATGCCCCCATTTCTCCAGATTGCCAGAGCTCTCTGAGGGGA 792
Qy 745 ATGATCGAAGTGTGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATTCCTTGG 804
Db 793 ATGATCGAAGTGTGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATTCCTTGG 852
Qy 805 TACTTAGGGGGGAAACGAGCCAGACCCGCTGCTGAGCCAGCCCTCTGCGCGCGGGTA 864
Db 853 TACTTAGGGGGGAAACGAGCCAGACCCGCTGCTGAGCCAGCCCTCTGCGCGCGGGTA 912
Qy 865 GCATGCGGAGCTTGCATCCAGAGAGCTGGAACCCGACGTCCTTAGAGAGCATGGCA 924
Db 913 GCATGCGGAGCTTGCATCCAGAGAGCTGGAACCCGACGTCCTTAGAGAGCATGGCA 972
Qy 925 TCACTGGGCTGTTTCAAGGACCGCGAGAGCTGCATCGAGCTGCGCAGTGTGAGAGAGAG 984
Db 973 TCACTGGGCTGTTTCAAGGACCGCGAGAGCTGCATCGAGCTGCGCAGTGTGAGAGAGAG 1032
Qy 985 AACCAAGAAAAAGATGATATATTTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044
Db 1033 AACCAAGAAAAAGATGATATATTTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1092
Qy 1045 GAGGACAGGACCTTGCCTCCCGGAATGATTTGACCCCCCGGAGAGCGTGTGATTCT 1104
Db 1093 GAGGACAGGACCTTGCCTCCCGGAATGATTTGACCCCCCGGAGAGCGTGTGATTCT 1152
Qy 1105 CCATGCTGAGCGCTCACGGGAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1164
Db 1153 CCATGCTGAGCGCTCACGGGAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1212
Qy 1165 ATCACCGATCCCGGGGTGGTCTCCCTGTATCCCAACCGAGCGGCTTTGGAGATGCCC 1224
Db 1213 ATCACCGATCCCGGGGTGGTCTCCCTGTATCCCAACCGAGCGGCTTTGGAGATGCCC 1272
Qy 1225 CAGCACAGCAGAGATCCCGTAGGCTCAGTGGAGCTTCCAGGGTCTGTCTCCAGGCCCT 1284
Db 1273 CAGCACAGCAGAGATCCCGTAGGCTTCCAGGGCTTCCAGGGGTCTGTCTCCAGGCCCT 1332
Qy 1285 CTAAAGACCCCAAGGAGTCCGTTCTTTTCTTTTTCACCGGAGCGGGGCTTGGAGATGAG 1344
Db 1333 CTAAAGACCCCAAGGAGTCCGTTCTTTTCTTTTTCACCGGAGCGGGGCTTGGAGATGAG 1392
Qy 1345 GCTCGAGCGGGGCTCTCCCGACTTCCAAAACGAGACGCTGCTTCTCGGGGCCCCCAGG 1404
Db 1393 GCTCGAGCGGGGCTCTCCCGACTTCCAAAACGAGACGCTGCTTCTCGGGGCCCCCAGG 1452
Qy 1405 GGTGGGGGCGCGGGGAGGAGCCCCCGCCCCCGAGTCCCGCTCCACACCCCTGCCCCG 1464
```

```
Db 1453 GGTGGGGCGCGGGGAGCAGCCCCCGCCCCCAGTGCCCGCTCCACACCCCTGCCCGG 1512
Qy 1465 CCCCAGAGCTCCCGCGCTCTCTGGGGGAGACCCCTTGGACTGCGCTTGTGCAACGCGCC 1524
Db 1513 CCCCAGAGCTCCCGCGCTCTCTGGGGGAGACCCCTTGGACTGCGCTTGTGCAACGCGCC 1572
Qy 1525 CGGGCAGTCCACCGGGACCCCGGGGACACACCCACCCCGGAGCGCGGGGCGGTC 1584
Db 1573 CGGGCAGTCCACCGGGACCCCGGGGACACACCCACCCCGGAGCGCGGGGCGGTC 1632
Qy 1585 GGGGAGCGCGCTGGAGAGTCTCTCAATCCCATCGCAACAGCTTCTGGGCTCCCT 1644
Db 1633 GGGGAGCGCGCTGGAGAGTCTCTCAATCCCATCGCAACAGCTTCTGGGCTCCCT 1692
Qy 1645 CGCTTTACCGGGCGAGATCGAGTCTCTCAATCCCATCGCAACAGCTTCTGGGCTCC 1704
Db 1693 CGCTTTACCGGGCGAGATCGAGTCTCTCAATCCCATCGCAACAGCTTCTGGGCTCC 1752
Qy 1705 GAGTCTCTCCCGGAGCTGGCAAGAGCTCTCTGGTTCGGGAATCTCATCTCTGGCAAA 1764
Db 1753 GAGTCTCTCCCGGAGCTGGCAAGAGCTCTCTGGTTCGGGAATCTCATCTCTGGCAAA 1812
Qy 1765 GAAGAAACAATATCTCTGCTCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824
Db 1813 GAAGAAACAATATCTCTGCTCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1872
Qy 1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 1884
Db 1873 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 1932
Qy 1885 AGGCGGAGTACAGGCGAGTGGGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1944
Db 1933 AGGCGGAGTACAGGCGAGTGGGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1992
Qy 1945 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGCGGAGCGGAGGT 2004
Db 1993 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGCGGAGCGGAGGT 2052
Qy 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGTTCAAGCGA 2064
Db 2053 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGTTCAAGCGA 2112
Qy 2065 GTGTGAGACCATCCAGGCAAGTCTGAGCACTCATGACAGCCCTCGTGTGAGGCC 2124
Db 2113 GTGTGAGACCATCCAGGCAAGTCTGAGCACTCATGACAGCCCTCGTGTGAGGCC 2172
Qy 2125 CTGGCAGACGAGAGAAACGGGGCCAGACCCGGGCTCTGTGTGTGTGTGTGTGTGTGTGTGT 2184
Db 2173 CTGGCAGACGAGAGAAACGGGGCCAGACCCGGGCTCTGTGTGTGTGTGTGTGTGTGTGTGT 2232
Qy 2185 CAGCCCCCAGCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGGCGGAGGCCCGCCCC 2244
Db 2233 CAGCCCCCAGCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGGCGGAGGCCCGCCCC 2292
Qy 2245 AAGGACAGAGCTCTGGGCCAACCAAGCGGACCCCTCTGCCC 2286
Db 2293 AAGGACAGAGCTCTGGGCCAACCAAGCGGACCCCTCTGCCC 2334
```

## RESULT 6

```
US-09-774-528-221
; Sequence 221, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
```

```
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774, 528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 221
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1787)
US-09-774-528-221
```

Query Match 42.8%; Score 980; DB 4; Length 1797;  
Best Local Similarity 75.4%; Pred. No. 1.2e-227;  
Matches 1470; Conservative 0; Mismatches 0; Indels 480; Gaps 1;

```
Qy 268 AGGTACCTGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAGAG 327
Db 87 AGGTACCTGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAGAG 146
Qy 328 GGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGSCCAGATTGTCTGCGCTGGAC 387
Db 147 GGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGSCCAGATTGTCTGCGCTGGAC 206
Qy 388 TTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACTCTCTTTTGGAT 447
Db 207 TTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACTCTCTTTTGGAT 266
Qy 448 GAGAAAAACAATCCCGATTGACAGATTGGGATGGGCTCCCTGAGGTGGGGACAGC 507
Db 267 GAGAAAAACAATCCCGATTGACAGATTGGGATGGGCTCCCTGAGGTGGGGACAGC 326
Qy 508 CTCTTGAGAGCAGCTCGGGTCCCGCATTTATCGGTGTCAGAGGTGATTAAAGGGGAA 567
Db 327 CTCTTGAGAGCAGCTCGGGTCCCGCATTTATCGGTGTCAGAGGTGATTAAAGGGGAA 386
Qy 568 AAATATGATGCGCCCGGCGAGACATGTGAGCTGTGAGTCACTCTTCCGCTCTGCTC 627
Db 387 AAATATGATGCGCCCGGCGAGACATGTGAGCTGTGAGTCACTCTTCCGCTCTGCTC 446
Qy 628 GTGGGGCTCTGCGCTTTGATGACGACAACTCCCGCAGCTGTGGAGAGGTGAAACGG 687
Db 447 GTGGGGCTCTGCGCTTTGATGACGACAACTCCCGCAGCTGTGGAGAGGTGAAACGG 506
Qy 688 GCGCTCTTCACATGCCCCACTTCATCTCCATGTCAGATGCGAGCTCTGAGGGGATG 747
Db 507 GCGCTCTTCACATGCCCCACTTCATCTCCATGTCAGATGCGAGCTCTGAGGGGATG 566
Qy 748 ATCGAAGTGGAGCCCGGAAAGAGGCTCAGTCTGAGCAAAATTCAGAAACATCTTGGTAC 807
Db 567 ATCGAAGTGGAGCCCGGAAAGAGGCTCAGTCTGAGCAAAATTCAGAAACATCTTGGTAC 626
Qy 808 CTAGCGGGGAAACAGCAGCCAGACCCGCTGCTGAGCCAGCCCTTGGCCCGGGTAGCC 867
Db 627 CTAGCGGGGAAACAGCAGCCAGACCCGCTGCTGAGCCAGCCCTTGGCCCGGGTAGCC 686
Qy 868 ATGCGGAGCTTCCATCCACGGAGAGTGGACCCCGAGCTCTTAGAGAGCATGCA 927
Db 687 ATGCGGAGCTTCCATCCACGGAGAGTGGACCCCGAGCTCTTAGAGAGCATGCA 746
Qy 928 CTGGGCTGCTTTCAGGGACCGGAGAGCTGATCGCGAGCTGCGCAGTGAGAGAGAAC 987
Db 747 CTGGGCTGCTTTCAGGGACCGGAGAGCTGATCGCGAGCTGCGCAGTGAGAGAGAAC 806
```

QY 988 CAAGAAAGATGATATATATCTGCTTTTGGATCGAAGGAGCGGTATCCAGCTGTGAG 1047  
Db 807 CAAAGAAAGATGATATATATCTGCTTTTGGATCGAAGGAGCGGTATCCAGCTGTGAG 866  
QY 1048 GACCAGGACCTGCTCCCGGAATGATTTGACCCCCCGGAAGCGGTGTGGATTTCTCC 1107  
Db 867 GACCAGGACCTGCTCCCGGAATGATTTGACCCCCCGGAAGCGGTGTGGATTTCTCC 926  
QY 1108 ATGCTGAGCCGTACCGGAAGCGGACCGAGGGAAGTCCATGGAAGTCCCTGAGCATC 1167  
Db 927 ATGCTGAGCCGTACCGGAAGCGGACCGAGGGAAGTCCATGGAAGTCCCTGAGCATC 986  
QY 1168 ACCGATCCCGGGGTGTGCTCCCTGTATACCAACCGAGCGGCTTGGAGATGGCCAG 1227  
Db 987 ACCGATCCCGGGGTGTGCTCCCTGTATACCAACCGAGCGGCTTGGAGATGGCCAG 1046  
QY 1228 CACAGCCAGAGATCCCGTAGCGTGTAGTGGAGCCTCCACAGGCTGTCTCCAGCCCTCTA 1287  
Db 1047 CACAGCCAGAG----- 1057  
QY 1288 AGCAGCCAGAGTCCCGTCTTTTCTTTTACCGGAGCGGGGCTGGAGATGAGGCT 1347  
Db 1058 ----- 1057  
QY 1348 CGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGTCTTCTCGGGGCCCGAGGGT 1407  
Db 1058 ----- 1057  
QY 1408 GGGGCGCCGGGAGAGAGCCCCCGCCAGTGTCCGCTCCACACCCCTGCCCGGCCCC 1467  
Db 1058 ----- 1057  
QY 1468 CCAGGCTCCCGGCTCTCTGGGGGACCCCTTGTGACCTCGCTCTGACAGCCCGG 1527  
Db 1058 ----- 1057  
QY 1528 GCCAGTCCACCGGAGCCCGGGGACAAACCAACCCCGGAGCCCGGGTGGCGTGG 1587  
Db 1058 ----- 1057  
QY 1588 GGAGCGGCTGGAGGAGTGTCTCACTCCATCCGACAGCTTCCTGGGCTCCCTCGC 1647  
Db 1058 ----- 1057  
QY 1648 TTTACCGGCAAGATGAGTCCCTACCGTGTGAGGAGATGTCCAGCTTGTGACCCAGAG 1707  
Db 1058 ----- 1057  
QY 1708 TCCTCCCGGAGCTGGCAAAACGCTCTGTGGTTCCGGAACTTCATCTCTTGGACAAAGAA 1767  
Db 1058 -----GCTGGCAAAACGCTCTGTGGTTCCGGAACTTCATCTCTTGGACAAAGAA 1106  
QY 1768 GAACAAATATCTCTGCTTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTC 1827  
Db 1107 GAACAAATATCTCTGCTTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTC 1166  
QY 1828 CATGCTTTCTGTCATCCAGCTGAGTCAAGTGTGTGTCTCAGCAGCATCAAGCAGCTTCAGG 1887  
Db 1167 CATGCTTTCTGTCATCCCGCTGAGTCAAGTGTGTGTCTCAGCAGCATTCAGG 1226  
QY 1888 GCCGAGTACAGGCGAGTGGGGCCCTCTCGTCTTCCAAAGCCCGTCCGCTTCCAGGTG 1947  
Db 1227 GCCGAGTACAGGCGAGTGGGGCCCTCTCGTCTTCCAAAGCCCGTCCGCTTCCAGGTG 1286  
QY 1948 GACATCAGTCTCTGAGGCTCCAGAGCCCTCCCGGAGCGGAGCGGAGTGGT 2007  
Db 1287 GACATCAGTCTCTGAGGCTCCAGAGCCCTCCCGGAGCGGAGCGGAGTGGT 1346  
QY 2008 GGCATCTACTCGGTCACTCTCATCTCGGCTCCAGCGGCTCGGTTCAGGCGAGTG 2067  
Db 1347 GGCATCTACTCGGTCACTCTCATCTCGGCTCCAGCGGCTCGGTTCAGGCGAGTG 1406  
QY 2068 GTGGAGACCATCCAGGCAAGCTCTGTGAGCACTCATGACCAACCCCTCCGTGCGAGCCCTG 2127

Db 1407 GTGGAGACCATCCAGGCAAGCTCTGTGAGCACTCATGACCACTCCGTGAGGCCCTG 1466  
QY 2128 GCAGAGGAAGAAACGGGGCCAGACCCGGCTGTGTGGTGGCCCAACCCCGAAGCCTGCGAG 2187  
Db 1467 GCAGAGGAAGAAACGGGGCCAGACCCGGCTGTGTGGTGGCCCAACCCCGAAGCCTGCGAG 1526  
QY 2188 CCCCCACCCGGCGCCCGCCAGACCCAGAGCTG 2217  
Db 1527 CCCCCACCCGGCGCCCGCCAGACCCAGAGCTG 1556  
RESULT 7  
US-09-930-181-3  
; Sequence 3, Application US/09930181  
; Patent No. 6455292  
; GENERAL INFORMATION:  
; APPLICANT: Origene Technologies  
; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas  
; FILE REFERENCE: 16U 101 V1  
; CURRENT APPLICATION NUMBER: US/09/930,181  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 3364  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (482)..(2239)  
US-09-930-181-3  
Query Match 34.1%; Score 780.4; DB 3; Length 3364;  
Best Local Similarity 68.0%; Pred. No. 3.6e-179;  
Matches 1279; Conservative 0; Mismatches 406; Indels 195; Gaps 6;  
QY 265 TTTAGGTACTGTCTTCTGGAGCAGCTCTCGGGGGTGTAGCTATTCGACTACCTGTTAAAG 324  
Db 500 TGTAGGTACTGTCTTCTAGAACACGTGTCTAGGTGTGTAGCTCTTCGACTACCTGTTGAAG 559  
QY 325 AAGGGGAGCTGACGCCCAAGGAGGCCGAAAGTTCTTCGCCAGATTTGTCTTGGCGCTG 384  
Db 560 AAGGGGAGCTGACGCCCAAGGAGGCCGAAAGTTCTTCGCCAGATCACTCTTGGCGCTG 619  
QY 385 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACTTAAAGCCCGAGAACTCTGCTTTTG 444  
Db 620 GACTTCTGCCACAGCTACTCCATCTGCCACAGGAGTCTGAAACCTGAAACCTCTCTGCTG 679  
QY 445 GATGAGAAACAAACATCCCGCATTCGAGCTTCGGCATGGCTCCCTGCGAGTGGGGAC 504  
Db 680 GACGAGAAACAAACATCCCGCATTCGAGCTTCGGCATGGCTCCCTGCGAGTGGGGAC 739  
QY 505 AGCTCTCTGAGACCAAGCTCGGGTCCCGCATTTATGCTGTCTCCAGAGGTGATTAAAGGG 564  
Db 740 AGCTCTTGGAGACCAAGCTGTGGTCCCGCATCTAGCCCTGCCCGAGGTGATCCGGGG 799  
QY 565 GAAATAATGATGCCCGCGGACAGATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG 624  
Db 800 GAGAAGTATGACGCCCGGAGCGAGCGTGTGGAGCTGCGGCGTCACTCTGTTCCGCCCTT 859  
QY 625 CTGTTGGGGCTCTGCCCTTTGATGAGCAACCTCCGCGAGCTGCTGGAGAGTGAAG 684  
Db 860 CTGTTGGGGCTCTGCCCTTCGAGATGACAACTTGGACAGCTGTGGAGAGGTGAG 919  
QY 685 CGGGCGCTTCTCCACATGCCCCCACTTCACTTCTCCAGATTGCCAGAGCTCTTCCAGGGGA 744  
Db 920 CGGGCGCTTCTCCACATGCCCCCACTTCACTTCTCCGCGGAGTCTGCTACGGGGC 979  
QY 745 ATGATCGAAGTGGAGCGGCAAAAGGCTGAGTGTGGAGCAATTCAGAAACATCTTGG 804  
Db 980 ATGATCGAAGTGGAGCGGCGCAACCGGCTCTACGCTAGAGCAATTCAGAAACATATGG 1039

```
QY 805 TACCTAGGCGGAAACACGAGCCAGACCCGTCCTGGAGCCAGCCCTCGGCGCGCGGTA 864
Db |||||
QY 1040 TATATAGGGGCAAGATAGAGCCGAACC-----AGAGCAGCCATTCTTCGCAAGGTG 1093
Db |||||
QY 865 GCCATGCGGAGCCTGCCATCCAAACGAGAGCTGGACCCCGACGTCCTAGAGAGCATGGCA 924
Db |||||
QY 1094 CAGATCCGCTCGCTGCCAGCCTGGAGGACATCGACCCCGAGCTGCTGGACAGCATGCAC 1153
Db |||||
QY 925 TCACTGGGCTGCTTCAGGAGACCGGAGAGGTGATCGGAGCTGCGCAGTGAAGGAGAG 984
Db |||||
QY 1154 TCACTGGGCTGCTTCGAGAGCCGCAACAAGCTGTGAGGACCTGCTGTCGAGAGGAG 1213
Db |||||
QY 985 AACCAAGAAAGATGATATATATCTCTTTGATCGGAAGAGCGGTATCCAGCTGT 1044
Db |||||
QY 1214 AACGAGAGAGATGATTTTCTCTCTCTGACCGAAGAAAGTATCCGAGCAG 1273
Db |||||
QY 1045 GAGGACGAGGACCTGCTCCCGGAATGATGTTGACCCCGGAGAGCGGTGTGATTTCT 1104
Db |||||
QY 1274 GAGGATGAGGACCTGCTCCCGGAAACGAGATAGACCTCCCGGAAAGCGTGTGACTCC 1333
Db |||||
QY 1105 CCNATGCTGAGCCTGACGGGAGCGGAGCCGACGAGAGGAGTGCATGGAAGTCTTGAGC 1164
Db |||||
QY 1334 CCGATGCTGAACCGGACGAGCGGCGGACAGACGCAAAATCCATGAGAGTGTCTCAGC 1393
Db |||||
QY 1165 ATCACCAGATGCGGGGTGGTCTCCCTGTCACCCACCGAGCGGCTTGGAGATGSCC 1224
Db |||||
QY 1394 GTGACGAGCGC-----GGTCCCGGTGCTCGCGCGCGGCAATGAGATGGCC 1444
Db |||||
QY 1225 CAGCAGACGAGAGATCCCGTAGCGTCAAGTGAGGCTCCAGCGGTCTGTCTCCAGGCT 1284
Db |||||
QY 1445 CAGCAGCGCCAGAGTCTCGGTTCATCAGCGGTGCTCTCAGGCTTTCACACAGCCCA 1504
Db |||||
QY 1285 CTAGAGACCCCAAGAGTGTGCGTCTTTTCTTTTCAACGGAGCGGGGCTGGAGATGAG 1344
Db |||||
QY 1505 CTCAGCAGCGCCCG----- 1518
Db |||||
QY 1345 GCTCAGGCGGGGCTCCCGACTTCCAAACGAGACGCTGCTCTCGGGGCCCCAGG 1404
Db |||||
QY 1519 ----- 1518
Db |||||
QY 1405 GGTGGGGGCGCGGGGAGCAGCCCGCCCGCCAGTGCCTCCACACACCCCTCCCGGC 1464
Db |||||
QY 1519 -----GGTGACCCCTCACCCCTCACCAGGGGAGTCCCTCCCGC--- 1558
Db |||||
QY 1465 CCCCCAGGCTCCCGGCTCTCTGGGCGGACCCCTTTGCACTCGCTCTGCAACAGGCC 1524
Db |||||
QY 1559 -----ACCCCAAGGGGACACCTGTCCACAGCCCA 1588
Db |||||
QY 1525 CGGCGCAGTCCACCGGGACCCCGGGACACACACCCCGCCAGCCCGGGGCTGGCGTC 1584
Db |||||
QY 1589 AAGGAGAGCCCGGTGGCAAGCCCAACCCCGCCCGGTCCAGCCCC-----AGCGTC 1642
Db |||||
QY 1585 GGGGAGCGGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1644
Db |||||
QY 1643 GGAGGGTGCCTTGAGGGGCGGCTCACTCCATCAAGACAGCTTCTGGGCTCACCC 1702
Db |||||
QY 1645 CGCTTTCAACCGGCAAGATGAGAGTCCCTACCGCTGAGGAGATGTCCAGCTTCAACGCCA 1704
Db |||||
QY 1703 CGCTTCCACCGCGGAAATGCAAGTTCCGAGCGCGGAGAGATGTCCAACCTGCACCA 1762
Db |||||
QY 1705 GAGTCTCCCGGAGCTGGCAAAAGCTCTCGGTTGCGGAATCTCATCTCTTGACAAA 1764
Db |||||
QY 1763 GAGTGTCTCCAGAGCTGGCGAAGTCTCTGGTTTGGGAATCTCATCAGCTGGAGAAG 1822
Db |||||
QY 1765 GAAGAAACAATATCTCTGCTTAAAGAGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824
Db |||||
QY 1823 GAGGAGCAGATCTTCTGCTGATCATCAAGACAAACCTCTGAGCTCATCAGGCTGACATC 1882
Db |||||
QY 1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTGCTGTCAACAGCAGCTTC 1884
Db |||||
QY 1883 GTGACGCTTCTGCTGATTCAGTCTCAGGTCACAGCGTCACTCCCAACAGGCTTC 1942
Db |||||
QY 1885 AGGCGGAGTACAAGGCGAGTGGGCGGCCCTCTCCGTCTTTCAAAAGCGCGTCCGCTTCAG 1944
Db |||||
```

```
Db 1943 CGGGCCGAGTACAAAGGCCACGGGGGGCCAGCCGTGTTCCAGAAGCCGGTCAAGTTCAG 2002
QY 1945 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGACGGCAGCGAGGT 2004
Db |||||
QY 2003 GTTGATATCACTACACGAGGGT-----GGGAGGGCGCAGAAGGAG 2044
Db |||||
QY 2005 GTTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGTCGGTTCAAGCGA 2064
Db |||||
QY 2045 AACGGCATCTACTCCGTCACCTTCACTCTCTCGAGCCCGGAGCCGTCGCTTCAAGAGG 2104
Db |||||
QY 2065 GTGTGAGAGACCATCCAGGACAGCTCTGAGCACTCATACCAAGCCCTCCGTCAGGCCC 2124
Db |||||
QY 2105 GTGTGAGAGACCATCCAGGACAGCTCTGAGCACTCATACCAAGCCCTCCGTCAGGCCC 2164
Db |||||
QY 2125 CTGGCAGACGAGAAGACGG 2144
Db |||||
QY 2165 TTGTCAACACCACTAACTG 2184
Db |||||

RESULT 8
US-09-930-181-1
; Sequence 1, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2908
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)..(2112)
US-09-930-181-1

Query Match 34.0%; Score 778.8; DB 3; Length 2908;
Best Local Similarity 68.0%; Pred. No. 8.3e-179;
Matches 1278; Conservative 0; Mismatches 407; Indels 195; Gaps 6;

QY 265 TTTAGGTACCTGGTTCTGAGACAGCTCTCGGGGGTGAAGTTCGACTACCTGTTAAAG 324
Db |||||
QY 373 TATTTGTACCTGGTGTAGAACACGTCAGGTGAGTCTTCGACTACCTGTTGAAG 432
Db |||||
QY 325 AAGGGAGACTGACGCCCAAGGAGGCGCCGAAAGTTCTTCGCGCAGATTGTCTGCGCTG 384
Db |||||
QY 433 AAGGGAGGCTGACGCCCTAAGGAGGCTCGAAGTTCTTCGCGCAGATCATCTCTGCGCTG 492
Db |||||
QY 385 GACTTCTGCACAGCTACTCCATCTGCCACAGACCTAAAGCCCGAGAACCTGCTTTTG 444
Db |||||
QY 493 GACTTCTGCACAGCCTACTCATATGACAGGATCTGAACCTGAAACCTCTGCTG 552
Db |||||
QY 445 GATGAGAAAAACAACATCCGCAATTCAGACTTCGCGCATGGCGTCCCTGAGGTGGGGAC 504
Db |||||
QY 553 GACGAGAAGAACACATCCGATCGCAGACTTTTGGCATGGGTCCTCGAGTTGGCGAC 612
Db |||||
QY 505 AGCTCTCTGAGACCAAGTGGGTTCCCGCATTTATGCGTGTCCAGAGGTGATTAAGGG 564
Db |||||
QY 613 AGCTGTGTGAGACCAAGTGGGTTCCCGCATTCACGCTGCCCCGAGGTGATCCGGGG 672
Db |||||
QY 565 GAAAAATATGATGGCCCGGCGCAGACATGTGGAGCTGTGGAGTCTCTCTCGCCCTG 624
Db |||||
QY 673 GAGAAGTATGACGCCCGGAGGCGAGCTGTGGAGCTGCGCGCTCATCTCTGTCCTTG 732
Db |||||
QY 625 CTGCTGGGGGCTCTGCCCTTTGATGAGCAACACCTCCGCGCAGCTGCTGGAGAGGTGAAA 684
Db |||||
QY 733 CTGCTGGGGGCTCTGCCCTTCGACGATGACAACTTTCGACAGCTGCTGGAGAGGTGAAG 792
Db |||||
```





Qy		511	CTGGAGACCGAGTGGGGTCCCCCATTTATGGGTGTCCAGAGGTGATTAAAGGGGGAAAA	570
Db		517	CTGGACACTTCTGTGGCAGTCCCCCTTATGTGCGCCAGAACTCTTCAGGGCCAAAAA	576
Qy		571	TATGATGCCCGCGGGCAGACATGTGGAGCTGTGGAGTCATCCTCTTCGCCCTGCTCGTG	630
Db		577	TATGATGACCCGAGTGGATGTGGAGCCTAGGAGTTATCCTCTATACACTGGTCAGC	636
Qy		631	GGGGCTGTGCCCTTTGATGACGACAACTCCGCCAGCTGCTGGAGAAAGGTGAAACGGGGC	690
Db		637	GGATCCCTGCCTTTGATGGACAGAACCTCAAGGAGCTCGGGAACGGGTACTGAGGGA	696
Qy		691	GTCCTTCCACATGCCCACTTCAATTCCTCAGANTGCCAGAGCCTCTGAGGGGAATGATC	750
Db		697	AAATACCGTATTCCATTTCTACATGTCCAGGACTGTGAAAACCTGTTAAGAAAATTTCTC	756
Qy		751	GAAGTGGAGCCGAAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAACATCCTTGGTACCTA	810
Db		757	ATTCTTAATCCAGCAAGAGAGGCACTTTAGAGCAAAATCATGAAGATCGATGGATGAAT	816
Qy		811	G-----GCGGAAACACGACCGACACCGTGCCTGGAGCCAGCCCTTGGCGCGCGGTA	864
Db		817	GTGGGTCAAGAAGATGTAACATAAAGCCTTAGTGGAGCCACTCCCTGACTACAAAGGAC	876
Qy		865	GCCATGCGGA	874
Db		877	CCCCGGCGGA	886

RESULT 10

```

RES001 10
US-09-949-016-2385
; Sequence 2385, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2385
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2385

```

Query Match	8.7%	Score 198.2;	DB 4;	Length 2224;
Best Local Similarity	59.2%	Pred. No. 2.3e-38;		
Matches 361;	Conservative	0;	Mismatches 243;	Indels 66;
				Gaps 1;

Qy	271	TACCTGTTCTGGAGCACGCTCTCGGGGGGTGAGCTATTGCGACTACTGTTAAAGAGGGG	330
Db	277	TACCTTGTGTCATGGAGTACGCTAGTGGCGAGAGGTATTGATTACTAGTGGCTCATGGC	336
Qy	331	AGACTGACGCCCCAGGAGGCGCGAAGTCTTCCGCCAGATTGTGTCTGGCTGGACCTTC	390
Db	337	AGGATGAAGAAAAAGAGGGCTCGAGCCAAATTCGCCAGATAGTGTCTCTGTGCAGTAC	396
Qy	391	TGCCACAGCTACTCCATCTGCCACAGACACCTTAAAGCCGAGAACTGCTTTTGGATGAG	450
Db	397	TGTCAACAGAGTTATTGTGTCATAGAGACTTAAAGGACGAAAACTGCTCTTGGATGCT	456
Qy	451	AAAAACAAATCCCGCATTTGCAGACTTCGGCATTTGGCGTCCCTGCAGGTGGGGACACGCTTC	510
Db	457	GATATGAACATCAAGATTGCAGACTTTGGCTTCAGCAATGAATTACCTTTGGGACACAG	516

Qy	511	CTGAGACACAGCTGGGTCCCCCATTTATCGGTGTCAGAGGTGATTAAAGGGGAAAAA	570
Db	517	CTGAGACACTTCTGTGGCAGTCCCTTATGCTGCCCAGAACTCTTCAGGGCAAAAAA	576
Qy	571	TATCATGCCGCCGGCGAGACATGTGGAGCTGTGGAGTCATCTTCCTTCGCCCTGCTCGTG	630
Db	577	TATGATGACCCGAGGTGGATGTGTGGAGCCTTAGAGTTATCTCTATACACTGGTCAGC	636
Qy	631	GGGGCTCTGCCCTTTTGATGACGACAACTCCGCCAGCTGCTGGAGAAAGGTGAAACGGGCG	690
Db	637	GGATCCCTGCCTTTTGATGGACAGAACTCAAGGAGCTGCCGGAACGGGTACTGAGGGGA	696
Qy	691	GTCCTTCCACATGCCCCACTTCATTTCTCCAGATTGCCAGAGCTCTCCTGAGGGGAATGATC	750
Db	697	AAATACCGTATTTCCTATTCTACATGTCCACGGACTGTGAAAACCTGCTTTAAGAAATTTCTC	756
Qy	751	GAACTGGAGCCCGAAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCCTTGGTACCTA	810
Db	757	ATTCTTAATCCACGACAGAGAGGCATTTAGAGCAAAATCATGAAGATGCGATGGATGAAT	816
Qy	811	G-----GCGGGAAACACGAGCCAGACCCGTGCCTGGAGGCCAGGCCCTCGGCCCGGGGTA	864
Db	817	GTGGGTCAAGNAGATGATGAACCTAAAGCCTTACGTGGAGGCCACTCCCTGACTACAAGGAC	876
Qy	865	GCCATGCGGA	874
Db	877	CCCCGGCGGA	886

## RESULT 11

```

RESULT 11
US-09-949-016-1546
; Sequence 1546, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1546
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1546

```

Query Match	8.7%	Score 199.2;	DB 4;	Length 2950;
Best Local Similarity	59.2%	Pred. No. 2.6e-38;		
Matches 361; Conservative		0; Mismatches 243;	Indels 6;	Gaps 1;

Qy	271	TACCTGGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAGAAAGGGG	330
Db	684	TACCTTGTTCATGGAGTAGCGCTAGTGGCGGAGAGGTATTGTGATTACCTAGTGGCTCATGGC	743
Qy	331	AGACTGACGCCCAAGGAGGGCCGAAAGTCTTCCGCCAGATTGTCTGCGCTGGACTTTC	390
Db	744	AGGATGAAGAAGAAAGAGGCTCGAGCCAAAATCCGCCAGATAGTGTCTGCTGTGCAGTAC	803
Qy	391	TGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTGGATGAG	450
Db	804	TGTCAACAGAAAGTTATTGTTCATAGAGACTTAAAGGCAGAAAACCTGCTCTTGGATGCT	863
Qy	451	AAAAACAACATCCGCATTTCAGACTTCGGGCATGGCGTCCCTGCAGGTGGGGGACAGCCCTC	510

Db 864 GATATGAACATCAAGATTGCAGACTTTGGCTTCAGCAATGAATTCACCTTTGGGAACAAG 923  
QY 511 CTGGAGACCACTGCGGGTCCCCCAATTATGCTGTCCAGAGGTGATTAAGGGGGAAGAAA 570  
Db 924 CTGGACACCTTCTGTGGCAGTCCCTTATGCTGCCCCAGAACTCTTCAGGGGCAAGAAA 983  
QY 571 TATGATGGCCCGCGGACAGATGTGGAGCTGTGGAGTCAATCTCTTGGCCCTGCTCGTG 630  
Db 984 TATGATGGACCCGAGGTGGATGTGGAGCTTAGGAGTTATCTCTATACACTGGTCAGC 1043  
QY 631 GGGGCTCTGCCCTTTGATGACGACAACTCCGCGAGCTGTGGAGAGGTGAAGCGGGG 690  
Db 1044 GGATCCCTGCTTTGATGACGACAACTCAAGAGCTGGGGAAACGGGTACTGAGGGGA 1103  
QY 691 GTCTTCCACATGCCCACTTCATTCCTCCAGATGCCAGAGCTCTGAGGGGAATGATC 750  
Db 1104 AATACCGGTATTCATTCCTAGATGTCCAGGACTGTGAAACCTGCTTAAGAAATTTCTC 1163  
QY 751 GAAGTGGAGCCGGAAGAGCTCAGTCTGAGCAAAATTCAGAAACATCTCTGTACCTA 810  
Db 1164 ATTCTTAATCCAGCAAGAGGACCTTTAGAGCAAAATCATGAAGATCGATGATGAAT 1223  
QY 811 G-----GCGGGAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGCGGGTA 864  
Db 1224 GTGGGTCAAGAGATGATGAATTAAGCCTTACGTGGAGCCACTCCCTGACTACAGGAC 1283  
QY 865 GCCATGCGGA 874  
Db 1284 CCGCGGGGA 1293

RESULT 12  
US-09-949-016-1547  
; Sequence 1547, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1547  
; LENGTH: 2950  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1547

Query Match 8.7%; Score 199.2; DB 4; Length 2950;  
Best Local Similarity 59.2%; Pred. No. 2.6e-38;  
Matches 361; Conservative 0; Mismatches 243; Indels 6; Gaps 1;  
QY 271 TACCTGGTTCTGGAGACACTCTCGGGGGGTGAGCTATTTCGACTACTCTGGTAAAGAGGG 330  
Db 684 TACCTGTCTAGGAGTACCTAGTGGCGGAGAGGTATTGTATTACCTAGTGGCTCATGGC 743  
QY 331 AGACTGACGCCCAAGAGAGCCGAAAGTTCTTCGCGAGATGTGTCTGCGCTGGACTTC 390  
Db 744 AGATGAAGAAAGAAAGAGGCTCGAGCAAAATTCGCGCAGATGATGTCTGTGTCAGTAC 803  
QY 391 TGCCACAGCTACTTCCATCTGCCACAGACCTTAAGCCCGAGAACTTGCTTTTGGATGAG 450  
Db 804 TGTCACCAAGAGTTTATTGTGCCATAGAGACTTAAGGACAGAAACCTCTCTTTGATGCT 863  
QY 451 AAAAAACAATCCGCAATTCAGACTTCGGCATGGCGTCCCTGCAGGTGGGGGACAGCCTC 510

Db 864 GATATGAACATCAAGATTGCAGACTTTGGCTTCAGCAATGAATTCACCTTTGGGAACAAG 923  
QY 511 CTGGAGACCACTGCGGGTCCCCCAATTATGCTGTCCAGAGGTGATTAAGGGGGAAGAAA 570  
Db 924 CTGGACACCTTCTGTGGCAGTCCCTTATGCTGCCCCAGAACTCTTCAGGGGCAAGAAA 983  
QY 571 TATGATGGCCCGCGGACAGATGTGGAGCTGTGGAGTCAATCTCTTGGCCCTGCTCGTG 630  
Db 984 TATGATGGACCCGAGGTGGATGTGGAGCTTAGGAGTTATCTCTATACACTGGTCAGC 1043  
QY 631 GGGGCTCTGCCCTTTGATGACGACAACTCCGCGAGCTGTGGAGAGGTGAAGCGGGG 690  
Db 1044 GGATCCCTGCTTTGATGACGACAACTCAAGAGCTGGGGAAACGGGTACTGAGGGGA 1103  
QY 691 GTCTTCCACATGCCCACTTCATTCCTCCAGATGCCAGAGCTCTGAGGGGAATGATC 750  
Db 1104 AATACCGGTATTCATTCCTAGATGTCCAGGACTGTGAAACCTGCTTAAGAAATTTCTC 1163  
QY 751 GAAGTGGAGCCGGAAGAGCTCAGTCTGAGCAAAATTCAGAAACATCTCTGTACCTA 810  
Db 1164 ATTCTTAATCCAGCAAGAGGACCTTTAGAGCAAAATCATGAAGATCGATGATGAAT 1223  
QY 811 G-----GCGGGAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGCGGGTA 864  
Db 1224 GTGGGTCAAGAGATGATGAATTAAGCCTTACGTGGAGCCACTCCCTGACTACAGGAC 1283  
QY 865 GCCATGCGGA 874  
Db 1284 CCGCGGGGA 1293

RESULT 13  
US-09-984-890-1  
; Sequence 1, Application US/09984890  
; Patent No. 6492156  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; THEREOF  
; FILE REFERENCE: CL001306  
; CURRENT APPLICATION NUMBER: US/09/984,890  
; CURRENT FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2175  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-984-890-1

Query Match 8.6%; Score 197.6; DB 4; Length 2175;  
Best Local Similarity 59.0%; Pred. No. 5.7e-38;  
Matches 360; Conservative 0; Mismatches 244; Indels 6; Gaps 1;  
QY 271 TACCTGGTTCTGGAGACACTCTCGGGGGGTGAGCTATTTCGACTACTCTGGTAAAGAGGG 330  
Db 376 TACCTTGTCTATGGAGTACGCTAGTGGCGGAGAGGTATTGATTACCTAGTGGCTCATGGC 435  
QY 331 AGACTGACGCCCAAGAGAGCCGAAAGTTCTTCGCGCAGATTTGTCTGCGCTGGACTTC 390  
Db 436 AGGATGAAGAAAGAAAGAGGCTCGAGCCAAATTCGCGCAGGTAGTGTCTGCTGTGCAGTAC 495  
QY 391 TGCCACAGCTACTCTCCATCTGCCACAGACCTTAAGCCCGAGAACCTCTTTTGGATGAG 450  
Db 496 TGTCAACAGAAAGTTTATTGTCTCATAGAGACTTAAGGCGAGAAACCTCTCTTTGATGCT 555  
QY 451 AAAAAACAATCCGCAATTCAGACTTCGGCATGGCGTCCCTGCAGGTGGGGGACAGCCTC 510  
Db 556 GATATGAACATCAAGATTGAGACTTTGGCTTTCAGCAATGAATTCACCTTTTGGGAACAAG 615  
QY 511 CTGGAGACCACTGCGGGTCCCGCCCATATTCGCTGTCCAGAGGTGATTAAAGGGGGAAGAAA 570

Db 616 CTGACACCTTCYGTGGCAGTCCCTTATGCTCCCGAGACTCTCCAGGGCAAAAA 675  
Qy 571 TATGATGCCCGCCGGGAGACATGAGAGCTGTGGAGTCAATCTCTTCGCGCTCTCGTG 630  
Db 676 TATGATGGACCCGAGGTGGATGTGTGGAGCTAGGAGTTATCTCTATACACTGGTCAGC 735  
Qy 631 GGGGCTCTGCGCTTTGATGACGACAACTCCGCGAGCTGTGGAGAGAGGTGAACGGGGC 690  
Db 736 GGATCCCTGCGCTTTGATGAGCAGAACCTCAAGAGAGCTGGGGAAACGGGTACTGAGGGGA 795  
Qy 691 GTCTTCCACATGCCCGCCCACTTCATCTCCAGATTGCCAGAGCCTCTGAGGGGAATGATC 750  
Db 796 AATACCGTATTCATTTCTACATGTCCAGGACTGTGAACCTGCTTTAGAAATTTCTC 855  
Qy 751 GAAGTGGAGCCGAAAAAGGCTCAGTCTGTGGAGCAAAATTCAGAAACATCTTGGTACCTA 810  
Db 856 ATTCTTAATCCAGCAAGAGAGGACATTTAGAGCAAAATCATGAAGATCGATGATGAAT 915  
Qy 811 G-----GCGGGAACAGAGCCAGACCGGTGCTGTGGAGCCAGCCCTTGGCGCGGGTA 864  
Db 916 GTGGGTCAACGAATGATGAATAAGCCTTACGTGGAGCCACTCCCTGACTACAAGGAC 975  
Qy 865 GCCATGCCGA 874  
Db 976 CCCCGCGGA 985

## RESULT 14

US-10-274-194-1  
; Sequence 1, Application US/10274194  
; Patent No. 6706511  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; FILE REFERENCE: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001306DIV  
; CURRENT APPLICATION NUMBER: US/10/274,194  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2175  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-274-194-1

Query Match 8.6%; Score 197.6; DB 4; Length 2175;  
Best Local Similarity 59.0%; Pred. No. 5.7e-38;  
Matches 360; Conservative 0; Mismatches 244; Indels 6; Gaps 1;  
Qy 271 TACCTGTCTCGGAGCAGCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAGAGGGG 330  
Db 376 TACCTGTCTGAGTACGTAGTGGCGGAGAGTATTGATACCTAGTGGCTCATGGC 435  
Qy 331 AGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCGAGATTTGTCTGCGCTGGACTTC 390  
Db 436 AGGATGAAGAAAGAGGCTCGAGCCAAATTCGCCAGGTAGTGTCTGTGTGCAGTAC 495  
Qy 391 TGCACAGCTACTCCATCTGCGACAGACCTAAAGCCCGAGAACCTGCTTTGGATGAG 450  
Db 496 TGTCAACAGAGTTTATTTGTCATAGAGACTTAAAGGAGAAACCTGCTCTTGGATGCT 555  
Qy 451 AAAAACAACATCCGATTCGAGACTTCGGCATGCGCTCCCTGCGAGTGGGGGACAGCTC 510  
Db 556 GATATGAACATCAAGATTGCACTTTGGCTTTCAGCAATGAATTCACCTTTGGAAACAAG 615  
Qy 511 CTGGAGACCAAGCTCGGGTCCCGCCATTATGCGTGTCCAGAGGTGATTAAAGGGGAAAAA 570  
Db 616 CTGGACACCTTCTGTGGCAGTCCCTTATGCTGCCCGCAGAACTCTTCAGGGGCAAAAA 675  
Qy 571 TATGATGGCCCGGGCAGACATGTGGAGCTGTGGAGTCAATCTCTTTCGCGCTCTCGTG 630

Db 676 TATGATGGACCCGAGGTGGATGTGTGGAGCTAGGAGTTATCTCTATACACTGGTCAGC 735  
Qy 631 GGGGCTCTGCGCTTTGATGACGACAACTCCGCGAGCTGTGGAGAGAGGTGAACGGGGC 690  
Db 736 GGATCCCTGCGCTTTGATGAGCAGAACCTCAAGAGAGCTGGGGAAACGGGTACTGAGGGGA 795  
Qy 691 GTCTTCCACATGCCCGCCCACTTCATCTCCAGATTGCCAGAGCCTCTGAGGGGAATGATC 750  
Db 796 AATACCGTATTCATTTCTACATGTCCAGGACTGTGAACCTGCTTTAGAAATTTCTC 855  
Qy 751 GAAGTGGAGCCGAAAAAGGCTCAGTCTGTGGAGCAAAATTCAGAAACATCTTGGTACCTA 810  
Db 856 ATTCTTAATCCAGCAAGAGAGGACATTTAGAGCAAAATCATGAAGATCGATGATGAAT 915  
Qy 811 G-----GCGGGAACAGAGCCAGACCGGTGCTGTGGAGCCAGCCCTTGGCGCGGGTA 864  
Db 916 GTGGGTCAACGAATGATGAATAAGCCTTACGTGGAGCCACTCCCTGACTACAAGGAC 975  
Qy 865 GCCATGCCGA 874  
Db 976 CCCCGCGGA 985

## RESULT 15

US-08-557-006C-38  
; Sequence 38, Application US/08557006C  
; Patent No. 6258547  
; GENERAL INFORMATION:  
; APPLICANT: Beri, Rajinder K.  
; APPLICANT: Forde, Robert A.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE  
; FILE REFERENCE: NGAP/PHM37588/UST  
; CURRENT APPLICATION NUMBER: US/08/557,006C  
; CURRENT FILING DATE: 1996-03-06  
; PRIOR APPLICATION NUMBER: PCT/GB94/01093  
; PRIOR FILING DATE: 1994-05-20  
; PRIOR APPLICATION NUMBER: GB 9310489.1  
; PRIOR FILING DATE: 1993-05-21  
; PRIOR APPLICATION NUMBER: GB 9318010.7  
; PRIOR FILING DATE: 1993-08-31  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 1742  
; TYPE: DNA  
; ORGANISM: Human AMP protein kinase  
US-08-557-006C-38

Query Match 7.1%; Score 163; DB 3; Length 1742;  
Best Local Similarity 56.7%; Pred. No. 1.3e-29;  
Matches 301; Conservative 0; Mismatches 230; Indels 0; Gaps 0;  
Qy 275 TGGTTCTGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAGAGGGGAGAC 334  
Db 272 TGGTAATGGAATATGTCTCTGGAGGTGAATTTGTCGACTACATCTGTAAACACAGGGAGGG 331  
Qy 335 TGACGCCCAAGGAGGCCGAAAGTTCTTCGCCAGATTGTCTGCGCTGGACTTCTGCC 394  
Db 332 TTGAAGAGGTGGAGCTCGCGGCTCTTCAGCAGATTTCTGTCTGCCGTGGACTACTGTC 391  
Qy 395 ACAGCTACTCCATCTGCGCACAGAGACCTAAAGCCCGAGAACCTCTTTTGGATGAGAAAA 454  
Db 392 ACAGGCACATGGTTGTCCACAGGGACCTGAAGCCAGAGAACGTTGCTGGACGCCGAGA 451  
Qy 455 ACAACATCCGATTCGAGACTTCGGCATGGCGTCCCTTGCAGAGTGGGGGAGACAGCTCTCG 514  
Db 452 TGAATGCTAAGATAGCTGACTTCGGACTCTCTAATATGATGTCAAGTGGTGAATTTCTAC 511  
Qy 515 AGACCACTCGGGTCCCGCCATTATGCGTGTCCAGAGGTGATTAAGGGGGAAAAAATG 574  
Db 512 GAACCTAGCTGTGATGCCCAAAATTAAGCAGACCGGAGGTCAATCTCAGGAAGGCTGTATG 571

Tue Feb 22 14:35:29 2005

Qy	575	ATGCGCCGCGGCGAGCATGTGAGCTGTGAGTCACTCTTCGCCCTGCTCGTGGGG	634
Db	572	CGGTCCTGAGGTTGATATCTGGAGCTGTGGTGTATCTCTGTATGCCCTTCTCTGTGGCA	631
Qy	635	CTCTGCCCTTTGATGACGACAACCTCCGCCAGCTGTGGAGAGGTGAACGGGGCGTCT	694
Db	632	CCCTCCCGTTGCGAGATGAGACGTGCTTACGCTCTTTAAGAAGATCCGAGGGGTGTGT	691
Qy	695	TCCACATGCCCCACTTCATTCTCTCCAGATTGCCAGAGCCTCTCTGAGGGGAATGATCGAAG	754
Db	692	TCTACATCCCGGAGTATCTCAACGGTTCTATTGCCACTCTGTCTGATGCACATGCTGCAGG	751
Qy	755	TGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCCTTGGT	805
Db	752	TGGACCCCTTGAGCGGAGCAACTATCAAGACATACGAGAGCATGAATGGT	802

Search completed: February 19, 2005, 14:27:39  
Job time : 415 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: February 17, 2005, 10:29:15 ; Search time 176 Seconds  
(without alignments)  
1674.497 Million cell updates/sec  
US-10-803-277-4  
Perfect score: 4056  
Sequence: 1 MGLEFGFLEAGNWSHPLPG.....PRRGPPKDKLLATNGTPLP 762  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_16Dec04:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4056	100.0	762	6	ABB98744 Human kin
2	3545	87.4	703	6	ABB98745 Human kin
3	3545	87.4	715	7	ADQ89184 Human kin
4	3545	87.4	715	7	ADQ89184 Human kin
5	3545	87.4	715	7	ADQ89184 Human kin
6	3545	87.4	715	7	ADQ89184 Human kin
7	3545	87.4	715	7	ADQ89184 Human kin
8	3545	87.4	715	7	ADQ89184 Human kin
9	3545	87.4	715	7	ADQ89184 Human kin
10	3545	87.4	715	7	ADQ89184 Human kin
11	3545	87.4	715	7	ADQ89184 Human kin
12	3545	87.4	715	7	ADQ89184 Human kin
13	3545	87.4	715	7	ADQ89184 Human kin
14	3545	87.4	715	7	ADQ89184 Human kin
15	3545	87.4	715	7	ADQ89184 Human kin
16	3545	87.4	715	7	ADQ89184 Human kin
17	3545	87.4	715	7	ADQ89184 Human kin
18	3545	87.4	715	7	ADQ89184 Human kin
19	3545	87.4	715	7	ADQ89184 Human kin
20	3545	87.4	715	7	ADQ89184 Human kin
21	3545	87.4	715	7	ADQ89184 Human kin
22	3545	87.4	715	7	ADQ89184 Human kin
23	3545	87.4	715	7	ADQ89184 Human kin
24	3545	87.4	715	7	ADQ89184 Human kin
25	3545	87.4	715	7	ADQ89184 Human kin

26	2386.5	58.8	668	8	ADH59076	Adh59076 Human KSE
27	2381.5	58.7	603	8	ADH59091	Adh59091 Human KSE
28	2381.5	58.7	674	5	AAM47830	Aam47830 Human pro
29	2381.5	58.7	674	6	ABR44014	AbR44014 Human ser
30	2366.5	58.3	636	6	AAO29859	Aao29859 Human kin
31	1590	39.2	851	4	ABB62061	Abb62061 Drosophil
32	1043	25.7	204	4	ABB11680	Abb11680 Human Ser
33	979	24.1	301	4	ABB11052	Abb11052 Human HRP
34	677	16.7	1518	6	ABR53219	ABr53219 Protein s
35	677	16.7	1518	7	ADK63724	Adk63724 Disease t
36	677	16.7	1518	8	ADI26784	Adi26784 Saccharom
37	677	16.7	1518	8	ADS43813	AdS43813 Bacterial
38	657	16.2	1462	8	ADI26788	Adi26788 Candida a
39	651	16.1	1349	4	AAG70854	Aag70854 C albican
40	648	16.0	1251	4	AAB65626	Aab65626 Novel pro
41	648	16.0	1309	7	ADG74678	Adg74678 Human kin
42	648	16.0	1311	8	ADI29232	Adi29232 Human MAR
43	648	16.0	1349	8	ADI26789	Adi26789 Candida a
44	648	16.0	1369	5	AAE21712	Aae21712 Human PKI
45	643.5	15.9	783	4	AAG65764	Aag65764 Human pro

ALIGNMENTS

RESULT 1  
ABB98744  
ID ABB98744 standard; protein; 762 AA.  
XX ABB98744;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human kinase #2.  
XX  
KW Human; kinase; chromosome 19.  
XX  
OS Homo sapiens.  
XX  
PN WO200281670-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 04-APR-2002; 2002WO-US010786.  
XX  
PR 06-APR-2001; 2001US-0282036P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Turner CA, Mathur B, Friddle CJ;  
XX  
DR WPI; 2003-058538/05.  
XX  
DR N-PSDB; ABV74558.  
XX  
PT New human kinase proteins useful for diagnosis, drug screening, clinical  
trial monitoring, treatment of disorders and diseases, and cosmetic and  
nutritional applications.  
XX  
PS Claim 5; Page 42-43; 47pp; English.  
XX  
CC The present sequence is a novel human kinase. The genomic locus encoding  
the kinase is thought to be on human chromosome 19. The kinase and its  
coding sequence are useful for diagnosis, drug screening, clinical trial  
monitoring, treatment of disorders and diseases, and cosmetic and  
nutritional applications  
XX  
SQ Sequence 762 AA;

Query Match 100.0%; Score 4056; DB 6; Length 762;  
Best Local Similarity 100.0%; Pred. No. 4.9e-270;  
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGLEFGFLEAGNWSHPLPGSDGNWNLFLPGINGNWSLFLPGTHGNWSLFLPRIMGIVL 60

Db 1 MGLEFGLAGGNWHLFGSDGNWNLFLPGINGNWSLFLPGTHGNSLFLPRIMGIVL 60  
Qy 61 CHOPEVEGDEALWSCTCPQPSAPSISPRYLVLHVSGGELFDYLVKKGRITPKEARX 120  
Db 61 CHOPEVEGDEALWSCTCPQPSAPSISPRYLVLHVSGGELFDYLVKKGRITPKEARX 120  
Qy 121 FROIVSALDFCHSYISICHRDLKPENLLDEKNNIRIADFGMASLQVGDLSLETSCGSPHY 180  
Db 121 FROIVSALDFCHSYISICHRDLKPENLLDEKNNIRIADFGMASLQVGDLSLETSCGSPHY 180  
Qy 181 ACEPIVKGKYGRRADWMSGVLFPALLVGVLPDDNLRQLLEKVKRGVFMHPIPP 240  
Db 181 ACEPIVKGKYGRRADWMSGVLFPALLVGVLPDDNLRQLLEKVKRGVFMHPIPP 240  
Qy 241 DCQSLRGMIEVEPEKRLSLEQIQKHPWYLGKGHEPDCLEPAPGRVAMRSIPLSNGELD 300  
Db 241 DCQSLRGMIEVEPEKRLSLEQIQKHPWYLGKGHEPDCLEPAPGRVAMRSIPLSNGELD 300  
Qy 301 PDVLESASLGCFRDRERLHRELSEENQEKMIYLLDRKERYPSCEDQDLPFRNDVD 360  
Db 301 PDVLESASLGCFRDRERLHRELSEENQEKMIYLLDRKERYPSCEDQDLPFRNDVD 360  
Qy 361 PPRKRVDSPLMRSHGKRPRPKSMVLSITDAGGGSPVPTRRALEMAQHSQRSVSVA 420  
Db 361 PPRKRVDSPLMRSHGKRPRPKSMVLSITDAGGGSPVPTRRALEMAQHSQRSVSVA 420  
Qy 421 STGLSSPLSPSPSPVFSFPEPCAGDEARGGSPSTOTLPSRGRGGGAGEQPPPPS 480  
Db 421 STGLSSPLSPSPSPVFSFPEPCAGDEARGGSPSTOTLPSRGRGGGAGEQPPPPS 480  
Qy 481 ARSTPLPGPCSPRSSGTPHLSPLHTPRASPTGTPCTTTPPPSPGGVGGAAWRSRLNSI 540  
Db 481 ARSTPLPGPCSPRSSGTPHLSPLHTPRASPTGTPCTTTPPPSPGGVGGAAWRSRLNSI 540  
Qy 541 RNSFLGSPFRHRRKQVPTAEEMSLTPESPPELAKRSWFCNFTISLDKEQIFLVLDKXP 600  
Db 541 RNSFLGSPFRHRRKQVPTAEEMSLTPESPPELAKRSWFCNFTISLDKEQIFLVLDKXP 600  
Qy 601 LSSIKADIVHAFLSIPLSHSVLSQTSFRAEYKASGSPVFKVRFQVDISSSEGEPS 660  
Db 601 LSSIKADIVHAFLSIPLSHSVLSQTSFRAEYKASGSPVFKVRFQVDISSSEGEPS 660  
Qy 661 PRDGGSGGGIYSVTFTLISGFSRRFRXVVTETIOALLSTHDQPSVQALADEKNGAATRP 720  
Db 661 PRDGGSGGGIYSVTFTLISGFSRRFRXVVTETIOALLSTHDQPSVQALADEKNGAATRP 720  
Qy 721 AGAPPRSLQPPGPPDPBELSSPRGPPKDKLLATNGTPLP 762  
Db 721 AGAPPRSLQPPGPPDPBELSSPRGPPKDKLLATNGTPLP 762

RESULT 2

ABB98745

ID ABB98745 standard; protein; 703 AA.

XX AC ABB98745;

XX DT 20-JAN-2003 (first entry)

XX DE Human kinase #3.

XX KW Human; kinase; chromosome 19.

XX OS Homo sapiens.

XX PN WO200281670-A1.

XX PD 17-OCT-2002.

XX PF 04-APR-2002; 2002WO-US010786.

XX PR 06-APR-2001; 2001US-0282036P.

XX (LEXI-) LEXICON GENETICS INC.  
XX Turner CA, Mathur B, Friddle CJ;  
XX WPI; 2003-058538/05.  
XX N-PSDB; ABV74559.  
XX New human kinase proteins useful for diagnosis, drug screening, clinical  
XX trial monitoring, treatment of disorders and diseases, and cosmetic and  
XX nutritional applications.  
XX Claim 5; Page 44-46; 47pp; English.  
XX The present sequence is a novel human kinase. The genomic locus encoding  
XX the kinase is thought to be on human chromosome 19. The kinase and its  
XX coding sequence are useful for diagnosis, drug screening, clinical trial  
XX monitoring, treatment of disorders and diseases, and cosmetic and  
XX nutritional applications  
XX Sequence 703 AA;

Query Match 87.4%; Score 3545; DB 6; Length 703;

Best Local Similarity 99.7%; Pred. No. 6.1e-235;

Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 89 FRYLVLEHVSGGELFDYLVKKGRITPKEARXFRQIVSALDFCHSYISICHRDLKPENILL 148

Db 30 YLYLVLEHVSGGELFDYLVKKGRITPKEARXFRQIVSALDFCHSYISICHRDLKPENILL 89

Qy 149 DEKNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIGKGYDGRADWMSGVLFPAL 208

Db 90 DEKNNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIGKGYDGRADWMSGVLFPAL 149

Qy 209 LVGALPFDDNLRQLLEKVKRGVFMHPIPPDCQSLRGMIEVEPEKRLSLEQIQKHPW 268

Db 150 LVGALPFDDNLRQLLEKVKRGVFMHPIPPDCQSLRGMIEVEPEKRLSLEQIQKHPW 209

Qy 269 YLGKGHEPDCLEPAPGRVAMRSIPLSNGELDPDVLESASLGCFRDRERLHRELSEEE 328

Db 210 YLGKGHEPDCLEPAPGRVAMRSIPLSNGELDPDVLESASLGCFRDRERLHRELSEEE 269

Qy 329 NQSKMIYLLDRKERYPSCEDQDLPFRNDVDPKRKRVDSPLMRSHGKRPRPKSMVLS 388

Db 270 NQSKMIYLLDRKERYPSCEDQDLPFRNDVDPKRKRVDSPLMRSHGKRPRPKSMVLS 329

Qy 389 ITDAGGGSPVPTRRALEMAQHSQRSVSAGSTGLSSPLSPSPSPVFSFSPPEAGDE 448

Db 330 ITDAGGGSPVPTRRALEMAQHSQRSVSAGSTGLSSPLSPSPSPVFSFSPPEAGDE 389

Qy 449 ARGGSPTSKTQTLPSRGRGGGAGEQPPPPSARSTPLPGPCSPRSSGTPHLSPLHTP 508

Db 390 ARGGSPTSKTQTLPSRGRGGGAGEQPPPPSARSTPLPGPCSPRSSGTPHLSPLHTP 449

Qy 509 RASPTGTPGTPPPSPGGVGGAAWRSRLNSIRNSFLGSPFRHRRKQVPTAEEMSLTP 568

Db 450 RASPTGTPGTPPPSPGGVGGAAWRSRLNSIRNSFLGSPFRHRRKQVPTAEEMSLTP 509

Qy 569 ESSPELAKRSWFCNFTISLDKEQIFLVLDKQKPSIKADIVHAFLSIPLSHSVLSQTSF 628

Db 510 ESSPELAKRSWFCNFTISLDKEQIFLVLDKQKPSIKADIVHAFLSIPLSHSVLSQTSF 569

Qy 629 RAEYKASGSPVFKVRFQVDISSSEGEPSPRRDGGGGIYSVTFTLISGFSRRFRK 688

Db 570 RAEYKASGSPVFKVRFQVDISSSEGEPSPRRDGGGGIYSVTFTLISGFSRRFRK 629

Qy 689 VVETIOALLSTHDQPSVQALADEKNGAATRPAGAPPRSLQPPGPPDPBELSSPRGPP 748

Db 630 VVETIOALLSTHDQPSVQALADEKNGAATRPAGAPPRSLQPPGPPDPBELSSPRGPP 689

Qy 749 KDKKLLATNGTPLP 762

Db 690 KDKKLLATNGTPLP 703



## RESULT 3

ID ADE71299 standard; protein; 715 AA.

XX AC ADE71299;

XX DT 29-JAN-2004 (first entry)

XX DE Novel human protein #53.

XX KW human; novel protein; drug.

XX OS Homo sapiens.

XX PN JP2002345493-A.

XX PD 03-DEC-2002.

XX PF 29-MAR-2001; 2002JP-00049046.

XX PR 29-MAR-2001; 2001JP-00095524.

XX PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.

XX DR WPI; 2003-460885/44.

XX DR N-PSDB; ADE71237.

XX PT A gene and a protein encoded by it, used in drugs.

XX PS Disclosure; Page 227-230; 257pp; Japanese.

XX CC The invention comprises the amino acid and coding sequences of novel human proteins. The DNA and protein sequences of the invention are used in drugs. The present amino acid sequence represents a novel human protein of the invention.

XX SQ Sequence 715 AA;

Query Match 87.4%; Score 3545; DB 7; Length 715;  
 Best Local Similarity 99.7%; Pred. No. 6.2e-235;  
 Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 89 FRYLVLEHVGGEFLDYLVKGRITPKKARFFQIVSALDFCHSYICHRLDKPENLL 148  
 : |||||  
 DB 42 YLYLVLEHVGGEFLDYLVKGRITPKKARFFQIVSALDFCHSYICHRLDKPENLL 101  
 |||||

QY 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADWMSGVILPAL 208  
 : |||||  
 DB 102 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADWMSGVILPAL 161  
 |||||

QY 209 LVGALPFDNRLRLLEKVKGVFHMHPFIIPDCQSLRLGMIEVEPEKRLSLEQIQKHPW 268  
 : |||||  
 DB 162 LVGALPFDNRLRLLEKVKGVFHMHPFIIPDCQSLRLGMIEVEPEKRLSLEQIQKHPW 221  
 |||||

QY 269 YLGKHEPDPCLPAPGRVAMRSLPSNGELDPDVLESMAISLGCFRDRERLHRELSEEE 328  
 : |||||  
 DB 222 YLGKHEPDPCLPAPGRVAMRSLPSNGELDPDVLESMAISLGCFRDRERLHRELSEEE 281  
 |||||

QY 329 NQEKMIYLLLDKRYPCSDQDLPRNDVDPKRVDSVMSLHGKRRPERKSMVLS 389  
 : |||||  
 DB 282 NQEKMIYLLLDKRYPCSDQDLPRNDVDPKRVDSVMSLHGKRRPERKSMVLS 341  
 |||||

QY 389 ITDAGGGSVPVTRALEMAHORSRSVSGASTGLSSPLSSPRSPVSPSPGAGDE 448  
 : |||||  
 DB 342 ITDAGGGSVPVTRALEMAHORSRSVSGASTGLSSPLSSPRSPVSPSPGAGDE 401  
 |||||

QY 449 ARGGGSPTKTQTLPSRPGCGAGEQPPPSARSTPLPGPGSPRSGGTPLHSPHT 508  
 : |||||  
 DB 402 ARGGGSPTKTQTLPSRPGCGAGEQPPPSARSTPLPGPGSPRSGGTPLHSPHT 461  
 |||||

QY 509 RASPTGTGTTTPPPSPGGVGGAAWRSLNIRNSFLGSPRFRHRKMQVPTAEEMSLTP 568  
 : |||||

DB 462 RASPTGTGTTTPPPSPGGVGGAAWRSLNIRNSFLGSPRFRHRKMQVPTAEEMSLTP 521  
 : |||||

QY 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKDKPLSSIKADIVHAFPLSIPSLSHSVLSQTSF 628  
 : |||||

DB 522 ESSPELAKRSWFGNFISLDKEEQIFLVLDKDKPLSSIKADIVHAFPLSIPSLSHSVLSQTSF 581  
 : |||||

QY 629 RAEYKASGSPSVFQKPVRFQVDISSSEGPSPSRDDSGGGGIYSVTFTLISGSRSPKR 688  
 : |||||

DB 582 RAEYKASGSPSVFQKPVRFQVDISSSEGPSPSRDDSGGGGIYSVTFTLISGSRSPKR 641  
 : |||||

QY 689 VVETIOAQLLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPGRDPPELSSSPRGGPP 748  
 : |||||

DB 642 VVETIOAQLLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPGRDPPELSSSPRGGPP 701  
 : |||||

QY 749 KDKKLLATNGTPLP 762  
 : |||||

DB 702 KDKKLLATNGTPLP 715  
 : |||||

## RESULT 4

ADF74177

ID ADF74177 standard; protein; 715 AA.

XX AC ADF74177;

XX DT 26-FEB-2004 (first entry)

XX DE Human novel brain/hippocampus protein #65.

XX KW Human; brain; hippocampus; gene therapy; mental illness;

XX OS Homo sapiens.

XX PN JP2003009886-A.

XX PD 14-JAN-2003.

XX PF 21-DEC-2001; 2001JP-00390441.

XX PR 22-DEC-2000; 2000JP-00389742.

XX PR 29-MAR-2001; 2001JP-00095524.

XX PR 25-APR-2001; 2001JP-00127066.

XX PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.

XX PA (PROT-) PROTEIN EXPRESS KK.

XX DR WPI; 2003-735084/70.

XX DR N-PSDB; ADF74247.

XX PT Novel isolated polypeptide useful for screening compounds which modulate the activity of polypeptide and thus have therapeutic applications.

XX PS Claim 1; SEQ ID NO 65; 319pp; Japanese.

XX CC The invention relates to an isolated human polypeptide consisting of a sequence of any one of 70 fully defined sequences (S1) appearing as ADF74113-ADF74182 being encoded by one of 70 disclosed cDNA sequences isolated from brain or hippocampus tissue, or a sequence of (S1) having deletion, substitution, or addition and essentially retaining the same biological activity of (S1). Also included are DNA that encodes the protein, DNA which hybridizes with the encoding DNA and codes a polypeptide which substantially as the same activity as that of a polypeptide above, a gene including the DNA, a recombinant polypeptide encoded by the gene, an antibody against the protein, DNA chip which comprises the DNA, a polypeptide chip comprising the protein, an antibody chip comprising the antibody, a recombinant vector containing the DNA, a transformed host cell containing the vector, an antisense polynucleotide which has a sequence complementary to the DNA, a kit for screening compounds that interact with the protein, test compounds which interact with the protein and homologous proteins having 70% sequence identity with (S1). The protein is useful for identifying compounds which interact

CC with the protein e.g., compounds which inhibit or activate the protein.  
CC Compounds that inhibit the protein activity are useful as therapeutic  
CC agents for treating disorders characterised by aberrant protein activity.  
CC The DNA is useful for producing the protein by recombinant techniques, as  
CC a probe in diagnostic techniques for detecting abnormalities in the gene,  
CC and in gene therapy techniques. The DNA is useful for creating animal  
CC models of disease. The DNA chips are useful for diagnosing any  
CC abnormalities of the DNA in biological samples obtained from human  
CC subjects, where the abnormalities result in mental illness. The antibody  
CC is useful for detecting the protein in biological samples. The protein  
CC chip is useful for functional analysis of the protein, e.g. expression of  
CC the protein, interaction of the protein, post-translational modification  
CC of the protein. The antibody chip is useful for analysing disease states  
CC associated with polypeptide. The antibody chip is also useful in proteome  
CC analysis. The present sequence represents a human brain/hippocampus  
CC protein of the invention.

XX SQ Sequence 715 AA;

Query Match 87.4%; Score 3545; DB 7; Length 715;  
Best Local Similarity 99.7%; Pred. No. 6.2e-235;  
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 89 FRYLVLEHVSGGELFDYLVKKGLTPEAKRFFQIVSALDFCHSYISICHRDLKPNLL 148  
DB 42 YLYLVLEHVSGGELFDYLVKKGLTPEAKRFFQIVSALDFCHSYISICHRDLKPNLL 101  
QY 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIGKEVDGRRADWMSGVILFAL 208  
DB 102 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIGKEVDGRRADWMSGVILFAL 161  
QY 209 LVGALPDDNNLRQLLEKVKRGVFMHFFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 268  
DB 162 LVGALPDDNNLRQLLEKVKRGVFMHFFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 221  
QY 269 YLGKHEPDCLEPAPGRVAMRSLPSNGELDPVLESMAISLCGFRDRRLHRLRESEE 328  
DB 222 YLGKHEPDCLEPAPGRVAMRSLPSNGELDPVLESMAISLCGFRDRRLHRLRESEE 281  
QY 329 NOEKMIYLLLDKRYEPCEDQDLPENDVDPRKRVDSPLSRHGKRRPERKSMVLS 388  
DB 282 NOEKMIYLLLDKRYEPCEDQDLPENDVDPRKRVDSPLSRHGKRRPERKSMVLS 341  
QY 389 ITDAGGSGSPVPTTRALEMAHQSRSSVSGASTGLSSPLSSPRSPVFSPPFGAGDE 448  
DB 342 ITDAGGSGSPVPTTRALEMAHQSRSSVSGASTGLSSPLSSPRSPVFSPPFGAGDE 401  
QY 449 ARGGSPTSKTOTLPSRGRGGAGEQPPPSARSTPLPGPRGSRSSGGTPLHSLHTP 508  
DB 402 ARGGSPTSKTOTLPSRGRGGAGEQPPPSARSTPLPGPRGSRSSGGTPLHSLHTP 461  
QY 509 RASPTGTCTTTPPPSGGVGGAWRSLNSTRNSFLGSPRFRHRRKMVPTAEEMSSLT 568  
DB 462 RASPTGTCTTTPPPSGGVGGAWRSLNSTRNSFLGSPRFRHRRKMVPTAEEMSSLT 521  
QY 569 ESSPELAKESWFGNFIISLKEQIFLVKDKPLSSIKADIVHAFIISPSLSHVSLSQTSF 628  
DB 522 ESSPELAKESWFGNFIISLKEQIFLVKDKPLSSIKADIVHAFIISPSLSHVSLSQTSF 581  
QY 629 RAEYKASGSPVQKRVFRQVDIISSEGEPPSPRDGGGGIYVFTTLISGSPRRFKR 688  
DB 582 RAEYKASGSPVQKRVFRQVDIISSEGEPPSPRDGGGGIYVFTTLISGSPRRFKR 641  
QY 689 VVETIOALLSHDQPSVALADEKNAGQTRPAGAPRSLQPPGPRDPELSSSPRRGPP 748  
DB 642 VVETIOALLSHDQPSVALADEKNAGQTRPAGAPRSLQPPGPRDPELSSSPRRGPP 701  
QY 749 KDKKLLATNGTLP 762  
DB 702 KDKKLLATNGTLP 715

ABB98743  
ID ABB98743 standard; protein; 778 AA.

XX ABB98743;

AC ABB98743;

DT 20-JAN-2003 (first entry)

XX Human kinase #1.

XX Human; kinase; chromosome 19.

XX Homo sapiens.

XX WO200281670-A1.

XX 17-OCT-2002.

XX 04-APR-2002; 2002WO-US010786.

XX 06-APR-2001; 2001US-0282036P.

XX (LEXI-) LEXICON GENETICS INC.

XX Turner CA, Mathur B, Friddle CJ;

XX WPI; 2003-058538/05.

XX N-PSDB; ABV74557.

XX New human kinase proteins useful for diagnosis, drug screening, clinical  
XX trial monitoring, treatment of disorders and diseases, and cosmetic and  
XX nutritional applications.

XX Claim 5; Page 40-41; 47pp; English.

XX The present sequence is a novel human kinase. The genomic locus encoding  
XX the kinase is thought to be on human chromosome 19. The kinase and its  
XX coding sequence are useful for diagnosis, drug screening, clinical trial  
XX monitoring, treatment of disorders and diseases, and cosmetic and  
XX nutritional applications

XX SQ Sequence 778 AA;

Query Match 87.4%; Score 3545; DB 6; Length 778;

Best Local Similarity 99.7%; Pred. No. 6.9e-235;

Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 89 FRYLVLEHVSGGELFDYLVKKGLTPEAKRFFQIVSALDFCHSYISICHRDLKPNLL 148

DB 105 YLYLVLEHVSGGELFDYLVKKGLTPEAKRFFQIVSALDFCHSYISICHRDLKPNLL 164

QY 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIGKEVDGRRADWMSGVILFAL 208

DB 165 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIGKEVDGRRADWMSGVILFAL 224

QY 209 LVGALPDDNNLRQLLEKVKRGVFMHFFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 268

DB 225 LVGALPDDNNLRQLLEKVKRGVFMHFFIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 284

QY 269 YLGKHEPDCLEPAPGRVAMRSLPSNGELDPVLESMAISLCGFRDRRLHRLRESEE 328

DB 285 YLGKHEPDCLEPAPGRVAMRSLPSNGELDPVLESMAISLCGFRDRRLHRLRESEE 344

QY 329 NOEKMIYLLLDKRYEPCEDQDLPENDVDPRKRVDSPLSRHGKRRPERKSMVLS 388

DB 345 NOEKMIYLLLDKRYEPCEDQDLPENDVDPRKRVDSPLSRHGKRRPERKSMVLS 404

QY 389 ITDAGGSGSPVPTTRALEMAHQSRSSVSGASTGLSSPLSSPRSPVFSPPFGAGDE 448

DB 405 ITDAGGSGSPVPTTRALEMAHQSRSSVSGASTGLSSPLSSPRSPVFSPPFGAGDE 464

QY 449 ARGGSPTSKTOTLPSRGRGGAGEQPPPSARSTPLPGPRGSRSSGGTPLHSLHTP 508

DB 465 ARGGSPTSKTOTLPSRGRGGAGEQPPPSARSTPLPGPRGSRSSGGTPLHSLHTP 524

Qy 509 RASPTGPTGTTTPSPGCGVCGAAWRSLNSIRNSFLGSPRFRHRRKQVPTAEEMSLTP 568  
 Db 525 RASPTGPTGTTTPSPGCGVCGAAWRSLNSIRNSFLGSPRFRHRRKQVPTAEEMSLTP 584  
 Qy 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628  
 Db 585 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644  
 Qy 629 RAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGGGGIYSVFTLLISGSPRRPKR 688  
 Db 645 RAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGGGGIYSVFTLLISGSPRRPKR 704  
 Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRRSLQPPGRDPPELSSSPRRGPP 748  
 Db 705 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRRSLQPPGRDPPELSSSPRRGPP 764  
 Qy 749 KDKKLLATNGTFLP 762  
 Db 765 KDKKLLATNGTFLP 778

RESULT 6  
 AAO23053  
 ID AAO23053 standard; protein; 778 AA.  
 AC AAO23053;  
 XX 17-SEP-2003 (first entry)  
 XX Human eukaryotic protein kinase 55053 protein.  
 KW Cardiant; antianginal; antiarteriosclerotic; antidiabetic; thyromimetic;  
 KW antiarrhythmic; cytostatic; nootropic; neuroprotective; antiparkinsonian;  
 KW anticonvulsant; antidepressant; tranquiliser; antimigraine; EPK 55053;  
 KW eukaryotic protein kinase; cellular growth disorder; angina; cancer;  
 KW cognitive; neurodegenerative; Alzheimer's disease; learning; hormone;  
 KW autonomic function; memory; neuropsychiatric; depression; reproductive;  
 KW musculoskeletal; immune system; human; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 214..231  
 FT /label= Transmembrane\_domain  
 XX  
 PN WO2003042371-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 15-NOV-2002; 2002WO-US036967.  
 XX  
 PR 15-NOV-2001; 2001US-00003690.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Curtis RAJ;  
 XX  
 WPI: 2003-449574/42.  
 DR N-PSDB; AAL55772.  
 XX  
 XX New isolated EPK-55053 nucleic acid and polypeptide, useful for  
 FT diagnosing and treating EPK-55053-related disorders, such as  
 PT hypertension, arteriosclerosis, myocardial infarction, diabetes mellitus,  
 PT cancer and/or epilepsy.  
 XX  
 PS Claim 12; Fig 1A-1B; 86pp; English.  
 XX  
 XX The invention relates to a novel isolated nucleic acid molecule  
 CC comprising a sequence which encodes a eukaryotic protein kinase (EPK) -  
 CC 55053 polypeptide. The polynucleotides and polypeptides of the invention  
 CC may play a role as modulating agents in regulating a variety of cellular  
 CC processes. Furthermore, the methods and compositions of the present

CC invention may be useful during the diagnosis, screening and treatment of  
 CC various disorders including cellular growth-related disorders such as  
 CC angina and cancer, cognitive and neurodegenerative disorders e.g.  
 CC Alzheimer's disease, autonomic function disorders, learning or memory  
 CC disorders and neuropsychiatric disorders such as depression. In addition,  
 CC disorders associated with the musculoskeletal, reproductive and immune  
 CC systems, as well as disorders which are cardiac or hormone related, may  
 CC be addressed by the present invention. The current sequence is that of  
 CC the human EPK-55053 protein of the invention  
 XX  
 SQ Sequence 778 AA;

Query Match 87.4%; Score 3545; DB 6; Length 778;  
 Best Local Similarity 99.7%; Pred. No. 6.9e-25; Indels 0; Gaps 0;  
 Matches 672; Conservative 1; Mismatches 1;  
 Qy 89 FRYLVLESHVSGGELFDYLVKKGRITPKAEKFFRQIVSALDFCHSYISICHRLDLPENLLL 148  
 Db :  
 Qy 105 YLYLVLESHVSGGELFDYLVKKGRITPKAEKFFRQIVSALDFCHSYISICHRLDLPENLLL 164  
 Db :  
 Qy 149 DEKNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIKGEYDGRADMMSCGVILPAL 208  
 Db :  
 Qy 165 DEKNIRIADFGMASLQVGDLSLETSCGSPHYACPEVIKGEYDGRADMMSCGVILPAL 224  
 Db :  
 Qy 209 LVGALPEDDDNLRQLLEKVRGVFHMHPFTPPDCQSLRGMIEVEPEKRLSLEQIQHPW 268  
 Db :  
 Qy 225 LVGALPEDDDNLRQLLEKVRGVFHMHPFTPPDCQSLRGMIEVEPEKRLSLEQIQHPW 284  
 Db :  
 Qy 269 YLGKKEPDPCLPEAPGRRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRLRSSEE 328  
 Db :  
 Qy 285 YLGKKEPDPCLPEAPGRRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRLRSSEE 344  
 Db :  
 Qy 329 NOEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388  
 Db :  
 Qy 345 NOEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 404  
 Db :  
 Qy 389 ITDAGGGSVPVTRALEMAHQSORRSVSGASTGLSSPLSSPSRSPVFSFSPRGAGDE 448  
 Db :  
 Qy 405 ITDAGGGSVPVTRALEMAHQSORRSVSGASTGLSSPLSSPSRSPVFSFSPRGAGDE 464  
 Db :  
 Qy 449 ARGGSPTSQTOTLPSRPGGGAGEQPPPSARSTPLPGPPGSPRSGGTPLHSPLHTP 508  
 Db :  
 Qy 465 ARGGSPTSQTOTLPSRPGGGAGEQPPPSARSTPLPGPPGSPRSGGTPLHSPLHTP 524  
 Db :  
 Qy 509 RASPTGPTGTTTPSPGCGVCGAAWRSLNSIRNSFLGSPRFRHRRKQVPTAEEMSLTP 568  
 Db :  
 Qy 525 RASPTGPTGTTTPSPGCGVCGAAWRSLNSIRNSFLGSPRFRHRRKQVPTAEEMSLTP 584  
 Db :  
 Qy 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628  
 Db :  
 Qy 585 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644  
 Db :  
 Qy 629 RAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGGGGIYSVFTLLISGSPRRPKR 688  
 Db :  
 Qy 645 RAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGGGGIYSVFTLLISGSPRRPKR 704  
 Db :  
 Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRRSLQPPGRDPPELSSSPRRGPP 748  
 Db :  
 Qy 705 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRRSLQPPGRDPPELSSSPRRGPP 764  
 Db :  
 Qy 749 KDKKLLATNGTFLP 762  
 Db :  
 Qy 765 KDKKLLATNGTFLP 778  
 Db :  
 XX

RESULT 7  
 ADE38431  
 ID ADE38431 standard; protein; 778 AA.  
 AC ADE38431;  
 XX 29-JAN-2004 (first entry)  
 XX

	Human protein 6862 amino acid sequence.
DE	tumorigenic disorder; angiogenic disorder; aberrant gene expression;
XX	aberrant protein activity; cystostatic; antithyroid; antidiabetic;
KW	ophthalmological cancer; breast cancer; colon cancer; lung cancer;
KW	prostatic cancer; Grave's disease; diabetic retinopathy; protein 6862.
XX	Homo sapiens.
OS	
PX	WO2003065006-A2.
NN	
PD	07-AUG-2003.
XX	
XX	30-JAN-2003; 2003WO-US002588.
XX	
XX	31-JAN-2002; 2002US-0353600P.
PR	15-MAR-2002; 2002US-0364517P.
PR	09-APR-2002; 2002US-0371075P.
PR	10-APR-2002; 2002US-0371507P.
PR	16-APR-2002; 2002US-0372984P.
PR	19-APR-2002; 2002US-0374194P.
PR	24-MAY-2002; 2002US-0382995P.
PR	31-MAY-2002; 2002US-0385023P.
PR	14-JUN-2002; 2002US-0388853P.
PR	17-JUN-2002; 2002US-0389395P.
PR	25-JUN-2002; 2002US-0391324P.
PR	15-JUL-2002; 2002US-0395944P.
PR	22-JUL-2002; 2002US-0397726P.
PR	13-AUG-2002; 2002US-0403046P.
PR	22-AUG-2002; 2002US-0405155P.
PR	27-AUG-2002; 2002US-0406361P.
PR	25-OCT-2002; 2002US-0421195P.
PR	12-NOV-2002; 2002US-0425456P.
PR	19-NOV-2002; 2002US-0427626P.
PR	10-DEC-2002; 2002US-0432122P.
XX	(MILL-) MILLENNIUM PHARM INC.
PA	
XX	Hunter JJ, Macbeth KJ, Tsai F, Lesoon A, Lightcap ES;
PI	Williamson MW, Rudolph-Owen LA;
XX	WPI; 2003-646176/61.
DR	N-PSTB; ADE38430.
XX	Treating subject having tumorigenic disorder or angiogenic disorder
PT	caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic
PT	acid, by administering a modulator.
XX	Disclosure; SEQ ID NO 92; 454pp; English.
PS	This invention relates to a novel method of treating a human subject
XX	having a tumorigenic disorder or angiogenic disorder, caused by aberrant
CC	gene expression or activity of an isolated protein, by administering a
CC	modulator. The modulator may have cytostatic, antithyroid, antidiabetic
CC	or ophthalmological activity. The method is useful for treating a subject
CC	having a tumorigenic or angiogenic disorder, in particular for treating
CC	cancer (for example breast cancer, colon cancer, lung cancer or prostatic
CC	cancer) and, for example, Grave's disease and diabetic retinopathy. The
CC	present sequence is the amino acid sequence of the novel isolated human
CC	protein 6862 of the invention.
XX	Sequence 778 AA;
SQ	
	Query Match 87.4%; Score 3545; DB 7; Length 778;
	Best Local Similarity 99.7%; Pred. No. 6.9e-235;
	Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0
OY	89 FYLVLEHVS GGELFDYL VKGRLTPKEARKFROI VSDFC HSYICHRDLKPENLLL 148
	:
DB	105 YILVLEHVS GGELFDYL VKGRLTPKEARKFROI VSDFC HSYICHRDLKPENLLL 164
	:
OY	149 DEKNINRIADFGNASIQVGDSLLETSCGSPHVACPEVIKGEKYDGRADMWSCGVILPAL 208
	:

KW human.  
 XX Homo sapiens.  
 OS US2004058355-A1.  
 PN 25-MAR-2004.  
 XX 25-APR-2003; 2003US-00423543.  
 XX 30-SEP-1998; 98US-00163821.  
 PR 27-JAN-1999; 99US-0117580P.  
 PR 25-MAR-1999; 99US-00276400.  
 PR 30-JUL-1999; 99US-00365162.  
 PR 09-SEP-1999; 99US-00392189.  
 PR 05-OCT-1999; 99US-00412210.  
 PR 23-NOV-1999; 99US-00448076.  
 PR 29-FEB-2000; 2000US-0186061P.  
 PR 28-APR-2000; 2000US-0200688P.  
 PR 19-MAY-2000; 2000US-0205447P.  
 PR 30-JUN-2000; 2000US-00608921.  
 PR 31-JUL-2000; 2000US-0221925P.  
 PR 25-SEP-2000; 2000US-0234922P.  
 PR 25-SEP-2000; 2000US-0235035P.  
 PR 08-NOV-2000; 2000US-0246669P.  
 PR 09-NOV-2000; 2000US-00711216.  
 PR 14-NOV-2000; 2000US-0248325P.  
 PR 15-NOV-2000; 2000US-0248893P.  
 PR 22-DEC-2000; 2000US-0257511P.  
 PR 05-JAN-2001; 2001US-0260166P.  
 PR 28-FEB-2001; 2001US-00797039.  
 PR 27-APR-2001; 2001US-00845044.  
 PR 20-JUL-2001; 2001US-00909743.  
 PR 31-JUL-2001; 2001US-00920346.  
 PR 13-AUG-2001; 2001US-00928531.  
 PR 14-AUG-2001; 2001US-00929218.  
 PR 15-AUG-2001; 2001US-0312539P.  
 PR 25-SEP-2001; 2001US-00963159.  
 PR 08-NOV-2001; 2001US-0008016.  
 PR 13-NOV-2001; 2001US-00012055.  
 PR 15-NOV-2001; 2001US-00003690.  
 PR 30-JAN-2002; 2002US-00060763.  
 PR 25-MAR-2002; 2002US-00105989.  
 PR 12-APR-2002; 2002US-00121911.  
 PR 12-AUG-2002; 2002US-00217168.  
 PR 22-OCT-2002; 2002US-00278036.  
 PR 02-JAN-2003; 2003US-00336489.  
 PR 03-JAN-2003; 2003US-00336153.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Kapeller-Libermann R, Hunter JJ, Meyers RE, Rudolph-Owen LA,  
 PI Curtis RAJ, Olandt PJ, Tsai F, Galvin KM, Chun M, Williamson MJ;  
 PI Silos-Santiago I, Bandaru R;  
 XX WPI; 2004-268788/25.  
 DR N-PSDB; ADL14127, ADL14129.  
 XX New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529,  
 PT 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593  
 PT nucleic acid molecules and proteins, useful for treating, e.g. cancer,  
 PT heart failure and angina.  
 XX Claim 4; SEQ ID NO 11; 139pp; English.  
 PS The invention describes an isolated 21910, 56634, 55053, 2504, 15977,  
 CC 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217,  
 CC 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising  
 CC any one of 40 nucleotide sequences (I). The nucleic acid molecules and  
 CC polypeptides are useful for diagnosing and treating a subject having a  
 CC disorder, or a subject at risk of developing a disorder, which is  
 CC associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,  
 CC 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983,

CC m1983, 38555 or 593 activity, such as cellular proliferative and/or  
 CC differentiative disorders, brain disorders, platelet disorders, breast  
 CC disorders, colon disorders, kidney (renal) disorders, lung disorders,  
 CC ovarian disorders, prostate disorders, cervical disorders, spleen  
 CC disorders, thymus disorders, thyroid disorders, testes disorders,  
 CC hematopoietic disorders, pancreatic disorders, skeletal muscle disorders,  
 CC skin (dermal) disorders, disorders associated with bone metabolism,  
 CC immune, e.g. inflammatory disorders, cardiovascular disorders,  
 CC endothelial cell disorders, liver disorders, viral diseases, pain  
 CC disorders, metabolic disorders, neurological or central nervous system  
 CC disorders, erythroid disorders, blood vessel disorders or angiogenic  
 CC disorders (all claimed), e.g. cancer, heart failure, hypertension,  
 CC angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's  
 CC disease, psoriasis, or asthma. The nucleic acid molecules and  
 CC polypeptides are also useful as modulating agents in regulating a variety  
 CC of cellular process, e.g. cell proliferation, differentiation, growth and  
 CC division. This is the amino acid sequence of a novel human protein of the  
 CC invention. Note: The sequences given in the specification are also  
 CC available in electronic format from  
 CC ftp.segdata.uspto.gov/sequence.html?DocID=20040058355.  
 XX  
 SQ Sequence 778 AA;  
 Query Match 87.4%; Score 3545; DB 8: Length 778;  
 Best Local Similarity 99.7%; Pred. No. 6.9e-235;  
 Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 89 FRYLVLEHVS GGLFDYLVKKGLTTPKEARKFRQIVSALDFCHSYICHRLDKPENLLL 148  
 DB 105 YLYLVLEHVS GGLFDYLVKKGLTTPKEARKFRQIVSALDFCHSYICHRLDKPENLLL 164  
 QY 149 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADMMSCGVILFAL 208  
 DB 165 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADMMSCGVILFAL 224  
 QY 209 LVGALPDDNNLRQLLEKVRGVFHMHPHFTPPCQSLLRGMIEVEPEKRSLLEQIQKHPW 268  
 DB 225 LVGALPDDNNLRQLLEKVRGVFHMHPHFTPPCQSLLRGMIEVEPEKRSLLEQIQKHPW 284  
 QY 269 YLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRELSEEE 328  
 DB 285 YLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRELSEEE 344  
 QY 329 NOEKMIYLLLDKRYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGRKRPKSMSEVLS 388  
 DB 345 NOEKMIYLLLDKRYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGRKRPKSMSEVLS 404  
 QY 389 ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSSLSPSPSPSPSPSPSPSPSPSPSP 448  
 DB 405 ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSSLSPSPSPSPSPSPSPSPSPSPSP 464  
 QY 449 ARGGGSPSTKTQTLPSRGRGGGAGEOPPPPSARSTPLPGPPSPSSGGTPLHSLPLHTP 508  
 DB 465 ARGGGSPSTKTQTLPSRGRGGGAGEOPPPPSARSTPLPGPPSPSSGGTPLHSLPLHTP 524  
 QY 509 RASPTGTPTTTPPPSPGGVGGAAWRSLRSLRSLRSLRSLRSLRSLRSLRSLRSLRSLRSL 568  
 DB 525 RASPTGTPTTTPPPSPGGVGGAAWRSLRSLRSLRSLRSLRSLRSLRSLRSLRSLRSLRSL 584  
 QY 569 ESSPELAKRSWFGNFTSLDKKEQIFLVLDKDKPLSSIKADIVHAFSLTSPSLSHSVLSQTSF 628  
 DB 585 ESSPELAKRSWFGNFTSLDKKEQIFLVLDKDKPLSSIKADIVHAFSLTSPSLSHSVLSQTSF 644  
 QY 629 RABYKASGGSPVFKPVRFOVDISSSEGGPSPRRDGGSGGGIYSVFTTILSGPSRRFKR 688  
 DB 645 RABYKASGGSPVFKPVRFOVDISSSEGGPSPRRDGGSGGGIYSVFTTILSGPSRRFKR 704  
 QY 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLOPPGPRDPPELSSSPRRGPP 748  
 DB 705 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLOPPGPRDPPELSSSPRRGPP 764  
 QY 749 KDKKLLATNGTPLP 762  
 DB |||||

Db	765 KDKLLATNGTPLP 778	
RESULT 9		
ADQ89184		
ID	ADQ89184 standard; protein; 778 AA.	
XX		
AC	ADQ89184;	
XX		
DT	21-OCT-2004 (first entry)	
XX		
DE	Human urological disorder related protein 55053 SEQ:136.	
XX		
KW	urological disorder; uropathic; cytostatic; urinary incontinence;	
KW	benign prostatic hyperplasia; human.	
XX		
OS	Homo sapiens.	
XX		
FN	WO2004065576-A2.	
XX		
PD	05-AUG-2004.	
XX		
PF	14-JAN-2004; 2004WO-US000750.	
XX		
PR	15-JAN-2003; 2003US-0440318P.	
PR	04-FEB-2003; 2003US-0444783P.	
PR	27-MAR-2003; 2003US-0457901P.	
PR	08-MAY-2003; 2003US-0468775P.	
PR	19-MAY-2003; 2003US-0471614P.	
PR	16-JUN-2003; 2003US-0478742P.	
PR	18-JUL-2003; 2003US-0498529P.	
PR	30-JUL-2003; 2003US-0491156P.	
PR	02-SEP-2003; 2003US-0499594P.	
PR	26-SEP-2003; 2003US-0506332P.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Karicheti V, Silos-Santiago I, Eliasof SD;	
XX		
DR	WPI; 2004-562167/54.	
DR	N-PSDB; ADQ89183.	
XX		
XX	Use of polypeptides related to urological disorders, e.g. 44390, 54181,	
PT	211 or for identifying a compound capable of treating a urological	
PT	disorder or identifying and treating a subject having a urological	
PT	disorder.	
XX		
XX	Claim 1; SEQ ID NO 136; 542pp; English.	
PS		
XX		
CC	The present invention describes the use of polypeptides related to,	
CC	urological disorders for identifying a compound capable of treating a	
CC	urological disorder, identifying a subject having a urological disorder,	
CC	or treating a subject having a urological disorder. Also described: (1) a	
CC	method for identifying a compound capable of treating a urological	
CC	disorder; and (2) a method for identifying a subject having a urological	
CC	disorder; and (3) a method for treating a subject having a urological	
CC	disorder. The compound has uropathic and cytostatic activities. The	
CC	polypeptides related to urological disorders are useful for identifying a	
CC	compound capable of treating a urological disorder. Identifying a subject	
CC	having a urological disorder, or treating a subject having a urological	
CC	disorder. Disorders include urinary incontinence and benign prostatic	
CC	hyperplasia. The present sequence represents a human urological disorder	
CC	related protein, which is used in the exemplification of the present	
CC	invention.	
XX		
XX	Sequence 778 AA;	
XX		
Query Match	87.4%; Score 3545; DB 8; Length 778;	
Best Local Similarity	99.7%; Pred. NO. 6.9e-235;	
Matches	672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	89 FRYLVLEHVSGGELFDYLVKKGRLTPKEARKFFRQIVSALDFCHSYICHRLDKPENLLL 148	



FT Domain 34..286  
 FT /note = Tyrosine kinase domain  
 FT Domain 34..285  
 FT /note = Eukaryotic protein kinase domain  
 FT Domain 152..164  
 FT /note = Serine/threonine kinase domain  
 FT Modified-site 208..211  
 FT /note = "Amidation site"  
 FT Domain 214..231  
 FT /note = Transmembrane domain  
 FT Modified-site 300..303  
 FT /note = "Amidation site"  
 FT Domain 315..356  
 FT /note = UBA domain  
 FT Modified-site 390..393  
 FT /note = "Amidation site"  
 FT Binding-site 682..685  
 FT /note = "Glycosaminoglycan attachment site"  
 FT US6787345-B1.  
 FT 07-SEP-2004.  
 FT 15-NOV-2001; 2001US-00003690.  
 FT 15-NOV-2000; 2000US-0248893P.  
 FT (MILL-) MILLENNIUM PHARM INC.  
 FT Curtis RAJ;  
 FT WPI; 2004-632931/61.  
 FT N-PSDB; ADS16425, ADS16427, ADS16433.  
 FT New isolated eukaryotic kinase (EPK-55053) nucleic acid and protein,  
 FT useful for diagnosing or treating EPK-55053 mediated or related  
 FT disorders, e.g. Alzheimer's disease, multiple sclerosis, depression,  
 FT ischemia, restenosis, or diabetes.  
 FT  
 FT Claim 2; SEQ ID NO 2; 55pp; English.  
 FT  
 FT The invention relates to an eukaryotic protein kinase-55053 (EPK-55053)  
 FT and its corresponding nucleic acid sequence. The EPK-55053 nucleic acid  
 FT molecules, proteins and antibodies are useful in screening assays,  
 FT diagnostic assays, prognostic assays, in monitoring clinical trials,  
 FT pharmacogenetics or for treating EPK-55053 mediated or related disorders.  
 FT EPK-55053 mediated or related disorders include CNS disorders  
 FT (Alzheimer's disease, Parkinson's disease, multiple sclerosis,  
 FT amyotrophic lateral sclerosis or epilepsy), autonomic function disorders  
 FT (sleep disorders, depression, mania, anxiety disorders or phobic  
 FT disorders), learning or memory disorders (amnesia or attention deficit  
 FT disorder), cardiovascular system disorders (arteriosclerosis, ischaemia,  
 FT reperfusion injury, restenosis or vascular heart disease), hormonal  
 FT disorders (diabetes or thyroid disorders) and reproductive or fertility  
 FT disorders. The present sequence is human EPK-55053 enzyme.  
 FT  
 FT Sequence 778 AA;  
 FT  
 FT Query Match 87.4%; Score 3545; DB 8; Length 778;  
 FT Best Local Similarity 99.7%; Pred. No. 6.9e-235;  
 FT Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 FT  
 FT 89 FRYLVLEHVSGLGELFDYLVKKGRITPKKARFFRQIVSALDFCHSYISICHRDLKPENLLL 148  
 FT :  
 FT 105 YLYLVLEHVSGLGELFDYLVKKGRITPKKARFFRQIVSALDFCHSYISICHRDLKPENLLL 164  
 FT  
 FT 149 DEKNIRIADPGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMMSCGVILFAL 208  
 FT  
 FT 165 DEKNIRIADPGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMMSCGVILFAL 224  
 FT  
 FT 209 LVGALPDDNNLRQLLEKVRGVFMPHFIPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 268  
 FT :  
 FT 225 LVGALPDDNNLRQLLEKVRGVFMPHFIPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 284

Qy 269 YLGSKHEPDCLEPAPGRRVAMRSLPSNGELDDPVLESMAISLGCFRDRERLHRLRSEE 328  
 Db 285 YLGSKHEPDCLEPAPGRRVAMRSLPSNGELDDPVLESMAISLGCFRDRERLHRLRSEE 344  
 Qy 329 NOEKMIYLLLDKRYPCEDODLPPRNDVDPPKRVDSFMLRHGKRRPERKSMVLS 388  
 Db 345 NOEKMIYLLLDKRYPCEDODLPPRNDVDPPKRVDSFMLRHGKRRPERKSMVLS 404  
 Qy 389 ITDAGGGSPVPTTRALEMAHQSRKSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE 448  
 Db 405 ITDAGGGSPVPTTRALEMAHQSRKSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE 464  
 Qy 449 ARGCGSPTSKTQTLPSRPGCGGAGEOPPPSARSTPLPGPPSPRSGGTPLHSPHTP 508  
 Db 465 ARGCGSPTSKTQTLPSRPGCGGAGEOPPPSARSTPLPGPPSPRSGGTPLHSPHTP 524  
 Qy 509 RASPTGPTGTTTPPSGCGVGGAAWRSLRSLRNSFLGSPFRHRRKMQVPTAEMSSLTP 568  
 Db 525 RASPTGPTGTTTPPSGCGVGGAAWRSLRSLRNSFLGSPFRHRRKMQVPTAEMSSLTP 584  
 Qy 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLSPSLSHSVLSQTSF 628  
 Db 585 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLSPSLSHSVLSQTSF 644  
 Qy 629 RAEYKASGSPSVFQKPVRFQVDISSSEGGPSPRRDGGGGGIYSVTFTLISGSPRRPKR 688  
 Db 645 RAEYKASGSPSVFQKPVRFQVDISSSEGGPSPRRDGGGGGIYSVTFTLISGSPRRPKR 704  
 Qy 689 VVETIQALLSTHDQPSVQALADEKNGAOTRPAAPPRLQPPGPDPELSSSPRRGPP 748  
 Db 705 VVETIQALLSTHDQPSVQALADEKNGAOTRPAAPPRLQPPGPDPELSSSPRRGPP 764  
 Qy 749 KDKKLLATNGTPLP 762  
 Db 765 KDKKLLATNGTPLP 778  
 RESULT 11  
 AAU03517  
 ID AAU03517 standard; protein; 794 AA.  
 AC AAU03517;  
 DT 12-SEP-2001 (first entry)  
 DE Human protein kinase #17.  
 KW Human; protein kinase; PK; STK; cancer; cardiovascular disease;  
 KW metabolic disorder; immune related disease; neurological disorder;  
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;  
 KW reproductive disorder.  
 OS Homo sapiens.  
 PN WO200138503-A2.  
 PD 31-MAY-2001.  
 PF 22-NOV-2000; 2000WO-US032085.  
 PR 24-NOV-1999; 99US-0167482P.  
 PA (SUGEN-) SUGEN INC.  
 PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
 PI Flanagan P, Clary D;  
 XX WPI; 2001-343950/36.  
 DR N-PSDB; AAS06717.  
 XX Nucleic acids encoding human kinase polypeptides, useful for preventing  
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and

PT neuronal-associated diseases, and microbial infections.

XX Claim 7; Fig 2; 433pp; English.

XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel  
XX protein kinases have been identified as members of the tyrosine or  
XX serine/threonine kinase (PTK and STK) families. The polynucleotides  
XX encoding protein kinases and the polypeptides may be used in the  
XX prevention, diagnosis and treatment of diseases associated with  
XX cancers (especially cancers of haematopoietic origin), cardiovascular  
XX disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
XX immune related diseases (e.g. rheumatoid arthritis), neurological  
XX disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
XX Parkinson's disease), inflammatory disorders (e.g. asthma), infectious  
XX disease (e.g. HIV), and reproductive disorders (e.g. infertility).  
XX Additionally, polynucleotides encoding protein kinases may be used for  
XX gene therapy and as DNA probes in diagnostic assays. The protein kinase  
XX polypeptides may be used as antigens in the production of antibodies  
XX against the protein kinases and in assays to identify modulators of  
XX protein kinase expression and activity

XX SQ Sequence 794 AA;

Query Match 87.4%; Score 3545; DB 4; Length 794;

Best Local Similarity 99.7%; Pred. No. 7.1e-235;  
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 89 FRYLVLEHVSGGELFDYLVKKGRITPKKARFFQIVSALDFCHSYISCHRDLPENLL 148  
DB : |||||  
QY 121 YLVLEHVSGGELFDYLVKKGRITPKKARFFQIVSALDFCHSYISCHRDLPENLL 180  
DB : |||||  
QY 149 DEKNIRIADFGMASLQVDSILSTSCGSHYACPEVIGKGYDGRADMWSCVILFAL 208  
DB 181 DEKNIRIADFGMASLQVDSILSTSCGSHYACPEVIGKGYDGRADMWSCVILFAL 240  
QY 209 LVGALPFDDNLRQLLEKVGKGVFHMHPFIIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 268  
DB 241 LVGALPFDDNLRQLLEKVGKGVFHMHPFIIPDCQSLLRGMIEVEPEKRLSLEIQKHPW 300  
QY 269 YLGKHEPDPCLEPAPGRVAMRSLPSNGELDDPVLESMSLGCGRFRERLHRLSEEE 328  
DB 301 YLGKHEPDPCLEPAPGRVAMRSLPSNGELDDPVLESMSLGCGRFRERLHRLSEEE 360  
QY 329 NOEKMIYLLLDKERYPSCEDQDLPFRNDVDPKRVDSPLMRSHGKRRPERKSMEVL 388  
DB 361 NOEKMIYLLLDKERYPSCEDQDLPFRNDVDPKRVDSPLMRSHGKRRPERKSMEVL 420  
QY 389 ITDAGGGSPVPTRRALEMAQHSQSRSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE 448  
DB 421 ITDAGGGSPVPTRRALEMAQHSQSRSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE 480  
QY 449 ARGGSPTSXTLTLSRGRGGAGGEOPPPBARSTPLPGPGSPRSSGGTPLHSLHTP 508  
DB 481 ARGGSPTSXTLTLSRGRGGAGGEOPPPBARSTPLPGPGSPRSSGGTPLHSLHTP 540  
QY 509 RASPTGTCTTPTTTPPGGPGVGAARSLNRSFLGSPRFRHKKMQVPTAEENSLTP 568  
DB 541 RASPTGTCTTPTTTPPGGPGVGAARSLNRSFLGSPRFRHKKMQVPTAEENSLTP 600  
QY 569 ESSPELAKGSWFGNFTSLDKERQIFLVLDKPLSSIKADIVHAFISLSHSLVLSQTSF 628  
DB 601 ESSPELAKGSWFGNFTSLDKERQIFLVLDKPLSSIKADIVHAFISLSHSLVLSQTSF 660  
QY 629 RAEYKASGSPVQKVRVQVDISSEGGPEPRDRGGGGGIYSVTFTLISGPPRRFR 688  
DB 661 RAEYKASGSPVQKVRVQVDISSEGGPEPRDRGGGGGIYSVTFTLISGPPRRFR 720  
QY 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRPSLPQPPGRPDPELSSSPRRGPP 748  
DB 721 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRPSLPQPPGRPDPELSSSPRRGPP 780  
QY 749 KDKKLLATNGTFLP 762

DB 781 KDKKLLATNGTFLP 794

RESULT 12

AAE16271

ID AAE16271 standard; protein; 794 AA.

XX AAE16271;

XX 26-MAR-2002 (first entry)

XX Human kinase PKIN-17 protein.

XX Human; kinase; PKIN-17; cancer; leukaemia; adenocarcinoma; osteoporosis;  
XX immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;  
XX Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;  
XX allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;  
XX autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;  
XX Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;  
XX rheumatoid arthritis; ulcerative colitis; cirrhosis; angina pectoris;  
XX hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;  
XX cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;  
XX congestive heart failure; ischaemic heart disease; lung tumour; gout;  
XX fatty liver; Niemann-Pick's disease; gene therapy.

XX Homo sapiens.

XX Location/Qualifiers

Key 50..301

Domain /note="Eukaryotic protein kinase domain"

Domain 51..292 /label= Protein\_kinase\_domain

Domain 52..292 /label= Protein\_kinase\_domain

Domain 71..292 /label= Protein\_kinase\_domain

XX W0200196547-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US019444.

XX 15-JUN-2000; 2000US-0212073P.

XX 23-JUN-2000; 2000US-0213467P.

XX 30-JUN-2000; 2000US-0215651P.

XX 07-JUL-2000; 2000US-0216605P.

XX 13-JUL-2000; 2000US-0218372P.

XX 25-AUG-2000; 2000US-0228056P.

XX (INCY-) INCYTE GENOMICS INC.

XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;

XX Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DM, Greenwald SR;

XX Runkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang Y;

XX Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;

XX Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;

XX Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;

XX WPI; 2002-090207/12.

XX N-PSDB; AAD26464.

XX New polypeptides, useful for diagnosing, treating or preventing disorders  
XX of growth and development, cardiovascular and lipid, and diseases such as  
XX cancer, comprise human kinase polypeptides.

XX Claim 1; Page 159-161; 197pp; English.

XX The invention relates to human kinase PKIN proteins and their

XX corresponding cDNAs. A composition containing PKIN agonist is useful for

XX treating a disease or condition associated with decreased expression of

XX PKIN and a composition comprising PKIN antagonist is useful for treating

a disease or condition associated with overexpression of PKIN. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atherosclerosis, anaemia, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease, osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protozoal and helminthic infections) growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio vascular disease (arteriovenous fistula, hypertension, vasculitis, aneurysms, congestive heart failure, angina pectoris, myocarditis, ischaemic heart disease, chronic bronchitis, lung tumours); lipid disorder (fatty liver, Fabry's disease, Niemann-Pick's disease, hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity of a test compound and in gene therapy. The present sequence is human PKIN-17 protein

XX Sequence 794 AA;

Query Match 87.4%; Score 3545; DB 5; Length 794;

Best Local Similarity 99.7%; Pred. No. 7.1e-235;

Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 89 FRYLVLEHVS GGELFDYLVKKGRUTPKARKFFRQIVSALDFCHSYSTCHRDLPENLL 148  
 Db : |||||  
 121 YLYLVLEHVS GGELFDYLVKKGRUTPKARKFFRQIVSALDFCHSYSTCHRDLPENLL 180  
 Qy 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMMSCGVILPAL 208  
 Db |||||  
 181 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMMSCGVILPAL 240  
 Qy 209 LVGALPPDDNLRQLLEKVRGVFHPHFIPDQCSSLRGMIYEVEPEKRLSLEQIQHPW 268  
 Db |||||  
 241 LVGALPPDDNLRQLLEKVRGVFHPHFIPDQCSSLRGMIYEVEPEKRLSLEQIQHPW 300  
 Qy 269 YLGKKEHPDPCLEPAPGRVAMRSLPSNGELDPDVLESMAISGCFRDRERLHRLSEEE 328  
 Db |||||  
 301 YLGKKEHPDPCLEPAPGRVAMRSLPSNGELDPDVLESMAISGCFRDRERLHRLSEEE 360  
 Qy 329 NQEKMIYLLLDKRYEPCEDQDLPVRNDVDPKRVDSMLSRHGKRRPERKSMVLS 388  
 Db |||||  
 361 NQEKMIYLLLDKRYEPCEDQDLPVRNDVDPKRVDSMLSRHGKRRPERKSMVLS 420  
 Qy 389 ITDAGGGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE 448  
 Db |||||  
 421 ITDAGGGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE 480  
 Qy 449 ARGCGSPSTKTQTLPSRPGCGGAGEQPPPSARSTPLPGPPSPRSSGGTFLHSLHTP 508  
 Db |||||  
 481 ARGCGSPSTKTQTLPSRPGCGGAGEQPPPSARSTPLPGPPSPRSSGGTFLHSLHTP 540  
 Qy 509 RASTGTPTGTTTPPSPGGVGGAWRSLNIRNSFLGSPRFRKQVPTAEEMSLTP 568  
 Db |||||  
 541 RASTGTPTGTTTPPSPGGVGGAWRSLNIRNSFLGSPRFRKQVPTAEEMSLTP 600  
 Qy 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIADIVHAFISLPSLSHSVLSQTSF 628  
 Db |||||  
 601 ESSPELAKRSWFGNFISLDKEEQIFLVLDKPLSSIADIVHAFISLPSLSHSVLSQTSF 660  
 Qy 629 RAEYKASGGSPVQKVRVQVDIISSESGEPSPRRDGGSGGGIYSVFTLISGSPRRFKR 688  
 Db |||||  
 661 RAEYKASGGSPVQKVRVQVDIISSESGEPSPRRDGGSGGGIYSVFTLISGSPRRFKR 720  
 Qy 689 VVETIQALLSTHQPVSQALADEKNGAQTPAGAPRSLQPPGRDPPELSSSPRRGPP 748  
 Db |||||  
 721 VVETIQALLSTHQPVSQALADEKNGAQTPAGAPRSLQPPGRDPPELSSSPRRGPP 780  
 Qy 749 KDKKLLATNGTPLP 762  
 Db |||||  
 781 KDKKLLATNGTPLP 794

RESULT 13  
 AAO16604

ID AAO16604 standard; protein; 754 AA.

XX AC AAO16604;

XX DT 08-MAY-2003 (first entry)

XX Human cell cycle-regulatory factor Cdr2.

XX Human; cell cycle-regulatory factor; Cdr2; kinase; proliferative disease;  
 anticancer agent; wound-healing drug.

XX Homo sapiens.

XX WO200299110-A1.

XX PD 12-DEC-2002.

XX 03-JUN-2002; 2002WO-JF005411.

XX 04-JUN-2001; 2001JP-00168792.

XX (TAIH ) TAIHO PHARM CO LTD.

XX (NAKA/) NAKANISHI M.

XX Nakanishi M;

XX WPI; 2003-156857/15.

XX N-PSDB; AAL51889.

XX Cell cycle-regulatory factor Cdr2 with kinase activity and encoded gene,  
 applicable in diagnosis of and screening drugs for proliferative diseases  
 e.g. anticancer agents and wound-healing drugs.

XX Claim 1; Fig 2 A-C; 63pp; Japanese.

XX The invention comprises the amino acid and coding sequence of the human  
 cell cycle-regulatory factor Cdr2 (with kinase activity). The DNA and  
 protein sequences of the invention are useful in diagnosing and screening  
 drugs for proliferative diseases (e.g. anticancer agents and wound-  
 healing drugs). The present amino acid sequence represents the human cell  
 cycle-regulatory factor Cdr2 protein

XX SQ Sequence 754 AA;

Query Match 82.9%; Score 3362; DB 6; Length 754;

Best Local Similarity 95.4%; Pred. No. 2.5e-222;

Matches 643; Conservative 1; Mismatches 6; Indels 24; Gaps 1;

Qy 89 FRYLVLEHVS GGELFDYLVKKGRUTPKARKFFRQIVSALDFCHSYSTCHRDLPENLL 148  
 Db : |||||  
 105 YLYLVLEHVS GGELFDYLVKKGRUTPKARKFFRQIVVACGLCHSYSTCHRDLPENLL 164  
 Qy 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMMSCGVILPAL 208  
 Db |||||  
 165 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADMMSCGVILPAL 224  
 Qy 209 LVGALPPDDNLRQLLEKVRGVFHPHFIPDQCSSLRGMIYEVEPEKRLSLEQIQHPW 268  
 Db |||||  
 225 LVGALPPDDNLRQLLEKVRGVFHPHFIPDQCSSLRGMIYEVEPEKRLSLEQIQHPW 284  
 Qy 269 YLGKKEHPDPCLEPAPGRVAMRSLPSNGELDPDVLESMAISGCFRDRERLHRLSEEE 328  
 Db |||||  
 285 YLGKKEHPDPCLEPAPGRVAMRSLPSNGELDPDVLESMAISGCFRDRERLHRLSEEE 344  
 Qy 329 NQEKMIYLLLDKRYEPCEDQDLPVRNDVDPKRVDSMLSRHGKRRPERKSMVLS 388  
 Db |||||  
 345 NQEKMIYLLLDKRYEPCEDQDLPVRNDVDPKRVDSMLSRHGKRRPERKSMVLS 404  
 Qy 389 ITDAGGGSPVPTTRALEMAHQSRSVSGASTGLSSPLSSPRSPVFSFSPFGAGDE 448

Db 405 ITDAGGGSPVPTTRALEMAQHSQSRVSGASTGLSSPLSPSPVFSFEPGAGDE 464  
Qy 449 ARGGSPTSTQTLPSRPGGAGGQPPPSARSTPLPGPGSPRSSGGTPLHSPHTP 508  
Db 465 ARGGSPTSTQTLPSRPGGAGGQPPPSARSTPLPGPGSPRSSGGTPLHSPHTP 500  
Qy 509 RASPTGPTTTPPPSGGAGGAAWRLNSIRNSFLGSPRFRHRRKQVPTAEEMSSLTP 568  
Db 501 RASPTGPTTTPPPSGGAGGAAWRLNSIRNSFLGSPRFRHRRKQVPTAEEMSSLTP 560  
Qy 569 ESSPELAKRWGFIQLDKEQIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLSQTSF 628  
Db 561 ESSPELAKRWGFIQLDKEQIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLSQTSF 620  
Qy 629 RAEYKASGGSPVOKPVRFOVDISSSEGPSPRRDGGGGGIYSVTFTLISGFSRRFKR 688  
Db 621 RAEYKASGGSPVOKPVRFOVDISSSEGPSPRRDGGGGGIYSVTFTLISGFSRRFKR 680  
Qy 689 VVETIQALLSTHDQPSVQALADEKGAQTRPAGAPPSLQPPGRDPPELSSPRGPP 748  
Db 681 VVETIQALLSTHDQPSVQALADEKGAQTRPAGAPPSLQPPGRDPPELSSPRGPP 740  
Qy 749 KDKLLATNGTPLP 762  
Db 741 KDKLLATNGTPLP 754

RESULT 14  
ADQ65624 standard; protein; 473 AA.  
AC ADQ65624;  
XX 07-OCT-2004 (first entry)  
XX Novel human protein sequence #597.  
DE osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
XX gene therapy; diagnostic marker; morbid state; osteoporosis;  
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;  
KW cancer.  
XX Homo sapiens.  
XX EF1440981-A2.  
XX 28-JUL-2004.  
XX 21-JAN-2004; 2004EP-00001196.  
XX 21-JAN-2003; 2003JP-00102206.  
XX 09-MAY-2003; 2003JP-00131392.  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Negai K, Irie R;  
XX WPI; 2004-535376/52.  
XX N-PSDB; ADQ63436.  
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,  
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX Claim 1; SEQ ID NO 2785; 2449pp; English.  
XX The invention relates to 2495 novel polynucleotides (I) and their encoded  
XX polypeptides, sequences hybridizing to these nucleotides, sequences  
XX encoding partial polypeptides and sequences having 70% or 90% identity to  
XX the nucleotide and protein sequences. The nucleotides and polypeptides  
XX are useful as diagnostic markers or therapeutic target for the diseases  
XX or morbid states. They are also useful for treating osteoporosis,

CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,  
CC dementia and various cancers. This sequence corresponds to a protein  
CC sequence of the invention.  
XX Sequence 473 AA;  
Query Match 60.8%; Score 2467; DB 8; Length 473;  
Beat Local Similarity 99.8%; Pred. No. 4.8e-161;  
Matches 472; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 290 MRSPLPSNGELDPDVLSEWASIGCFDRERLHRELSEENQEKMIYLLLDKRYPSCE 349  
Db 1 MRSPLPSNGELDPDVLSEWASIGCFDRERLHRELSEENQEKMIYLLLDKRYPSCE 60  
Qy 350 DQDLPRNDVDPKRKRVDSPLSRHGKRRPERKSMVLSITDAGGGSPVPTTRALEMAQ 409  
Db 61 DQDLPRNDVDPKRKRVDSPLSRHGKRRPERKSMVLSITDAGGGSPVPTTRALEMAQ 120  
Qy 410 HSQRSRSVSGASTGLSSPLSPSPVFSFEPGAGDEARGGSPSTQTLPSRGRPG 469  
Db 121 HSQRSRSVSGASTGLSSPLSPSPVFSFEPGAGDEARGGSPSTQTLPSRGRPG 180  
Qy 470 GGAGEQPPPPSARSTPLPGPGSPRSSGGTPLHSPHTPRASTGTCTTTPPPSGGAGV 529  
Db 181 GGAGEQPPPPSARSTPLPGPGSPRSSGGTPLHSPHTPRASTGTCTTTPPPSGGAGV 240  
Qy 530 GAAWRLNSIRNSFLGSPRFRHRRKQVPTAEEMSSLTPSESPELAKRWGFIQLDKE 589  
Db 241 GAAWRLNSIRNSFLGSPRFRHRRKQVPTAEEMSSLTPSESPELAKRWGFIQLDKE 300  
Qy 590 EQIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLSQTSFRAEYKASGGSPVOKPVRFOV 649  
Db 301 EQIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLSQTSFRAEYKASGGSPVOKPVRFOV 360  
Qy 650 DISSSEGPSPRRDGGGGGIYSVTFTLISGFSRRFKRVVETIQALLSTHDQPSVQAL 709  
Db 361 DISSSEGPSPRRDGGGGGIYSVTFTLISGFSRRFKRVVETIQALLSTHDQPSVQAL 420  
Qy 710 ADEKGAQTRPAGAPPSLQPPGRDPPELSSPRGPPKDKLLATNGTPLP 762  
Db 421 ADEKGAQTRPAGAPPSLQPPGRDPPELSSPRGPPKDKLLATNGTPLP 473

RESULT 15  
ADR50797 standard; protein; 766 AA.  
XX ADR50797;  
XX 18-NOV-2004 (first entry)  
XX Human c-bramy3018357 protein kinase SeqID 20.  
XX human, enzyme; kinase; screening method; hepatic carcinoma; renal cancer;  
XX testis cancer; hepatitis; liver cirrhosis; nephritis; diabetes;  
XX inflammatory disease.  
XX Homo sapiens.  
XX WO2004074485-A1.  
XX 02-SEP-2004.  
XX 24-FEB-2004; 2004WO-JP002133.  
XX 24-FEB-2003; 2003JP-00046606.  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX (ZORG-) ZOEGENE CORP.  
XX Isogai T, Sugiyama T, Wakamatsu A, Irie R, Ishii S, Kawai K;  
PI Kajl T, Nakajima M, Miyama N, Kishimoto T, Kondo J;  
XX

DR WPI: 2004-652962/63.  
DR N-PSDB; ADR50785.  
XX Novel protein having kinase activity, useful for diagnosing diseases e.g.  
PT hepatic carcinoma, renal cancer, testis cancer, hepatitis, liver  
PT cirrhosis, nephritis, diabetes or inflammatory disease.  
XX  
PS Claim 1; SEQ ID NO 20; 288pp; Japanese.  
XX  
CC This invention relates to novel isolated nucleic acid molecules that  
CC encode proteins with a kinase activity. Specifically, it refers to the  
CC analysis of cDNA clones contained within a full length cDNA library and  
CC the identification of the physiological activity of the encoded protein  
CC thereof. The present invention describes a recombinant vector and host  
CC cell for expression of the nucleic acids of interest, as well as  
CC antisense oligos and antibodies that can be used to modulate expression  
CC and neutralise kinase activity respectively. In particular, these  
CC proteins can be used for screening regulatory substances in order to  
CC detect and measure a change in kinase activity. Accordingly, these can be  
CC developed into pharmaceutical compositions that are useful for diagnosing  
CC diseases such as hepatic carcinoma, renal cancer, testis cancer,  
CC hepatitis, liver cirrhosis, nephritis, diabetes or inflammatory disease.  
CC This polypeptide sequence is an exemplary human kinase protein of the  
CC invention.  
XX  
SQ Sequence 766 AA;  
Query Match 59.2%; Score 2400; DB 8; Length 766;  
Best Local Similarity 68.5%; Pred. No. 3.5e-156;  
Matches 475; Conservative 59; Mismatches 65; Indels 94; Gaps 10;  
QY 89 FRYLVLEHVSQGEFLDYLVKKGRITPKEARFFQIVSALDFCHSYICHRLDAPENLLL 148  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 136  
YLVLVLEHVSQGEFLDYLVKKGRITPKEARFFQIIISALDFCHSHICHRLDAPENLLL 195  
QY 149 DEKNRIADFGMASLQVDSLLTSCGSPHYACPEVTKGKYDGRADMWCGVILFAL 208  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 196  
DEKNRIADFGMASLQVDSLLTSCGSPHYACPEVIRGEKYDGRADVWSCGVILFAL 255  
QY 209 LVGALPFDDNNLRQLLEKVRGVFMPHFIPDCQSLLRGMIEVEPEKRLSLEQIQHPW 268  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 256  
LVGALPFDDNNLRQLLEKVRGVFMPHFIPDCQSLLRGMIEVDAAARLTLEHIQHHW 315  
QY 269 YLGKKEPDPCLPEAPGRVAVMSLPSNGELDPVLESMAISLGCPRERLHRLRSEEE 328  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 316  
YIGKNEPEP-EQIP-P-KVQIRSLPSLEDIDPDVLSMHSLSGCFDRNKLQDLLSEEE 373  
QY 329 NQEKMIYLLLDKRYPSCEDQLPRNDVDPKRVDSPLSHGKRPRPERKSMVLS 388  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 374  
NQEKMIYLLLDKRYPSQEDQLPRNEIDPPKRVDSPLNLRHGRKRPRPERKSMVLS 433  
QY 389 ITDAGGGGSPVPTRRALMAHQSRSVSGASTGLSSPLSSPSRSPVFSPEPGAGDE 448  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 434  
VTD---GGSPVARRAEMAHQGRSRSISGASSGLSTSPSSPR-----TPVHTP 475  
QY 449 ARGCGSPSTKQTPLPSRPGGAGEPPPPSARSTPLPGPGSPRSGGTFPLHSPLHTP 508  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 476  
-----VTPHPSRGSPLTPKG-----TPVHTP 498  
QY 509 RASPTGTPTTPPSGGVGAARSLNSIRNSFLGSPFRHRRKMQVPTAEEMSSILTP 568  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 499  
KESPAQTNPPTPPSSP--SVGGVPWRLNLSIRNSFLGSPFRHRRKMQVPTPEEMSNLTP 556  
QY 569 ESSPELAKRSWFGNFIISLDEEQIFVLKDKKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 557  
ESSPELAKRSWFGNFIISLDEEQIFVVKDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 616  
QY 629 RAEYKASGGSPVQKVRVQVDISSESGPEPSPRDGGGGGIYSVFTTLISGSPRRFKR 688  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 617  
RAEYKATGGPAVQKVRVQVDITVTEGGEAQKE-----NGIYSVFTTLISGSPRRFKR 670  
QY 689 VVETIQALLSTHDPQSVQALA-----DEKNGAQTRPAGAPPR-----726  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 671 VVETIQALLSTHDPQSVQALA-----DEKNGAQTRPAGAPPR 730  
QY 727 -----SLQPPPG--RPDPSELSSSPRRGPPKDKK 752  
Db 731 LGDSAAAGPGPGGDAEYPTGKDTAKMGPTARR 763  
Search completed: February 17, 2005, 10:44:25  
Job time : 183 secs

This Page Blank (uspto)



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2005, 10:39:03 ; Search time 47 Seconds  
(without alignments)  
1210.268 Million cell updates/sec

Title: US-10-803-277-4

Perfect score: 4056

Sequence: 1 MGLEFGFLEAGGNWSHPLPG.....PRRGPPKDKLLATNGTPLP 762

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4056	100.0	762	4	US-10-116-326-4
2	3545	87.4	703	4	US-10-116-326-6
3	3545	87.4	778	4	US-10-116-326-2
4	3545	87.4	778	4	US-10-003-690-2
5	2390.5	58.9	585	4	US-09-930-181-4
6	2386.5	58.8	668	4	US-09-930-181-2
7	2381.5	58.7	603	4	US-09-930-181-17
8	637	15.7	691	4	US-09-949-016-8255
9	637	15.7	691	4	US-09-949-016-8256
10	636	15.7	724	4	US-09-984-890-2
11	636	15.7	724	4	US-10-274-194-2
12	636	15.7	745	4	US-09-523-849-36
13	631	15.6	722	4	US-09-984-890-4
14	631	15.6	722	4	US-10-274-194-4
15	629	15.5	722	4	US-08-817-832B-32
16	610	15.0	724	4	US-09-949-016-8234
17	608	15.0	713	4	US-09-538-092-1022
18	608	15.0	713	4	US-09-949-016-6214
19	606	14.9	729	2	US-08-677-298-2
20	606	14.9	729	4	US-08-523-849-33
21	604	14.9	776	4	US-09-523-849-34
22	603.5	14.9	602	4	US-09-949-016-7417
23	603.5	14.9	602	4	US-09-949-016-7418
24	602	14.8	1203	4	US-09-799-875-5
25	595	14.7	793	4	US-09-523-849-32
26	593	14.6	511	4	US-08-633-328B-4
27	589	14.5	511	4	US-09-633-328B-2

28	579	14.3	149	4	US-09-930-181-18	Sequence 18, Appl
29	577.5	14.2	779	4	US-08-817-832B-31	Sequence 31, Appl
30	569.5	14.0	360	4	US-09-248-796A-20497	Sequence 20497, A
31	564	13.9	915	4	US-09-538-092-63	Sequence 63, Appl
32	551.5	13.6	557	4	US-09-949-016-10174	Sequence 10174, A
33	548.5	13.5	552	4	US-09-538-092-1212	Sequence 1212, Ap
34	548.5	13.5	552	4	US-09-824-735-4	Sequence 4, Appli
35	545.5	13.4	521	4	US-09-949-016-7570	Sequence 7570, Ap
36	542.5	13.4	552	3	US-08-557-006C-40	Sequence 40, Appl
37	541	13.3	633	3	US-08-557-006C-43	Sequence 43, Appl
38	541	13.3	633	4	US-09-538-092-1212	Sequence 212, App
39	541	13.3	633	4	US-09-633-328B-3	Sequence 3, Appli
40	541	13.3	633	4	US-09-824-735-3	Sequence 3, Appli
41	539.5	13.3	345	3	US-09-101-146-1	Sequence 1, Appli
42	533	13.1	257	3	US-09-101-146-6	Sequence 6, Appli
43	531.5	13.1	604	4	US-09-523-849-35	Sequence 35, Appl
44	502.5	12.4	418	4	US-09-248-796A-18441	Sequence 18441, A
45	494.5	12.2	257	2	US-07-857-224B-25	Sequence 25, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-116-326-4

; Sequence 4, Application US/10116326

; Patent No. 6777545

; GENERAL INFORMATION:

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Mathur, Brian

; APPLICANT: Friddle, Carl Johan

; TITLE OF INVENTION: No. 6777545sel Human Kinases and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0332-USA

; CURRENT APPLICATION NUMBER: US/10116,326

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,036

; PRIOR FILING DATE: 2001-04-06

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 762

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-116-326-4

Query Match 100.0%; Score 4056; DB 4; Length 762;  
Best Local Similarity 100.0%; Pred. No. 5.7e-266;  
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGLEFGFLEAGGNWSHPLPGSDGNWNFLPFGINGNWSLFLPGTHGNWSLFLPRIMGIGVL	60
Db	1	MGLEFGFLEAGGNWSHPLPGSDGNWNFLPFGINGNWSLFLPGTHGNWSLFLPRIMGIGVL	60
Qy	61	CHQEPVEVGDEALWSSSTCPQSPAPSSFRYLVLHVHSGGELFDYLVKKGRLTPKEARKF	120
Db	61	CHQEPVEVGDEALWSSSTCPQSPAPSSFRYLVLHVHSGGELFDYLVKKGRLTPKEARKF	120
Qy	121	FRQIVSALDCHSYISICHRDLKPENLLDKNNIRIADFGWASLQVGSLLLETSCGSPHY	180
Db	121	FRQIVSALDCHSYISICHRDLKPENLLDKNNIRIADFGWASLQVGSLLLETSCGSPHY	180
Qy	181	ACPEVIKGEYDGRADMWSCGVILFALLVGALPFDNNLRQLLEKVKRGVFMHPHFIPP	240
Db	181	ACPEVIKGEYDGRADMWSCGVILFALLVGALPFDNNLRQLLEKVKRGVFMHPHFIPP	240
Qy	241	DCQSLRGMTVEVEPEKRLSLEQIKHPWYLGCKHEPDCLEPAPGRVAMRSLPSNGELD	300
Db	241	DCQSLRGMTVEVEPEKRLSLEQIKHPWYLGCKHEPDCLEPAPGRVAMRSLPSNGELD	300
Qy	301	PDVLESNASLGCPRDRRLHRELSEENQEKMIYYILLDRKERYPSCEDQLPDRNDVD	360
Db	301	PDVLESNASLGCPRDRRLHRELSEENQEKMIYYILLDRKERYPSCEDQLPDRNDVD	360

```
QY 361 PPRKRVDSPLSRHGKRRPERKSMVLSITDAGGGSPVTRRALEMAQHSQSRVSQA 420
Db 361 PPRKRVDSPLSRHGKRRPERKSMVLSITDAGGGSPVTRRALEMAQHSQSRVSQA 420
QY 421 STGLSSPLSSPRSPVFSFEPGAGDEARGGSPSTKTQTLPSRGRGGGAGEQPPPPS 480
Db 421 STGLSSPLSSPRSPVFSFEPGAGDEARGGSPSTKTQTLPSRGRGGGAGEQPPPPS 480
QY 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTPPTPPPGGAGVGAARSLNSI 540
Db 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTPPTPPPGGAGVGAARSLNSI 540
QY 541 RNSFLGSPRHRKMQVPTAEEMSSLTPESSPELAKRSWFGNFISLDKEQIFLVLDKDP 600
Db 541 RNSFLGSPRHRKMQVPTAEEMSSLTPESSPELAKRSWFGNFISLDKEQIFLVLDKDP 600
QY 601 LSIKADIVHAFSLPSLSHVSLSQTSFRAEYKASGSPSVFKPVRFOVDISSSEGEPS 660
Db 601 LSIKADIVHAFSLPSLSHVSLSQTSFRAEYKASGSPSVFKPVRFOVDISSSEGEPS 660
QY 661 PRDGGGGGIYSVTFTLISGPRRRFRVVTETIOAQLLSTHDSVQALADEKNGAOTRP 720
Db 661 PRDGGGGGIYSVTFTLISGPRRRFRVVTETIOAQLLSTHDSVQALADEKNGAOTRP 720
QY 721 AGAPRSLQPPGRDPDELSSSPRRGPKDKLLATNGTLP 762
Db 721 AGAPRSLQPPGRDPDELSSSPRRGPKDKLLATNGTLP 762

RESULT 2
US-10-116-326-6
; Sequence 6, Application US/10116326
; Patent No. 6777545
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 703
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-116-326-6

Query Match 87.4%; Score 3545; DB 4; Length 703;
Best Local Similarity 99.7%; Pred. No. 1.7e-231;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 89 FRYLVLEHVS GGELFDYLVKKGRITPKARKFFRQIVSALDFCHSYSICHRLDKPENLLL 148
Db 30 YLYLVLEHVS GGELFDYLVKKGRITPKARKFFRQIVSALDFCHSYSICHRLDKPENLLL 89
QY 149 DEKNIRIADFGMASLQVGSLSLETSCGSPHYACPEVIKGEKYDGRADWMSCGVILFAL 208
Db 90 DEKNIRIADFGMASLQVGSLSLETSCGSPHYACPEVIKGEKYDGRADWMSCGVILFAL 149
QY 209 LVGALPDDNNLRLLLEKVKRGVFMHPHFTPPDCQSLRGMIEVEPEKRLSLEQIQHPW 268
Db 150 LVGALPDDNNLRLLLEKVKRGVFMHPHFTPPDCQSLRGMIEVEPEKRLSLEQIQHPW 209
QY 269 YLGKKEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLGCFRDRRLHRLRESEEE 328
Db 210 YLGKKEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLGCFRDRRLHRLRESEEE 269
QY 329 NOEKMIYLLDRKERYPSCEDQDLPVRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388
Db 329 NOEKMIYLLDRKERYPSCEDQDLPVRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388
```

```
Db 270 NOEKMIYLLDRKERYPSCEDQDLPVRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 329
QY 389 ITDAGGGSPVTRRALEMAQHSQSRVSQTSGLSSPLSSPRSPVFSFEPGAGDE 448
Db 330 ITDAGGGSPVTRRALEMAQHSQSRVSQTSGLSSPLSSPRSPVFSFEPGAGDE 389
QY 449 ARGGGSPSTKTQTLPSRGRGGGAGEQPPPGARSTPLPGPGSPRSSGGTPLHSPHT 508
Db 390 ARGGGSPSTKTQTLPSRGRGGGAGEQPPPGARSTPLPGPGSPRSSGGTPLHSPHT 449
QY 509 RASPTGTPPTPPPGGAGVGAARSLNSIRNSFLGSPRHRKMQVPTAEEMSSLT 568
Db 450 RASPTGTPPTPPPGGAGVGAARSLNSIRNSFLGSPRHRKMQVPTAEEMSSLT 509
QY 569 ESSPELAKRSWFGNFISLDKEQIFLVLDKDPKLLSIKADIVHAFSLPSLSHVSLSQTSF 628
Db 510 ESSPELAKRSWFGNFISLDKEQIFLVLDKDPKLLSIKADIVHAFSLPSLSHVSLSQTSF 569
QY 629 RAEYKASGSPSVFKPVRFOVDISSSEGEPEPRRDGGGGGIYSVTFTLISGPRRRFKR 688
Db 570 RAEYKASGSPSVFKPVRFOVDISSSEGEPEPRRDGGGGGIYSVTFTLISGPRRRFKR 629
QY 689 VVETIOAQLLSTHDSVQALADEKNGAOTRPAQAPRSLQPPGRDPDELSSSPRRGPP 748
Db 630 VVETIOAQLLSTHDSVQALADEKNGAOTRPAQAPRSLQPPGRDPDELSSSPRRGPP 689
QY 749 KDKKLLATNGTLP 762
Db 690 KDKKLLATNGTLP 703

RESULT 3
US-10-116-326-2
; Sequence 2, Application US/10116326
; Patent No. 6777545
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 778
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-116-326-2

Query Match 87.4%; Score 3545; DB 4; Length 778;
Best Local Similarity 99.7%; Pred. No. 2e-231;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 89 FRYLVLEHVS GGELFDYLVKKGRITPKARKFFRQIVSALDFCHSYSICHRLDKPENLLL 148
Db 105 YLYLVLEHVS GGELFDYLVKKGRITPKARKFFRQIVSALDFCHSYSICHRLDKPENLLL 164
QY 149 DEKNIRIADFGMASLQVGSLSLETSCGSPHYACPEVIKGEKYDGRADWMSCGVILFAL 208
Db 165 DEKNIRIADFGMASLQVGSLSLETSCGSPHYACPEVIKGEKYDGRADWMSCGVILFAL 224
QY 209 LVGALPDDNNLRLLLEKVKRGVFMHPHFTPPDCQSLRGMIEVEPEKRLSLEQIQHPW 268
Db 225 LVGALPDDNNLRLLLEKVKRGVFMHPHFTPPDCQSLRGMIEVEPEKRLSLEQIQHPW 284
QY 269 YLGKKEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLGCFRDRRLHRLRESEEE 328
Db 285 YLGKKEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLGCFRDRRLHRLRESEEE 344
```

```
Qy 329 NOEKMIYYLLLDKERYPSCEDQDLPPRNDVDPPRKRVDSPMLSRHGKRRPERKSMVLS 388
Db 345 NOEKMIYYLLLDKERYPSCEDQDLPPRNDVDPPRKRVDSPMLSRHGKRRPERKSMVLS 404
Qy 389 ITDAGGGSPVPTRRALMAQHSQSRSSVSGASTGLSSSPSSPLSSPRSPVFSFSPGAGDE 448
Db 405 ITDAGGGSPVPTRRALMAQHSQSRSSVSGASTGLSSSPSSPLSSPRSPVFSFSPGAGDE 464
Qy 449 ARGGGSPSTKTQTLPSRGRGGAGQQPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 508
Db 465 ARGGGSPSTKTQTLPSRGRGGAGQQPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 524
Qy 509 RASPTGTPGTTPPSPCGGVGGAAWRSLRSLRNSFLGSRFRHRRKQVPTAEEMSLTP 568
Db 525 RASPTGTPGTTPPSPCGGVGGAAWRSLRSLRNSFLGSRFRHRRKQVPTAEEMSLTP 584
Qy 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
Db 585 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644
Qy 629 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGIYSVTFTLISGFSRFRKR 688
Db 645 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGIYSVTFTLISGFSRFRKR 704
Qy 689 VVETIOALLSTHDQPSVQALADEKGAQTRPAGAPRSLQPPGRDPDELSSSPRGPP 748
Db 705 VVETIOALLSTHDQPSVQALADEKGAQTRPAGAPRSLQPPGRDPDELSSSPRGPP 764
Qy 749 KDKKLLATNGTPLP 762
Db 765 KDKKLLATNGTPLP 778
```

## RESULT 4

```
US-10-003-690-2
; Sequence 2, Application US/10003690
; Patent No. 6787345
; GENERAL INFORMATION:
; APPLICANT: RORY A.J. CURTIS
; TITLE OF INVENTION: 55053, A No. 6787345el Human Eukaryotic Kinase
; FILE REFERENCE: WNI-206
; CURRENT APPLICATION NUMBER: US/10/003,690
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/248,893
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-690-2
```

```
Query Match 87.4%; Score 3545; DB 4; Length 778;
Best Local Similarity 99.7%; Pred. No. 2e-231;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 89 FRYLVLEHVS GGELFDYLVKKGRLLTPKEARFFRQIVSALDFCHSYISICHRDLKPENLLL 148
Db 105 YLYLVLEHVS GGELFDYLVKKGRLLTPKEARFFRQIVSALDFCHSYISICHRDLKPENLLL 164
Qy 149 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADWMSGVILFAL 208
Db 165 DEKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADWMSGVILFAL 224
Qy 209 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEQIQKHPW 268
Db 225 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEQIQKHPW 284
Qy 269 YLGKHEPDDCLEPAGRRVAMRSLPSNGELDPDVLDSMASLGCFRDRERLHRELSEEE 328
Db 285 YLGKHEPDDCLEPAGRRVAMRSLPSNGELDPDVLDSMASLGCFRDRERLHRELSEEE 344
```

```
Qy 329 NOEKMIYYLLLDKERYPSCEDQDLPPRNDVDPPRKRVDSPMLSRHGKRRPERKSMVLS 388
Db 345 NOEKMIYYLLLDKERYPSCEDQDLPPRNDVDPPRKRVDSPMLSRHGKRRPERKSMVLS 404
Qy 389 ITDAGGGSPVPTRRALMAQHSQSRSSVSGASTGLSSSPSSPLSSPRSPVFSFSPGAGDE 448
Db 405 ITDAGGGSPVPTRRALMAQHSQSRSSVSGASTGLSSSPSSPLSSPRSPVFSFSPGAGDE 464
Qy 449 ARGGGSPSTKTQTLPSRGRGGAGQQPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 508
Db 465 ARGGGSPSTKTQTLPSRGRGGAGQQPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 524
Qy 509 RASPTGTPGTTPPSPCGGVGGAAWRSLRSLRNSFLGSRFRHRRKQVPTAEEMSLTP 568
Db 525 RASPTGTPGTTPPSPCGGVGGAAWRSLRSLRNSFLGSRFRHRRKQVPTAEEMSLTP 584
Qy 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
Db 585 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644
Qy 629 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGIYSVTFTLISGFSRFRKR 688
Db 645 RAEYKASGGSPVFOKPVRFQVDISSSEGGPSPRRDGGGGIYSVTFTLISGFSRFRKR 704
Qy 689 VVETIOALLSTHDQPSVQALADEKGAQTRPAGAPRSLQPPGRDPDELSSSPRGPP 748
Db 705 VVETIOALLSTHDQPSVQALADEKGAQTRPAGAPRSLQPPGRDPDELSSSPRGPP 764
Qy 749 KDKKLLATNGTPLP 762
Db 765 KDKKLLATNGTPLP 778
```

## RESULT 5

```
US-09-930-181-4
; Sequence 4, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: ORIGENE Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-181-4
```

```
Query Match 58.9%; Score 2390.5; DB 4; Length 585;
Best Local Similarity 74.4%; Pred. No. 1.4e-153;
Matches 465; Conservative 51; Mismatches 44; Indels 65; Gaps 7;
```

```
Qy 90 RYLVLEHVS GGELFDYLVKKGRLLTPKEARFFRQIVSALDFCHSYISICHRDLKPENLLL 149
Db 8 RYLVLEHVS GGELFDYLVKKGRLLTPKEARFFRQIVSALDFCHSYISICHRDLKPENLLL 67
Qy 150 EKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADWMSGVILFAL 209
Db 68 EKNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEYDGRADWMSGVILFAL 127
Qy 210 VGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEQIQKHPW 269
Db 128 VGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCSSLRGMIEVEPEKRLSLEQIQKHPW 187
Qy 270 LGKHEPDDCLEPAGRRVAMRSLPSNGELDPDVLDSMASLGCFRDRERLHRELSEEN 329
Db 188 ICKNPEEP-EQIP-RKVIRSLPSLEDDIPDVLDSMHSLGCFRDRKLLQDLSSEEN 245
Qy 330 QEKMIYYLLLDKERYPSCEDQDLPPRNDVDPPRKRVDSPMLSRHGKRRPERKSMVLSI 389
```

449 ARGGSPTSXTQTLPSRGRGGAGBQPPPPSARSTPLPPOPPGSPRSSGGTPLHSLHTP 508  
 430 -----VTPHPSRGSPLTPKG-----TPVHTP 452  
 509 RASPTGPTTTPPPSGGGVGGAAWRSRLNSIRNSFLGSPFRHRRKMVPTAEMSSLT 568  
 453 KESDAGTNPPTPSSP--SVGGVPMRRLNSIKNSFLGSPFRHRRKLQVPTPEMNLTP 510  
 569 ESSPELAKRSWFGNFISLDKEQIFLVLDKPLSSIKADIVHAFLSIPSLSHVLSQTSF 628  
 511 ESSPELAKRSWFGNFISLDKEQIFLVLDKPLSSIKADIVHAFLSIPSLSHVLSQTSF 570  
 629 RAEYKASGSPVFOKPVRFQVDISSSEGPSPRDRGSGGGIYSVTFTLISGSPRFRK 688  
 571 RAEYKATGPAVFOKPVRFQVDITYTEGGEAQE-----NGIYSVTFTLLSGSPRFRK 624  
 689 VVETIOALLSTHDQPSVQALADEKN 714  
 625 VVETIOALLSTHDQPSVQALADEKN 650  
 RESULT 7  
 US-09-930-181-17  
 ; Sequence 17, Application US/09930181  
 ; Patent No. 6455292  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Origene Technologies  
 ; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas  
 ; FILE REFERENCE: 16U 101 V1  
 ; CURRENT APPLICATION NUMBER: US/09/930,181  
 ; CURRENT FILING DATE: 2001-08-16  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 17  
 ; LENGTH: 603  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-930-181-17  
 Query Match 58.7%; Score 2381.5; DB 4; Length 603;  
 Best Local Similarity 71.8%; Pred. No. 6.1e-153;  
 Matches 468; Conservative 53; Mismatches 46; Indels 85; Gaps 9;

246 QEKMIYFLLLDKRYEYPSQEDDLPPRNEIDPPRKVDSPMLNRHKKRPERKSMVEVLSV 305  
 390 TDAGGGSPVPTTRALEMAHQRSVSAGASTGLSSSLSPSPRSPVFSFSPGAGDEA 449  
 306 TD---GGSPVARRALEMAHQRSISISGASGLSTSLSSPR-----TPVHTPK 370  
 450 RGGGSPTSXTQTLPSRGRGGAGBQPPPPSARSTPLPPOPPGSPRSSGGTPLHSLHTP 509  
 347 -----VTPHPSRGSPLTPKG-----TPVHTPK 370  
 510 ASPTGPTTTPPPSGGGVGGAAWRSRLNSIRNSFLGSPFRHRRKMVPTAEMSSLTPE 569  
 371 ESPAGTNPPTPSSP--SVGGVPMRRLNSIKNSFLGSPFRHRRKLQVPTPEMNLTP 510  
 570 SSPELAKRSWFGNFISLDKEQIFLVLDKPLSSIKADIVHAFLSIPSLSHVLSQTSF 628  
 429 SSPELAKRSWFGNFISLDKEQIFLVLDKPLSSIKADIVHAFLSIPSLSHVLSQTSF 488  
 630 RAEYKASGSPVFOKPVRFQVDISSSEGPSPRDRGSGGGIYSVTFTLISGSPRFRK 688  
 489 RAEYKATGPAVFOKPVRFQVDITYTEGGEAQE-----NGIYSVTFTLLSGSPRFRK 542  
 690 VVETIOALLSTHDQPSVQALADEKN 714  
 543 VVETIOALLSTHDQPSVQALADEKN 567  
 RESULT 6  
 US-09-930-181-2  
 ; Sequence 2, Application US/09930181  
 ; Patent No. 6455292  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Origene Technologies  
 ; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas  
 ; FILE REFERENCE: 16U 101 V1  
 ; CURRENT APPLICATION NUMBER: US/09/930,181  
 ; CURRENT FILING DATE: 2001-08-16  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 668  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-930-181-2  
 Query Match 58.8%; Score 2386.5; DB 4; Length 668;  
 Best Local Similarity 74.1%; Pred. No. 3.2e-153;  
 Matches 464; Conservative 52; Mismatches 45; Indels 65; Gaps 7;

```
Db 382 KESPACTPNTPPSP--SUGGVFWRLKNSIKNSFLSGPRFHRKQVPTPEMSNLTP 439
Qy 569 ESSPELAKRSWFGNFIISLDKEQIFLVLDKDKPLSSIKADIVHAFSLSPSLSHSLSQTSF 628
Db 440 ESSPELAKRSWFGNFIISLDKEQIFLVLDKDKPLSSIKADIVHAFSLSPSLSHSLSQTSF 499
Qy 629 RAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGGGGGIIYVTFLLISGSRPRKR 688
Db 500 RAEYKATGGPAVFOKPVRFQVDITYTEGGEAQKE-----NGIYSVTFLLISGSRPRKR 553
Qy 689 VVETIQALLSTHDPQSVQALADEKNGAQTRPAGAPPRSLQPPRGRDPDELS 740
Db 554 VVETIQALLSTHDPQAAQHL-----EPPP--PAGLS 585

RESULT 8
US-09-949-016-8255
; Sequence 8255, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8255
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8255

Query Match 15.7%; Score 637; DB 4; Length 691;
Best Local Similarity 29.3%; Pred. No. 5.6e-35;
Matches 197; Conservative 93; Mismatches 241; Indels 142; Gaps 24;

Qy 91 YLVLEHVSGBGLFDYLVKKGRLTPKEARKFPRQIVSALDFCHSYICHRLKPNLLIDE 150
Db 93 YLVMEYASGGVEFDYLVHAGRMKEKARAKFQIVSAVOYCHQKFIHVHDLKAENLLDA 152
Qy 151 KNNIRIADFGWASLQVDSLETSCGSPHYACPEVIGKGYDGRADWMSGCVILFALLV 210
Db 153 DMNIIKADFGSNEFTFGNKLDTFCGSPPYAAPELFQKKYDGPVDVMSGLVILYTLVS 212
Qy 211 GALPDDNNLRQLLEKVKRGVFMHPFI PDCOSLLRGMIEVEPEKLSLEQIOKHPWYL 270
Db 213 GSLPFDGQNLKELRVLRGKRIPIFYMTSDCNLLKKFLINPSKRGTLQIWKDRWN 272
Qy 271 GKGHEPD---PCLEPAPGRVAMRSLPNSGELDPVLSEMASLGCPRDRRLHRLRSEE 327
Db 273 VG-HEDELKPYEPLPDYK-----DPRTELVMVSMG--YTREIQDSLQVQR 317
Qy 328 ENQEKMIYLLDLRKERYPSCEDODLPPRNDVDPPRKVDSP--MLSRHGKRRPERKSM 385
Db 318 YN-EVMATYLLGLYKSSLEGGDTITLKPSPADLTNSAPSPSHKVQSVSANPKQRRF- 375
Qy 386 VLSITDAGGSGSPVPTTRALE---MAQHSQRSVSGASTGLSSPLSSPRSPVFSPE 442
Db 376 -----SDQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKAS--STAKVPA---SPL 424
Qy 443 PGAGDEARGGSGPTSKTTLPSRPGRGGAGEQPPPSARSTPL--PGPPGSPRSSGGTP 500
Db 425 PGL---ERKTTPTSTNSVLSTSTN-----RSRNSPLLRASLQASIQNGKD 470
```

```
Qy 501 LHSPLHTPRASPT-----GTPGTT-----PPp 522
Db 471 STAPQRFVFAVSAHNISSGGAPDRTNFPRGVSSRSTFHAGQLQRVDRDQONLPGVTPA 530
Qy 523 SPGGVGGAARGLNIRNSFLSGPRFHRKQVPTAEB--MSLTP----- 568
Db 531 SPGHSQGR--RGASGIFSKF--TSKEVRNLNEPESKDRVETLRPHVVGSGGNDKEKE 586
Qy 569 ---ESSPELAKRSW-FGNFISLDKEQIFLVLDKDKPLSSIKADIVHAFSLSPSLSHSLS 624
Db 587 EFREAKPRSLFTWSMKTSTSMENMRBIRKVLANSQSELHKEYMLL--CMHGTPG 644
Qy 625 QTSFRAEYKASGGPSVFOKPVRFQVDISSSEGPSPRRDGGGGGIIYVTFLLISGSR 684
Db 645 HEDF-----VQMEMEVCK-----LPRLSLNG-----VRPKRISGTSM 676

Qy 685 RFKRVVETIQAL 697
Db 677 AFKNIAISKIANEL 689

RESULT 9
US-09-949-016-8256
; Sequence 8256, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8256
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8256

Query Match 15.7%; Score 637; DB 4; Length 691;
Best Local Similarity 29.3%; Pred. No. 5.6e-35;
Matches 197; Conservative 93; Mismatches 241; Indels 142; Gaps 24;

Qy 91 YLVLEHVSGBGLFDYLVKKGRLTPKEARKFPRQIVSALDFCHSYICHRLKPNLLIDE 150
Db 93 YLVMEYASGGVEFDYLVHAGRMKEKARAKFQIVSAVOYCHQKFIHVHDLKAENLLDA 152
Qy 151 KNNIRIADFGWASLQVDSLETSCGSPHYACPEVIGKGYDGRADWMSGCVILFALLV 210
Db 153 DMNIIKADFGSNEFTFGNKLDTFCGSPPYAAPELFQKKYDGPVDVMSGLVILYTLVS 212
Qy 211 GALPDDNNLRQLLEKVKRGVFMHPFI PDCOSLLRGMIEVEPEKLSLEQIOKHPWYL 270
Db 213 GSLPFDGQNLKELRVLRGKRIPIFYMTSDCNLLKKFLINPSKRGTLQIWKDRWN 272
Qy 271 GKGHEPD---PCLEPAPGRVAMRSLPNSGELDPVLSEMASLGCPRDRRLHRLRSEE 327
Db 273 VG-HEDELKPYEPLPDYK-----DPRTELVMVSMG--YTREIQDSLQVQR 317
Qy 328 ENQEKMIYLLDLRKERYPSCEDODLPPRNDVDPPRKVDSP--MLSRHGKRRPERKSM 385
Db 318 YN-EVMATYLLGLYKSSLEGGDTITLKPSPADLTNSAPSPSHKVQSVSANPKQRRF- 375
Qy 386 VLSITDAGGSGSPVPTTRALE---MAQHSQRSVSGASTGLSSPLSSPRSPVFSPE 442
Db 376 -----SDQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKAS--STAKVPA---SPL 424
```

QY 443 PGAGDEARGGSGTSKQTLPSPRGGGAGEQPPPSARSTPL--PGPEGSPRSSGGTP 500  
DB 425 PGL---ERKKTTPSTNSVLSTSTN-----RSRNSPLLERASLGQASIQNGKD 470  
QY 501 LHSPLHTPRASPT-----GTFGTT-----PPP 522  
DB 471 STAPQRPVAPSAHNISSGGAPDRTPPRGVSSRSTFHAGQLQVRDQQLPYGVTEA 530  
QY 523 SPGGVGGAARSLRSLRNSFLGSPRFRHRKQVPTAE--MSSLTP-----568  
DB 531 SPGSHSQGR--RGASGSIKFK--TSKFVRNLNPEPKDRVETLRPHVVGSGNDKEKE 586  
QY 569 ---ESSPELAKRW-FGNFISLDKEQIFLVLDKPLSSIKADIVHAFISLPSLSHVSLS 624  
DB 587 EFREAKPRSLRFTSMKTTSSMEPNEMREIRKVLNDANSQSELHEKYMLL--CMHGTPG 644  
QY 625 QTSFRAEYKASGGSPVFQKPRFQVDISSSEGEPEPRDRDGGGGGYSVFTLLSGPSR 684  
DB 645 HEDF-----VQWEMEVC-----LPRLSLNG-----VRFKRISGTSM 676  
QY 685 RFKRVVETIOAQL 697  
DB 677 AFKNIAASKIANEL 689

## RESULT 10

US-09-984-890-2  
; Sequence 2, Application US/09984890  
; Patent No. 6492156  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001306  
; CURRENT APPLICATION NUMBER: US/09/984,890  
; CURRENT FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 724  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-984-890-2

Query Match 15.7%; Score 636; DB 4; Length 724;  
Best Local Similarity 29.1%; Pred. No. 6.9e-35;  
Matches 196; Conservative 94; Mismatches 241; Indels 142; Gaps 24;

QY 91 YLVLEHVGSGELFDYLVKKGRLTPKEARKFRQIVSALDFCHSYISCHRDLPENLLLDE 150  
DB 126 YLVMEYASGGEVFDYLVAGHMKKEARAKFRQVSAVQYCHQKFIHVDLKAENLLDA 185  
QY 151 KNNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKEKDGRRADWMSGCVILFALLV 210  
DB 186 DMNIIADFGSNEFTFGNKLDTFCGSPPYAAPLFCQKYYDGVDMVSLGVILYTLVS 245  
QY 211 GALPDDNNLRQLLEKVKRGVFMHPHFPDPCOSLLRGMIEVEPEKRLSLEQIOKHPWYL 270  
DB 246 GSLPFDGQNLKRLRVLRGKRIPIFYMTSDCNLLKKFLINFSKRGTLQIWKDRWN 305  
QY 271 GKGHEPD---PCLEPAPGRVAMRSLPSNGELDDPVLESMSLGCPRDRRLHRLRSEE 327  
DB 306 VG-HEDELKPYVEPLPDYK-----DPRTELWVSMG--YTRREIQDSLVGQR 350  
QY 328 ENQEKMIYVLLDRKERYPCEDQDLPRANDVDPKRVDSP--MLSRHGKRPERKSM 385  
DB 351 YN-EVMATYLLGLYKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVQSVSANPKQRRF- 408  
QY 386 VLSITDAGGSGSPVPTTRALE---MAQHSQRSRVSGASTGLSSPLSSPRSPVFSFPE 442  
DB 409 -----SDQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKAS--STAKVPA---SPL 457

QY 443 PGAGDEARGGSGTSKQTLPSPRGGGAGEQPPPSARSTPL--PGPPGSPRSSGGTP 500  
DB 458 PGL---ERKKTTPSTNSVLSTSTN-----RSRNSPLLERASLGQASIQNGKD 503  
QY 501 LHSPLHTPRASPT-----GTFGTT-----PPP 522  
DB 504 STAPQRPVAPSAHNISSGGAPDRTPPRGVSSRSTFHAGQLQVRDQQLPYGVTEA 563  
QY 523 SPGGVGGAARSLRSLRNSFLGSPRFRHRKQVPTAE--MSSLTP-----568  
DB 564 SPGSHSQGR--RGASGSIKFK--TSKFVRNLNPEPKDRVETLRPHVVGSGNDKEKE 619  
QY 569 ---ESSPELAKRW-FGNFISLDKEQIFLVLDKPLSSIKADIVHAFISLPSLSHVSLS 624  
DB 620 EFREAKPRSLRFTSMKTTSSMEPNEMREIRKVLNDANSQSELHEKYMLL--CMHGTPG 677  
QY 625 QTSFRAEYKASGGSPVFQKPRFQVDISSSEGEPEPRDRDGGGGGYSVFTLLSGPSR 684  
DB 678 HEDF-----VQWEMEVC-----LPRLSLNG-----VRFKRISGTSM 709  
QY 685 RFKRVVETIOAQL 697  
DB 710 AFKNIAASKIANEL 722

## RESULT 11

US-10-274-194-2  
; Sequence 2, Application US/10274194  
; Patent No. 6706511  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001306DIV  
; CURRENT APPLICATION NUMBER: US/10/274,194  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 724  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-274-194-2

Query Match 15.7%; Score 636; DB 4; Length 724;  
Best Local Similarity 29.1%; Pred. No. 6.9e-35;  
Matches 196; Conservative 94; Mismatches 241; Indels 142; Gaps 24;

QY 91 YLVLEHVGSGELFDYLVKKGRLTPKEARKFRQIVSALDFCHSYISCHRDLPENLLLDE 150  
DB 126 YLVMEYASGGEVFDYLVAGHMKKEARAKFRQVSAVQYCHQKFIHVDLKAENLLDA 185  
QY 151 KNNIRIADFGMASLQVGSLLTSCGSPHYACPEVIGKEKDGRRADWMSGCVILFALLV 210  
DB 186 DMNIIADFGSNEFTFGNKLDTFCGSPPYAAPLFCQKYYDGVDMVSLGVILYTLVS 245  
QY 211 GALPDDNNLRQLLEKVKRGVFMHPHFPDPCOSLLRGMIEVEPEKRLSLEQIOKHPWYL 270  
DB 246 GSLPFDGQNLKRLRVLRGKRIPIFYMTSDCNLLKKFLINFSKRGTLQIWKDRWN 305  
QY 271 GKGHEPD---PCLEPAPGRVAMRSLPSNGELDDPVLESMSLGCPRDRRLHRLRSEE 327  
DB 306 VG-HEDELKPYVEPLPDYK-----DPRTELWVSMG--YTRREIQDSLVGQR 350  
QY 328 ENQEKMIYVLLDRKERYPCEDQDLPRANDVDPKRVDSP--MLSRHGKRPERKSM 385  
DB 351 YN-EVMATYLLGLYKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVQSVSANPKQRRF- 408  
QY 386 VLSITDAGGSGSPVPTTRALE---MAQHSQRSRVSGASTGLSSPLSSPRSPVFSFPE 442  
DB 409 -----SDQAGPAIPTNSYSKKTQSNNAENKRPEDRESGRKAS--STAKVPA---SPL 457



328	Qy	ENQEKIYYILLDRKERYSCCEDODILPPRNDVD-----PPRKVD 367
318	Db	YN-EVMATYLLLYGKSELEGDITITLKPRPSADLTNSSAQFPGHKVQSVSANPKORRFS 376
368	Qy	S-----PMLSRHGK-----RRPE-----RKSM-----384
377	Db	DOAGPALPITSNSYSKKTOSNAENKPEEDRESGRKASSTAKVPASPLPGLERKKTTP 436
385	Qy	---EVLISITDAGGGGVPFTRRALEMA---QHSQRSSVSG---ASTGLSSSPLSPR---433
437	Db	STNSVLSTSTNTRGRNSPFLERASLGOASIQNGKDSLTPMGSRASSTASASAASVAAARPROH 496
434	Qy	--SPVSFSPEPCAGDEARGGSPSTKOTLPKRGP-----RGGCAGSQ---PPP 478
497	Db	QKMSASVHNKASGLPPTESNCEVPSPSTAPORVPVASPAHNISSSGGAPDRTNPRG 556
479	Qy	PSARSTPLPGPPGSPRSSGGTPLHSPHLTPRASPTGTPPPSPGGVGGGAARSLN 538
557	Db	VSSRSTFHAGLAQRVDQONLP-----GVT-PASPSGHSGQR--RCASG 598
539	Qy	SIRNSFLGSPRPHRRKMOVPTAE-MSSLTP-----ESSPELAKRSM-P 580
599	Db	SIFSKEF--TSKFFVRNLPNEPESKDRVETLPHVYVVGSGNDKEKEEFREAKPRSLRFTWSM 656
581	Qy	GNFISLIDKEBQIFVLVKDKPLSSIKADIVHAFSLIPSLSHSVLSQTSFRAEYKASGSPSV 640
657	Db	KTTSSMEPNEMWEIRKVLNDANSQSLEHKEYMLL--CHGTFQCHEDF-----702
641	Qy	FQKVPARQVDISSEGEPSPRDGGGGGIYVFTFLISGPRRRFKRVVETTAQL 697
703	Db	---VOWEMEVCK-----LPRLSLNG-----VRFKRIISGTSMAFNIAASKIANEL 743

```

      657  KTTSSMEPNMWEIRKVLNDANSCQSELHEKYMLL---CHGTFQGHEDF----- 702
      641  FQKVPRAFQVDISSGEGPEPSPRDDGGSGGGGIYVFTFLISGPPRRFRKRVVETQAOQL 697
      703  ---VQWEMEVCVCK-----LPRLSLNG-----VRFKRISGTSMAFKNIASKIANEL 743

RESULT 13
US-09-984-890-4
; Sequence 4, Application US/09984890
; Patent NO. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-984-890-4

```

Query Match	15.6%	Score 631;	DB 4;	Length 722;
Best Local Similarity	30.1%;	Pred. No. 1.5e-34;		
Matches 203;	Conservative	90;	Mismatches 235;	Indels 146;
Gaps	25;			
Qy	91	YLVLEHVSGGELDYLVKKGRLPTKEARKEFRQIVSALDFCHSYSI	CHRDLPENLLDE	150
Db	126	YLVMEYASGGVEFDYLVAHGMRKEKEARFRQIVSAVQYCHQKFI	VHRDLKAENLLDA	185
Qy	151	KNNIRIADFGWASLOVGDLSLETSCGSPHYACBEVIKGEKVDGERAD	WMSGVILFALLV	210
Db	186	DMNIKIADFGFSEFTFGNKLDTFCGSPPPYAAAPELFGKKYDGEVD	WMSGVILYITLVS	245
Qy	211	GALPFDNDNLRLLEKVKRGVFTMHPIIPDCQSLLRGMIEVPEKLSLE	QIQKHWPYL	270
Db	246	GSLPFDQNLKEURERVLRGKYRIPTFYMSTDCENLLKKFLLINPS	KGTLEQIMKDRWN	305
Qy	271	GKGHPD---PCLEPAGRRVAMRSLPSNGELPDVLESMASLCGCFRDR	RLHRLRSEE	327
Db	306	VG-HEDELKPYVEPLDYK-----DPRRTELMVSMD--YTREIIQDSLV	QVQR	350



QY 328 ENQEKMIYLLDRKERYPCSCDQDLPRLNDVD-----PPRKRVDS 368  
DB 351 YN-EVMATYLLGKYSSELEGDTITLKPRPSADLTNSAPSHPKHQVRSVANSKQRRSS 409  
QY 369 -----PMLSRHCK-----RRPERKSMVLSITDAGGGSPVPTTRALEMAHQSHQ 412  
DB 410 QDAVPAIPTNSYSKKTQSNNAENKPEBETGRKASST-AKVPAASPPLP-----GLD 459  
QY 413 RSRVSGASTG--LSSSPLSSPRSPVFSPEPAGDEARGGSPSTKTQTLPSRGP-- 467  
DB 460 RKKTPTPTNSVLSLTSTNRNSPLLD---RASLGQASIQNGKDSAPORVPVAPSAH 516  
QY 468 ---RGGGAGEQ---PPPPSARSTPLPGPPSPSSCGTPLHSPHLPTRASPTGPTTTP 521  
DB 517 NISSSGAPDRTNPPRGVSSRSTFHAGQLQRVDRQNLPE-----GVT-P 560  
QY 522 PSPGGVGGAAWRSRLNSIRNSPLGSPFRHRRKMQVPTAE-MSSLTP----- 568  
DB 561 ASPGHSQGR--RGASGSIFSKF--TSKFVRRNLNPEKSDRVETLPHVVGGGTDKEK 616  
QY 569 ----ESSPELAKRSM-FGNFISLDKEEQIFVLVKDKPLSSIKADIVHAFLSIPSLSHSVL 623  
DB 617 EEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDSQSELHERYMLL--CVHGTP 674  
QY 624 SOTSFRAYKASGSPVQKPRQVDIISSEGEPEPSRRDGGGGGIYSVFTFLISGSPS 683  
DB 675 GHENF-----VQWEMEVC-----LPRLSLNG-----VRPKRISGTS 706  
QY 684 RRFKRVVETIQAL 697  
DB 707 MAFKNIASKIANEL 720

## RESULT 14

US-10-274-194-4  
; Sequence 4, Application US/10274194  
; Patent No. 6706511  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001306DIV  
; CURRENT APPLICATION NUMBER: US/10/274,194  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 722  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-274-194-4

Query Match 15.6%; Score 631; DB 4; Length 722;  
Best Local Similarity 30.1%; Pred. No. 1.5e-34;  
Matches 203; Conservative 90; Mismatches 235; Indels 146; Gaps 25;  
QY 91 YLVLEHVSGLGELDYLVKKRLTPKEARKEFRQIVSALDFCHSVSICHRLDKPENLLDE 150  
DB 126 YLVNEVASGGEVFDYLVHAGRMKEKARFRQIVSAVQYCHQKFIHVRDLKAENLLDA 185  
QY 151 KNNIRIADFQWASIQVDSILLETSCGSPHYACPEVIKGEYDGRADRMWSCGVILFALLV 210  
DB 186 DMNIIKIDFGSNEFTGNKLDITFCGSPPPYAAPFLFGKDYDGPVDVWLSGLVILYTLVS 245  
QY 211 GALPFDNDNRQLLEKVRGVFHFPHFIPDPCOSLLRGMTEVPEPKLSLEQIKHPWYL 270  
DB 246 GSLPFDQNLKELRERVLGKIRIPFYMTSDCNLLKKFLILNPSKRGTLQIMKDRWN 305  
QY 271 GKGHEPD---PCLEPAPGRVAMRSLPSNGELPDVLESWASLGCPCDRDLRHRSEE 327  
DB 306 VG-HEDELKPYVEPLDYK-----DPRTELMSVWG--YTRIEIQDSLVGQR 350

Query Match 15.5%; Score 629; DB 4; Length 722;  
Best Local Similarity 30.1%; Pred. No. 2e-34;

QY 328 ENQEKMIYLLDRKERYPCSCDQDLPRLNDVD-----PPRKRVDS 368  
DB 351 YN-EVMATYLLGKYSSELEGDTITLKPRPSADLTNSAPSHPKHQVRSVANSKQRRSS 409  
QY 369 -----PMLSRHCK-----RRPERKSMVLSITDAGGGSPVPTTRALEMAHQSHQ 412  
DB 410 QDAVPAIPTNSYSKKTQSNNAENKPEBETGRKASST-AKVPAASPPLP-----GLD 459  
QY 413 RSRVSGASTG--LSSSPLSSPRSPVFSPEPAGDEARGGSPSTKTQTLPSRGP-- 467  
DB 460 RKKTPTPTNSVLSLTSTNRNSPLLD---RASLGQASIQNGKDSAPORVPVAPSAH 516  
QY 468 ---RGGGAGEQ---PPPPSARSTPLPGPPSPSSCGTPLHSPHLPTRASPTGPTTTP 521  
DB 517 NISSSGAPDRTNPPRGVSSRSTFHAGQLQRVDRQNLPE-----GVT-P 560  
QY 522 PSPGGVGGAAWRSRLNSIRNSPLGSPFRHRRKMQVPTAE-MSSLTP----- 568  
DB 561 ASPGHSQGR--RGASGSIFSKF--TSKFVRRNLNPEKSDRVETLPHVVGGGTDKEK 616  
QY 569 ----ESSPELAKRSM-FGNFISLDKEEQIFVLVKDKPLSSIKADIVHAFLSIPSLSHSVL 623  
DB 617 EEFREAKPRSLRFTWSMKTTSMEPNEMREIRKVLDSQSELHERYMLL--CVHGTP 674  
QY 624 SOTSFRAYKASGSPVQKPRQVDIISSEGEPEPSRRDGGGGGIYSVFTFLISGSPS 683  
DB 675 GHENF-----VQWEMEVC-----LPRLSLNG-----VRPKRISGTS 706  
QY 684 RRFKRVVETIQAL 697  
DB 707 MAFKNIASKIANEL 720

## RESULT 15

US-08-817-832B-32  
; Sequence 32, Application US/08817832B  
; Patent No. 6579691  
; GENERAL INFORMATION:  
; APPLICANT: MANDELKOW, Eckhard, et al.  
; TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 S. Wacker Drive, 6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: US  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,832B  
; FILING DATE: 28-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/04258  
; FILING DATE: 30-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94 11 7122.5  
; FILING DATE: 28-OCT-1994  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 722 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-817-832B-32

```
Matches 203; Conservative 90; Mismatches 235; Indels 146; Gaps 25;
Qy 91 YLVLHVSGLLEFDYLYKKGLTPEAKRPFQIVTSALDPCHSYISICHRODKPENLILDE 150
Db 126 YLVMEYASGGGVFDYLYVAHGRMKKEAKRPFQIVTSAVQYCHHKFIIVHDLKAENLLDA 185
Qy 151 KNNIRIADFGMASIQVGDLSLETSCGSPHYACPEVIGKEKYDGRRADWMSCGVILFALLV 210
Db 186 DMNIIADFGSNEFTGKLDTCGSPFYAAPLFGKKYDGVVDVWSLGVILYTLVS 245
Qy 211 GALPFDNDLRQLLEKVRGVFMHPFIPPCQSLLRGMIEVEPEKRLSLEQIQKHFWYL 270
Db 246 GSLPFDQNLKELRERVLRGKRYIPFYMTSTDCENLLKKFLILNPSKRGTLQIMKDRWN 305
Qy 271 GKKHEPD---PCLEPAPGRRVAMRSLPSNGELDDVLESMAISLCFDRRLHRLRSEE 327
Db 306 VG-HEDDELKPYVEPLDYK-----DPRRTLMVSMG--YTREEIQDSLVGQR 350
Qy 328 ENQEKMIYVYLLDRKERYPCEDQDLPRNDVD-----PPRKEVDS 368
Db 351 YN-EVMATYLLGLGYKSSELEGGDTITLKPRAADLTNSAFSPSHKVORSVSANPKQRSS 409
Qy 369 -----PMLSRHGK-----RRPERKSMEVLSITDAGGGGSPVPTRRALEMAQHSQ 412
Db 410 DQAVPAIPTNSYSYKTSQNNNAENKRPHEETGRKASST-AKVPASPLP-----GLD 459
Qy 413 RRSVSGASTG--LSSGPLSPRPFVSPFPEAGDEARGGSPSTKQTLPSRGP---467
Db 460 RKKTPTFTSTNSVLSTSTNRSRNSPLLD---RASLQOASIQNGKDXSTAPQRPVVASPSAH 516
Qy 468 ---RGGGAGEQ---PPPPSARSTPLGPPGSPRSSGGTPLHSLHTPRASFTGTGTPPP 521
Db 517 NISSSGAPORTNPRGVSSRSTFHAGQLRQVRDQQLPF-----GVT-P 560
Qy 522 PSPGGGVGAARSLNSIRNSFLGSPRFRHRKMQVPTAE-MSSLTP-----568
Db 561 ASPGHSQGR--RGPSGSIFSKF--TSKFVYRNLENEPESKDRVETLPHVVVGGGTDKEK 616
Qy 569 -----ESSPELAKRW-FGNFISLDKEEQIFLVKDKPLSLIKADIVHAFISIPLSHSVL 623
Db 617 EEFREAKPRSLRFTWSMKTTSSMEPNEMWREIRKVLDA NSCQSELHERYMLL--CVHGTP 674
Qy 624 SQTSPRAEYKASGGSPVQKPVRFQVDISSSEGEPEPSPRDGGCGGGIYSVTFLLISGPS 683
Db 675 GHENF-----VQWEMEVCX-----LPRLSLNG-----VRFKRISGTS 706
Qy 684 RRFKRVVETIQAO 697
Db 707 MAFKNIASKIANEL 720
```

Search completed: February 17, 2005, 11:04:18

Job time : 51 secs

This Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2005, 10:47:38 ; Search time 139 Seconds  
(without alignments)  
1793.940 Million cell updates/sec

Title: US-10-803-277-4  
Perfect score: 4056  
Sequence: 1 MGLEFGLEAGGNSHFLPG.....PRRGPPKXKLLATNGTFLP 762

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4056	100.0	762	14	US-10-116-326-4
2	4056	100.0	762	16	US-10-803-277-4
3	3545	87.4	703	14	US-10-116-326-6
4	3545	87.4	703	16	US-10-803-277-6
5	3545	87.4	778	14	US-10-354-358-92
6	3545	87.4	778	14	US-10-116-326-2
7	3545	87.4	778	15	US-10-423-543-11
8	3545	87.4	778	16	US-10-803-277-2
9	3545	87.4	778	16	US-10-757-262-136
10	3545	87.4	794	15	US-10-311-034-17
11	3362	82.9	754	16	US-10-479-532-1
12	2654	65.4	506	15	US-10-425-114-54189
13	2390.5	58.9	585	14	US-10-195-072-4

14	2390.5	58.9	585	14	US-10-195-071-4	Sequence 4, Appli
15	2387.5	58.9	674	14	US-10-283-247-2	Sequence 2, Appli
16	2387.5	58.9	674	16	US-10-618-941-78	Sequence 78, Appli
17	2386.5	58.8	608	13	US-10-054-579-4	Sequence 4, Appli
18	2386.5	58.8	664	15	US-10-288-798-18	Sequence 18, Appli
19	2386.5	58.8	664	15	US-10-362-892-18	Sequence 18, Appli
20	2386.5	58.8	668	13	US-10-054-579-2	Sequence 2, Appli
21	2386.5	58.8	668	14	US-10-195-072-2	Sequence 2, Appli
22	2386.5	58.8	668	14	US-10-195-071-2	Sequence 17, Appli
23	2381.5	58.7	603	14	US-10-195-072-17	Sequence 17, Appli
24	2381.5	58.7	603	14	US-10-195-071-17	Sequence 9, Appli
25	2381.5	58.7	614	14	US-10-283-247-9	Sequence 17, Appli
26	2381.5	58.7	614	14	US-10-283-247-10	Sequence 10, Appli
27	2381.5	58.7	614	9	US-09-842-582-2	Sequence 2, Appli
28	2381.5	58.7	674	14	US-10-283-247-7	Sequence 7, Appli
29	2381.5	58.7	674	14	US-10-283-247-8	Sequence 8, Appli
30	2366.5	58.3	636	14	US-10-283-247-5	Sequence 5, Appli
31	2366.5	58.3	688	15	US-10-425-114-54467	Sequence 54467, A
32	1043	25.7	204	15	US-10-276-774-2050	Sequence 2050, Ap
33	979	24.1	301	15	US-10-276-774-1422	Sequence 1422, Ap
34	677	16.7	1518	9	US-09-801-368-152	Sequence 152, App
35	677	16.7	1518	15	US-10-369-493-22243	Sequence 22243, A
36	677	16.7	1518	15	US-10-618-581-11	Sequence 11, Appli
37	657	16.2	1462	15	US-10-618-581-15	Sequence 15, Appli
38	648	16.0	1349	15	US-10-618-581-16	Sequence 16, Appli
39	648	16.0	1369	15	US-10-288-798-7	Sequence 7, Appli
40	648	16.0	1369	15	US-10-362-892-7	Sequence 2, Appli
41	643.5	15.9	783	9	US-09-815-915-2	Sequence 90, Appli
42	643.5	15.9	783	9	US-09-823-187-90	Sequence 2, Appli
43	643.5	15.9	783	14	US-10-393-316-2	Sequence 2, Appli
44	643.5	15.9	826	15	US-10-425-114-54182	Sequence 54182, A
45	637	15.7	691	9	US-09-919-585-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-10-116-326-4  
; Sequence 4, Application US/10116326  
; Publication No. US20030166889A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. US20030166889A1el Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0332-USA  
; CURRENT APPLICATION NUMBER: US/10/116,326  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/282,036  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 762  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-116-326-4

Query Match	100.0%	Score	4056	DB	14	Length	762
Best Local Similarity	100.0%	Pred. NO.	1e-203				
Matches	762	Conservative	0	Mismatches	0	Indels	0
		Gaps	0				
Qy	1	MGLEFGLEAGGNSHFLPGSDGNWNLFLPGINGNSLFLPGTHGNWSLFLPRIMGVGL	60				
Db	1	MGLEFGLEAGGNSHFLPGSDGNWNLFLPGINGNSLFLPGTHGNWSLFLPRIMGVGL	60				
Qy	61	CHQEPVEVGEALWSSTCPQPAPSPISFRYLVLHVHSGGELFDYLVKKGLTPEAKRF	120				
Db	61	CHQEPVEVGEALWSSTCPQPAPSPISFRYLVLHVHSGGELFDYLVKKGLTPEAKRF	120				
Qy	121	FRQIVSALDFCHSYISCHRDLPENLLLDKNNIRIADFQVMSIQVSGDSLETSCGSPHY	180				
Db	121	FRQIVSALDFCHSYISCHRDLPENLLLDKNNIRIADFQVMSIQVSGDSLETSCGSPHY	180				

```
Db 121 FRQIVSALDFCHSYSTCHRDLPENLLDEKKNIRIADFGMASLQVGDSDLLETSCGSPHY 180
QY 181 ACEPVILKGYDGRADMMSCGVILFALLVGLPFDNDNLRLQLEKVKRGVFMHPHFIPP 240
Db 181 ACEPVILKGYDGRADMMSCGVILFALLVGLPFDNDNLRLQLEKVKRGVFMHPHFIPP 240
QY 241 DCOSLLRGMIEVEPEKRLSLEQIQKHPWYLGKGHEPDPCLPAPGRRVAMRSLPSNGELD 300
Db 241 DCOSLLRGMIEVEPEKRLSLEQIQKHPWYLGKGHEPDPCLPAPGRRVAMRSLPSNGELD 300
QY 301 PDVLESWASLGCGRDRERLHRELRSSEENQEKMIYLLDLRKERYPSCEDODLPPRNDVD 360
Db 301 PDVLESWASLGCGRDRERLHRELRSSEENQEKMIYLLDLRKERYPSCEDODLPPRNDVD 360
QY 361 PPRKRVDS PMLSRHGKRRRPERKSMVLSITDAGGSGSPVTRRALEMAQHSQSRSVSGA 420
Db 361 PPRKRVDS PMLSRHGKRRRPERKSMVLSITDAGGSGSPVTRRALEMAQHSQSRSVSGA 420
QY 421 STGLSSPLSSPRSPVFSFSPGAGDEARGGSPSTKTQTLPSRPGRGGAGEQPPPPS 480
Db 421 STGLSSPLSSPRSPVFSFSPGAGDEARGGSPSTKTQTLPSRPGRGGAGEQPPPPS 480
QY 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTGTTTTPPPSPGGVGGAAWRSLNSI 540
Db 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTGTTTTPPPSPGGVGGAAWRSLNSI 540
QY 541 RNSFLGSPRHRKQVPTAEEMSSLTPESSPELAKRSWFGNFI SLDKEQI FLVLKDKP 600
Db 541 RNSFLGSPRHRKQVPTAEEMSSLTPESSPELAKRSWFGNFI SLDKEQI FLVLKDKP 600
QY 601 LSSIKADIVHAFSLPSLSHSLVLSQTSFRAEYKASGSPSVFQKPVRFQVDISSEGEPS 660
Db 601 LSSIKADIVHAFSLPSLSHSLVLSQTSFRAEYKASGSPSVFQKPVRFQVDISSEGEPS 660
QY 661 PRDGGGGGIYSVTFTLISGSPRRFRKRVVETIQAQLLSTHDQPSVQALADEKNGAOTRP 720
Db 661 PRDGGGGGIYSVTFTLISGSPRRFRKRVVETIQAQLLSTHDQPSVQALADEKNGAOTRP 720
QY 721 AGAPPSLQPPGPRDPELSSSPRRGPPKDKLLATNGTPLP 762
Db 721 AGAPPSLQPPGPRDPELSSSPRRGPPKDKLLATNGTPLP 762

RESULT 2
US-10-803-277-4
; Sequence 4, Application US/10803277
; Publication No. US20040180416A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/803,277
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 762
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-803-277-4

Query Match 100.0%; Score 4056; DB 16; Length 762;
Best Local Similarity 100.0%; Pred. No. 1e-203;
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLEFGLGAGNWSHFLPGSDGNWNLFLPGINGNWSLFLPGTHGNWSLFLPRIMGIVL 60
```

```
Db 1 MGLEFGLGAGNWSHFLPGSDGNWNLFLPGINGNWSLFLPGTHGNWSLFLPRIMGIVL 60
QY 61 CHQEPVEVGEALMSSTCFQPSAPISFRYLVLHVSGGELFDYLVKKGRLTTPKEARKF 120
Db 61 CHQEPVEVGEALMSSTCFQPSAPISFRYLVLHVSGGELFDYLVKKGRLTTPKEARKF 120
QY 121 FRQIVSALDFCHSYSTCHRDLPENLLDEKKNIRIADFGMASLQVGDSDLLETSCGSPHY 180
Db 121 FRQIVSALDFCHSYSTCHRDLPENLLDEKKNIRIADFGMASLQVGDSDLLETSCGSPHY 180
QY 181 ACEPVILKGYDGRADMMSCGVILFALLVGLPFDNDNLRLQLEKVKRGVFMHPHFIPP 240
Db 181 ACEPVILKGYDGRADMMSCGVILFALLVGLPFDNDNLRLQLEKVKRGVFMHPHFIPP 240
QY 241 DCOSLLRGMIEVEPEKRLSLEQIQKHPWYLGKGHEPDPCLPAPGRRVAMRSLPSNGELD 300
Db 241 DCOSLLRGMIEVEPEKRLSLEQIQKHPWYLGKGHEPDPCLPAPGRRVAMRSLPSNGELD 300
QY 301 PDVLESWASLGCGRDRERLHRELRSSEENQEKMIYLLDLRKERYPSCEDODLPPRNDVD 360
Db 301 PDVLESWASLGCGRDRERLHRELRSSEENQEKMIYLLDLRKERYPSCEDODLPPRNDVD 360
QY 361 PPRKRVDS PMLSRHGKRRRPERKSMVLSITDAGGSGSPVTRRALEMAQHSQSRSVSGA 420
Db 361 PPRKRVDS PMLSRHGKRRRPERKSMVLSITDAGGSGSPVTRRALEMAQHSQSRSVSGA 420
QY 421 STGLSSPLSSPRSPVFSFSPGAGDEARGGSPSTKTQTLPSRPGRGGAGEQPPPPS 480
Db 421 STGLSSPLSSPRSPVFSFSPGAGDEARGGSPSTKTQTLPSRPGRGGAGEQPPPPS 480
QY 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTGTTTTPPPSPGGVGGAAWRSLNSI 540
Db 481 ARSTPLPGPGSPRSSGGTPLHSPHTPRASPTGTGTTTTPPPSPGGVGGAAWRSLNSI 540
QY 541 RNSFLGSPRHRKQVPTAEEMSSLTPESSPELAKRSWFGNFI SLDKEQI FLVLKDKP 600
Db 541 RNSFLGSPRHRKQVPTAEEMSSLTPESSPELAKRSWFGNFI SLDKEQI FLVLKDKP 600
QY 601 LSSIKADIVHAFSLPSLSHSLVLSQTSFRAEYKASGSPSVFQKPVRFQVDISSEGEPS 660
Db 601 LSSIKADIVHAFSLPSLSHSLVLSQTSFRAEYKASGSPSVFQKPVRFQVDISSEGEPS 660
QY 661 PRDGGGGGIYSVTFTLISGSPRRFRKRVVETIQAQLLSTHDQPSVQALADEKNGAOTRP 720
Db 661 PRDGGGGGIYSVTFTLISGSPRRFRKRVVETIQAQLLSTHDQPSVQALADEKNGAOTRP 720
QY 721 AGAPPSLQPPGPRDPELSSSPRRGPPKDKLLATNGTPLP 762
Db 721 AGAPPSLQPPGPRDPELSSSPRRGPPKDKLLATNGTPLP 762

RESULT 3
US-10-116-326-6
; Sequence 6, Application US/10116326
; Publication No. US20030166889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20030166889A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 703
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-116-326-6
```

```
Query Match      87.4%; Score 3545; DB 14; Length 703;
Best Local Similarity 99.7%; Pred. No. 4.4e-177;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 89 FRYLVLEHVS GGELFDYLVKKGR LTPKEARKFFRQIVSALDFCHSY SICH RDLPEN LLL 148
Db 30 YLYLVLEHVS GGELFDYLVKKGR LTPKEARKFFRQIVSALDFCHSY SICH RDLPEN LLL 89

Qy 149 DEKNIRIADFGMASLQVGD SLLTSCGSHYACPEVIKGEKYDGRADMMW SCGVILFAL 208
Db 90 DEKNIRIADFGMASLQVGD SLLTSCGSHYACPEVIKGEKYDGRADMMW SCGVILFAL 149

Qy 209 LVGALPDDDDNLRLQLLEKVG VFMHPHFIPDQCOSLLRGMIEVEPEKRLSLEQIQHPW 268
Db 150 LVGALPDDDDNLRLQLLEKVG VFMHPHFIPDQCOSLLRGMIEVEPEKRLSLEQIQHPW 209

Qy 269 YLGKKEHPDPCLEPAPGR RVAMRSLPSNGELDPDVLESMA SLGCFRDRERLHRELSEEE 328
Db 210 YLGKKEHPDPCLEPAPGR RVAMRSLPSNGELDPDVLESMA SLGCFRDRERLHRELSEEE 269

Qy 329 NOEKMIYYLLLD RKRYPSCEDQDLP RNDVDP RKRVDSPMLSRHGKRRPERKSM EVLS 388
Db 270 NOEKMIYYLLLD RKRYPSCEDQDLP RNDVDP RKRVDSPMLSRHGKRRPERKSM EVLS 329

Qy 389 ITDAGGGGSPVPTRRAL EMAHQSRSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 448
Db 330 ITDAGGGGSPVPTRRAL EMAHQSRSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 389

Qy 449 ARGGGSPSTKTQTLPSRG PRGGAGEQPPPSARSTPLPGPGSPRSGGTP LHSPLHTP 508
Db 390 ARGGGSPSTKTQTLPSRG PRGGAGEQPPPSARSTPLPGPGSPRSGGTP LHSPLHTP 449

Qy 509 RASPTGTGTPTTTPSPG GVGAAWRSLRNSIRNSFLGSPFRHRRKMQVPTAEEMSS LTP 568
Db 450 RASPTGTGTPTTTPSPG GVGAAWRSLRNSIRNSFLGSPFRHRRKMQVPTAEEMSS LTP 509

Qy 569 ESSPELAKRSWFGNFISLDKEEQIFLV LKDKPLSSI KADIVHAF LSIPLSHSVLSQTSF 628
Db 510 ESSPELAKRSWFGNFISLDKEEQIFLV LKDKPLSSI KADIVHAF LSIPLSHSVLSQTSF 569

Qy 629 RAEYKASGGPVFOKPVRFQVDI SSSEGPSPRRDGSGGGIYSVFTLISGSPRRFKR 688
Db 570 RAEYKASGGPVFOKPVRFQVDI SSSEGPSPRRDGSGGGIYSVFTLISGSPRRFKR 629

Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPG RDPPELSSSPRRGPP 748
Db 630 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPG RDPPELSSSPRRGPP 689

Qy 749 KDKKLLATNGTPLP 762
Db 690 KDKKLLATNGTPLP 703

RESULT 4
US-10-803-277-6
; Sequence 6, Application US/10803277
; Publication No. US20040180416A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/803,277
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 703
```

```
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-803-277-6
```

```
Query Match      87.4%; Score 3545; DB 16; Length 703;
Best Local Similarity 99.7%; Pred. No. 4.4e-177;
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 89 FRYLVLEHVS GGELFDYLVKKGR LTPKEARKFFRQIVSALDFCHSY SICH RDLPEN LLL 148
Db 30 YLYLVLEHVS GGELFDYLVKKGR LTPKEARKFFRQIVSALDFCHSY SICH RDLPEN LLL 89

Qy 149 DEKNIRIADFGMASLQVGD SLLTSCGSHYACPEVIKGEKYDGRADMMW SCGVILFAL 208
Db 90 DEKNIRIADFGMASLQVGD SLLTSCGSHYACPEVIKGEKYDGRADMMW SCGVILFAL 149

Qy 209 LVGALPDDDDNLRLQLLEKVG VFMHPHFIPDQCOSLLRGMIEVEPEKRLSLEQIQHPW 268
Db 150 LVGALPDDDDNLRLQLLEKVG VFMHPHFIPDQCOSLLRGMIEVEPEKRLSLEQIQHPW 209

Qy 269 YLGKKEHPDPCLEPAPGR RVAMRSLPSNGELDPDVLESMA SLGCFRDRERLHRELSEEE 328
Db 210 YLGKKEHPDPCLEPAPGR RVAMRSLPSNGELDPDVLESMA SLGCFRDRERLHRELSEEE 269

Qy 329 NOEKMIYYLLLD RKRYPSCEDQDLP RNDVDP RKRVDSPMLSRHGKRRPERKSM EVLS 388
Db 270 NOEKMIYYLLLD RKRYPSCEDQDLP RNDVDP RKRVDSPMLSRHGKRRPERKSM EVLS 329

Qy 389 ITDAGGGGSPVPTRRAL EMAHQSRSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 448
Db 330 ITDAGGGGSPVPTRRAL EMAHQSRSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 389

Qy 449 ARGGGSPSTKTQTLPSRG PRGGAGEQPPPSARSTPLPGPGSPRSGGTP LHSPLHTP 508
Db 390 ARGGGSPSTKTQTLPSRG PRGGAGEQPPPSARSTPLPGPGSPRSGGTP LHSPLHTP 449

Qy 509 RASPTGTGTPTTTPSPG GVGAAWRSLRNSIRNSFLGSPFRHRRKMQVPTAEEMSS LTP 568
Db 450 RASPTGTGTPTTTPSPG GVGAAWRSLRNSIRNSFLGSPFRHRRKMQVPTAEEMSS LTP 509

Qy 569 ESSPELAKRSWFGNFISLDKEEQIFLV LKDKPLSSI KADIVHAF LSIPLSHSVLSQTSF 628
Db 510 ESSPELAKRSWFGNFISLDKEEQIFLV LKDKPLSSI KADIVHAF LSIPLSHSVLSQTSF 569

Qy 629 RAEYKASGGPVFOKPVRFQVDI SSSEGPSPRRDGSGGGIYSVFTLISGSPRRFKR 688
Db 570 RAEYKASGGPVFOKPVRFQVDI SSSEGPSPRRDGSGGGIYSVFTLISGSPRRFKR 629

Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPG RDPPELSSSPRRGPP 748
Db 630 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPRSLQPPG RDPPELSSSPRRGPP 689

Qy 749 KDKKLLATNGTPLP 762
Db 690 KDKKLLATNGTPLP 703
```

```
RESULT 5
US-10-354-358-92
; Sequence 92, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
```

1 ; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,  
2 ; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,  
3 ; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,  
4 ; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32336, 2099,  
5 ; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES  
6 ; FILE REFERENCE: WPI02-020P1RNN0N1M  
7 ; CURRENT APPLICATION NUMBER: US/10/354,358  
8 ;  
9 ; CURRENT FILING DATE: 2003-01-30  
10 ; PRIOR APPLICATION NUMBER: US 60/353,600  
11 ; PRIOR FILING DATE: 2002-01-31  
12 ; PRIOR APPLICATION NUMBER: US 60/364,517  
13 ; PRIOR FILING DATE: 2002-03-15  
14 ; PRIOR APPLICATION NUMBER: US 60/371,075  
15 ; PRIOR FILING DATE: 2002-04-09  
16 ; PRIOR APPLICATION NUMBER: US 60/371,507  
17 ; PRIOR FILING DATE: 2002-04-10  
18 ; PRIOR APPLICATION NUMBER: US 60/372,984  
19 ; PRIOR FILING DATE: 2002-04-16  
20 ; PRIOR APPLICATION NUMBER: US 60/374,194  
21 ; PRIOR FILING DATE: 2002-04-19  
22 ; PRIOR APPLICATION NUMBER: US 60/382,995  
23 ; PRIOR FILING DATE: 2002-05-24  
24 ; PRIOR APPLICATION NUMBER: US 60/385,023  
25 ; PRIOR FILING DATE: 2002-05-31  
26 ; PRIOR APPLICATION NUMBER: US 60/388,853  
27 ; PRIOR FILING DATE: 2002-06-14  
28 ; PRIOR APPLICATION NUMBER: US 60/389,395  
29 ; PRIOR FILING DATE: 2002-06-17  
30 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
31 ; NUMBER OF SEQ ID NOS: 122  
32 ; SOFTWARE: FastSeq for Windows Version 4.0  
33 ; SEQ ID NO 92  
34 ; LENGTH: 778  
35 ; TYPE: PRT  
36 ; ORGANISM: Homo sapiens  
37 ;  
38 ; US-10-354-358-92

Query Match 87.4%; Score 3545; DB 14; Length 778;  
Best Local Similarity 99.7%; Pred. No. 4.9e-177;  
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 89 FRYLVLEHVSGGELFDYLVKKGRITPKKARKFFROIIVSALDFCHSYISICHRDLKPNL 148  
DB 105 YLYLVLEHVSGGELFDYLVKKGRITPKKARKFFROIIVSALDFCHSYISICHRDLKPNL 164  
QY 149 DEKNIRIADFGMASLQVGSILLETSCGSPHYACPEVIGKGYDGRADWMSGVL 208  
DB 165 DEKNIRIADFGMASLQVGSILLETSCGSPHYACPEVIGKGYDGRADWMSGVL 224  
QY 209 LVGALPDDNLRQLLEKVRGVFHMHPFIIPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 268  
DB 225 LVGALPDDNLRQLLEKVRGVFHMHPFIIPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 284  
QY 269 YLGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLCGFRDRERLHRLSEEE 328  
DB 285 YLGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLCGFRDRERLHRLSEEE 344  
QY 329 NOEKMIYLLLDKERYPSCEDQDLPVRNDVDPKRVDSPLMSRHGKRRPERKSMVLS 388  
DB 345 NOEKMIYLLLDKERYPSCEDQDLPVRNDVDPKRVDSPLMSRHGKRRPERKSMVLS 404  
QY 389 ITDAGGGSVPVTRRALEMAHQSRSSVSGASTGLSSPLSSPSRVSFSPSPGAGDE 448  
DB 405 ITDAGGGSVPVTRRALEMAHQSRSSVSGASTGLSSPLSSPSRVSFSPSPGAGDE 464  
QY 449 ARGGGSPTKTOTLPSRGRGGAGEOPPPPSARSTPLPGPGSPRSSGGTFLHSLHTP 508  
DB 465 ARGGGSPTKTOTLPSRGRGGAGEOPPPPSARSTPLPGPGSPRSSGGTFLHSLHTP 524  
QY 509 RASPTGTPTTTPPPSGGVGGAARSLNRSIRNSFLGSPRFRHRKQVPTAEENSSLTP 568  
DB 525 RASPTGTPTTTPPPSGGVGGAARSLNRSIRNSFLGSPRFRHRKQVPTAEENSSLTP 584

QY 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKXPLSIKADIIVHAFISIPSLSHSVLSQTSF 628  
DB 585 ESSPELAKRSWFGNFISLDKEEQIFLVLDKXPLSIKADIIVHAFISIPSLSHSVLSQTSF 644  
QY 629 RAEYKASGSPVQKPVRFQVDIISSEGEPEPSPRDGGGGIYSVTTLISGPRRRPKR 688  
DB 645 RAEYKASGSPVQKPVRFQVDIISSEGEPEPSPRDGGGGIYSVTTLISGPRRRPKR 704  
QY 689 VVETIQALLSTHDOPSVOALADENKGAQTRPAGAPRSLQPPGPRDPPELSSSPRRGPP 748  
DB 705 VVETIQALLSTHDOPSVOALADENKGAQTRPAGAPRSLQPPGPRDPPELSSSPRRGPP 764  
QY 749 KDKLLATNGTLP 762  
DB 765 KDKLLATNGTLP 778  
RESULT 6  
US-10-116-326-2  
; Sequence 2, Application US/10116326  
; Publication No. US20030166889A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. US20030166889A1  
; FILE REFERENCE: LEX-0332-USA  
; CURRENT APPLICATION NUMBER: US/10/116,326  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/282,036  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 778  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; US-10-116-326-2

Query Match 87.4%; Score 3545; DB 14; Length 778;  
Best Local Similarity 99.7%; Pred. No. 4.9e-177;  
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 89 FRYLVLEHVSGGELFDYLVKKGRITPKKARKFFROIIVSALDFCHSYISICHRDLKPNL 148  
DB 105 YLYLVLEHVSGGELFDYLVKKGRITPKKARKFFROIIVSALDFCHSYISICHRDLKPNL 164  
QY 149 DEKNIRIADFGMASLQVGSILLETSCGSPHYACPEVIGKGYDGRADWMSGVL 208  
DB 165 DEKNIRIADFGMASLQVGSILLETSCGSPHYACPEVIGKGYDGRADWMSGVL 224  
QY 209 LVGALPDDNLRQLLEKVRGVFHMHPFIIPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 268  
DB 225 LVGALPDDNLRQLLEKVRGVFHMHPFIIPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 284  
QY 269 YLGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLCGFRDRERLHRLSEEE 328  
DB 285 YLGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLCGFRDRERLHRLSEEE 344  
QY 329 NOEKMIYLLLDKERYPSCEDQDLPVRNDVDPKRVDSPLMSRHGKRRPERKSMVLS 388  
DB 345 NOEKMIYLLLDKERYPSCEDQDLPVRNDVDPKRVDSPLMSRHGKRRPERKSMVLS 404  
QY 389 ITDAGGGSVPVTRRALEMAHQSRSSVSGASTGLSSPLSSPSRVSFSPSPGAGDE 448  
DB 405 ITDAGGGSVPVTRRALEMAHQSRSSVSGASTGLSSPLSSPSRVSFSPSPGAGDE 464  
QY 449 ARGGGSPTKTOTLPSRGRGGAGEOPPPPSARSTPLPGPGSPRSSGGTFLHSLHTP 508  
DB 465 ARGGGSPTKTOTLPSRGRGGAGEOPPPPSARSTPLPGPGSPRSSGGTFLHSLHTP 524  
QY 509 RASPTGTPTTTPPPSGGVGGAARSLNRSIRNSFLGSPRFRHRKQVPTAEENSSLTP 568



Db 525 RASPTGPTGTTTPPSGGVGAARSLRNSIRNSFLSGSPRFRHRRKMQVPTAEEMSLTP 584  
Qy 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628  
Db 585 ESSPELAKRSWFGNFISLDKEEQIFLVLDKDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644  
Qy 629 RAEYKASGGPSVFOKPVRFQVDISSSGSPSPRSDGSGGGIYVTFLLISGSPRRFKR 688  
Db 645 RAEYKASGGPSVFOKPVRFQVDISSSGSPSPRSDGSGGGIYVTFLLISGSPRRFKR 704  
Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPPRSLQPPGRDPPELSSSPRRGPP 748  
Db 705 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPPRSLQPPGRDPPELSSSPRRGPP 764  
Qy 749 KDKKLLATNGTPLP 762  
Db 765 KDKKLLATNGTPLP 778

## RESULT 7

US-10-423-543-11  
; Sequence 11, Application US/10423543  
; Publication No. US20040058355A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Libermann, Rosana K.  
; APPLICANT: Hunter, John J.  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Rudolph-Owen, Laura A.  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Olandt, Peter J.  
; APPLICANT: Tsai, Fong-Ying  
; APPLICANT: Galvin, Katherine M.  
; APPLICANT: Chun, Miyoung  
; APPLICANT: Williams, Mark J.  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Bandaru, Rajasekhar  
; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,  
; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,  
; TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MPI03-0230NM  
; CURRENT APPLICATION NUMBER: US/10/423,543  
; CURRENT FILING DATE: 2003-04-25  
; PRIOR APPLICATION NUMBER: US 10/278,036  
; PRIOR FILING DATE: 2002-10-22  
; PRIOR APPLICATION NUMBER: US 09/711,216  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US 60/205,447  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 10/012,055  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/248,325  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 10/003,690  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/248,893  
; PRIOR FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: US 09/797,039  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US 60/186,061  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 10/217,168  
; PRIOR FILING DATE: 2002-08-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 778  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-423-543-11

Query Match 87.4%; Score 3545; DB 15; Length 778;  
Best Local Similarity 99.7%; Pred. No. 4.9e-177;  
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 89 FRYLVLEHVS GGSLFDYLVKKGLTTPKEARKFRQIVSALDFCHSYICHRLDKPENLLL 148  
Db :|||||  
Qy 105 YLVLEHVS GGSLFDYLVKKGLTTPKEARKFRQIVSALDFCHSYICHRLDKPENLLL 164  
Db :|||||  
Qy 149 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADMMSCVILPAL 208  
Db DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADMMSCVILPAL 224  
Qy 209 LVGALPDNDNLKQLLEKVKRGVFMHPHFIPPCQSLLRGMI EVEPEKRLSLEQIQHPW 268  
Db LVGALPDNDNLKQLLEKVKRGVFMHPHFIPPCQSLLRGMI EVEPEKRLSLEQIQHPW 284  
Qy 269 YLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLESMASTGLCFRDRERLHRELSEEE 328  
Db YLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLESMASTGLCFRDRERLHRELSEEE 344  
Qy 329 NQEKMIYYLLLDKRYPCSCDQDLPNRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388  
Db NQEKMIYYLLLDKRYPCSCDQDLPNRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 404  
Qy 389 ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSSLSPSRSPVFSFSPGAGDE 448  
Db ITDAGGGSPVPTTRALEMAHQSRSSVSGASTGLSSSLSPSRSPVFSFSPGAGDE 464  
Qy 449 ARGGGSPSTKTQTLPSRGRGGGAGGEOPPPSARSTPLPGPPSGSPSSGGTPLHSLHTP 508  
Db ARGGGSPSTKTQTLPSRGRGGGAGGEOPPPSARSTPLPGPPSGSPSSGGTPLHSLHTP 524  
Qy 509 RASPTGPTGTTTPPSGGVGAARSLRNSIRNSFLSGSPRFRHRRKMQVPTAEEMSLTP 568  
Db RASPTGPTGTTTPPSGGVGAARSLRNSIRNSFLSGSPRFRHRRKMQVPTAEEMSLTP 584  
Qy 569 ESSPELAKRSWFGNFISLDKEEQIFLVLDKDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628  
Db ESSPELAKRSWFGNFISLDKEEQIFLVLDKDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 644  
Qy 629 RAEYKASGGPSVFOKPVRFQVDISSSGSPSPRSDGSGGGIYVTFLLISGSPRRFKR 688  
Db RAEYKASGGPSVFOKPVRFQVDISSSGSPSPRSDGSGGGIYVTFLLISGSPRRFKR 704  
Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPPRSLQPPGRDPPELSSSPRRGPP 748  
Db VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPPRSLQPPGRDPPELSSSPRRGPP 764  
Qy 749 KDKKLLATNGTPLP 762  
Db KDKKLLATNGTPLP 778

## RESULT 8

US-10-803-277-2  
; Sequence 2, Application US/10803277  
; Publication No. US20040180416A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0332-USA  
; CURRENT APPLICATION NUMBER: US/10/803,277  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/10/116,326  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/282,036  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 778

; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-803-277-2  
  
Query Match 87.4%; Score 3545; DB 16; Length 778;  
Best Local Similarity 99.7%; Pred. No. 4.9e-177; Indels 0; Gaps 0;  
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
; FILE OF INVENTION: 55053  
; FILE REFERENCE: MPI03-007PIRNMNIM  
; CURRENT APPLICATION NUMBER: US/10/757,262  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/444,783  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/478,742  
; PRIOR FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/488,529  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/491,156  
; PRIOR FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 60/499,594  
; PRIOR FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US 60/506,332  
; PRIOR FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 136  
; LENGTH: 778  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-757-262-136

Query Match 87.4%; Score 3545; DB 16; Length 778;  
Best Local Similarity 99.7%; Pred. No. 4.9e-177; Indels 0; Gaps 0;  
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 89 FRVLVLEHVGSGELFDYLVKKGLRTPKEARKEFRQIVSALDFCHSYISCHRDLPENL 148  
DB 105 YLVLVLEHVGSGELFDYLVKKGLRTPKEARKEFRQIVSALDFCHSYISCHRDLPENL 164  
  
QY 149 DEKNIRIADFGNASIQVDSLETSCGSPHYACPEVIKGEKIDRRADWNSCGVILPAL 208  
DB 165 DEKNIRIADFGNASIQVDSLETSCGSPHYACPEVIKGEKIDRRADWNSCGVILPAL 224  
  
QY 209 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCQLLRGMIEVEPEKRLSLEQIQKHPW 268  
DB 225 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCQLLRGMIEVEPEKRLSLEQIQKHPW 284  
  
QY 269 YLGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLGCFFDRRLHRELSEEE 328  
DB 285 YLGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLGCFFDRRLHRELSEEE 344  
  
QY 329 NQEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388  
DB 345 NQEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 404  
  
QY 389 ITDAGGGSPVPTTRALEMAHQSRSVSGASTGLSSSPSSPSPSPSPSPSPSPSPSPSP 448  
DB 405 ITDAGGGSPVPTTRALEMAHQSRSVSGASTGLSSSPSSPSPSPSPSPSPSPSPSPSP 464  
  
QY 449 ARGGSPTSXTQTLPSPRGGGAGEQPPPPSARSTPLPGPGSPSSSGGTPHLSPLHTP 508  
DB 465 ARGGSPTSXTQTLPSPRGGGAGEQPPPPSARSTPLPGPGSPSSSGGTPHLSPLHTP 524  
  
QY 509 RASPTGTPTTTPPSGGVGGAAWRSLNRSFLGSPFRHRRKMQVPTAEEMSSLTP 568  
DB 525 RASPTGTPTTTPPSGGVGGVGGAAWRSLNRSFLGSPFRHRRKMQVPTAEEMSSLTP 584  
  
QY 569 ESSPELAKRSWFGNFISLDKEEQIFLVKOKPLSSIKADIHAFPLSPSHSVLSQTSF 628  
DB 585 ESSPELAKRSWFGNFISLDKEEQIFLVKOKPLSSIKADIHAFPLSPSHSVLSQTSF 644

; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-803-277-2  
  
Query Match 87.4%; Score 3545; DB 16; Length 778;  
Best Local Similarity 99.7%; Pred. No. 4.9e-177; Indels 0; Gaps 0;  
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 89 FRVLVLEHVGSGELFDYLVKKGLRTPKEARKEFRQIVSALDFCHSYISCHRDLPENL 148  
DB 105 YLVLVLEHVGSGELFDYLVKKGLRTPKEARKEFRQIVSALDFCHSYISCHRDLPENL 164  
  
QY 149 DEKNIRIADFGNASIQVDSLETSCGSPHYACPEVIKGEKIDRRADWNSCGVILPAL 208  
DB 165 DEKNIRIADFGNASIQVDSLETSCGSPHYACPEVIKGEKIDRRADWNSCGVILPAL 224  
  
QY 209 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCQLLRGMIEVEPEKRLSLEQIQKHPW 268  
DB 225 LVGALPDDNNLRQLLEKVKRGVFMHPHFIPDQCQLLRGMIEVEPEKRLSLEQIQKHPW 284  
  
QY 269 YLGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLGCFFDRRLHRELSEEE 328  
DB 285 YLGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAISLGCFFDRRLHRELSEEE 344  
  
QY 329 NQEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 388  
DB 345 NQEKMIYLLLDKERYPSCEDQDLPPRNDVDPKRKVDSPMLSRHGKRRPERKSMVLS 404  
  
QY 389 ITDAGGGSPVPTTRALEMAHQSRSVSGASTGLSSSPSSPSPSPSPSPSPSPSPSPSP 448  
DB 405 ITDAGGGSPVPTTRALEMAHQSRSVSGASTGLSSSPSSPSPSPSPSPSPSPSPSPSP 464  
  
QY 449 ARGGSPTSXTQTLPSPRGGGAGEQPPPSARSTPLPGPGSPSSSGGTPHLSPLHTP 508  
DB 465 ARGGSPTSXTQTLPSPRGGGAGEQPPPSARSTPLPGPGSPSSSGGTPHLSPLHTP 524  
  
QY 509 RASPTGTPTTTPPSGGVGGVGGAAWRSLNRSFLGSPFRHRRKMQVPTAEEMSSLTP 568  
DB 525 RASPTGTPTTTPPSGGVGGVGGAAWRSLNRSFLGSPFRHRRKMQVPTAEEMSSLTP 584  
  
QY 569 ESSPELAKRSWFGNFISLDKEEQIFLVKOKPLSSIKADIHAFPLSPSHSVLSQTSF 628  
DB 585 ESSPELAKRSWFGNFISLDKEEQIFLVKOKPLSSIKADIHAFPLSPSHSVLSQTSF 644  
  
QY 629 RAEYKASGSPVQKPVRFQVDIISSEGEPSPRDGGGGGIYVTTLLISGFSRRFKR 688  
DB 645 RAEYKASGSPVQKPVRFQVDIISSEGEPSPRDGGGGGIYVTTLLISGFSRRFKR 704  
  
QY 689 VVETIQALLSTHDQPSVQALADEKNGAQTTRPAGAPRSLQPPGPDPELSSSPRRGPP 748  
DB 705 VVETIQALLSTHDQPSVQALADEKNGAQTTRPAGAPRSLQPPGPDPELSSSPRRGPP 764  
  
QY 749 KDKKLLATNGTLP 762  
DB 765 KDKKLLATNGTLP 778  
  
RESULT 9  
US-10-757-262-136  
; Sequence 136, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karicheti, Venkateswarlu  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Eliasof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,  
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,  
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,  
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,  
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,  
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,  
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,

Qy 629 RAEYKASGSPVFOKPVRFQVDISSSEGPSPRRDGGGGGGIYVTFLLISGSPRRFKR 688  
Db 645 RAEYKASGSPVFOKPVRFQVDISSSEGPSPRRDGGGGGGIYVTFLLISGSPRRFKR 704  
Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTTPAGAPRRSLQPPRGRDPPELSSSPRRGPP 748  
Db 705 VVETIQALLSTHDQPSVQALADEKNGAQTTPAGAPRRSLQPPRGRDPPELSSSPRRGPP 764  
Qy 749 KDKKLLATNGTPLP 762  
Db 765 KDKKLLATNGTPLP 778

RESULT 10  
US-10-311-034-17  
; Sequence 17, Application US/10311034  
; Publication No. US20040023242A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YUE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BOROWSKY, Mark L.  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: LU, Yan  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: LU, Dyung Aina M.  
; APPLICANT: GREENWALD, Sara R.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: KEARNEY, Liam  
; APPLICANT: BURFORD, Neil  
; APPLICANT: NGUYEN, Dannel B.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: HE, Ann  
; APPLICANT: THORNTON, Michael  
; APPLICANT: HAPALIA, April  
; APPLICANT: ARVIZU, Chandra S.  
; APPLICANT: GURURAJAN, Rajagopal  
; APPLICANT: LO, Terence P.  
; APPLICANT: KHAH, Farrah A.  
; APPLICANT: RECIPON, Shirley A.  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: POLICKY, Jennifer L.  
; APPLICANT: DING, Li  
; APPLICANT: GRETHER, Megan  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: BATRA, Sajeev  
; APPLICANT: ISON, Craig H.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0125 PCT  
; CURRENT APPLICATION NUMBER: US/10/311.034  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
60/228,056  
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PERL Program  
; SEQ ID NO 17  
; LENGTH: 794  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7477486CD1  
US-10-311-034-17

Query Match 87.4%; Score 3545; DB 15; Length 794;  
Best Local Similarity 99.7%; Pred. No. 5e-177;  
Matches 672; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 89 FRYLVLEHVHSGGELFDYLVKKGRLTPKEARKFFRQIVSALDFCHSYSGICHRLDKPENLLL 148  
Db 121 YLYLVLEHVHSGGELFDYLVKKGRLTPKEARKFFRQIVSALDFCHSYSGICHRLDKPENLLL 180  
Qy 149 DEKNRIADFGMASLQVGSLLTSCGSPHYACPEVIGKEKYDGRADWMSGCVILPAL 208  
Db 181 DEKNRIADFGMASLQVGSLLTSCGSPHYACPEVIGKEKYDGRADWMSGCVILPAL 240  
Qy 209 LVGALPDDNDNLQLEKVRGVFHPHF1PPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 268  
Db 241 LVGALPDDNDNLQLEKVRGVFHPHF1PPDCQSLLRGMIEVEPEKRLSLEQIQKHPW 300  
Qy 269 YLGGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAASLGCFRDRERLHRELSEEE 328  
Db 301 YLGGKHEPDPCLPAPGRRVAMRSLPSNGELDPDVLESMAASLGCFRDRERLHRELSEEE 360  
Qy 329 NOEKMIYLLLDKRYPCEDQDLPPRNDVDPKRVDSFMLSRRHGRKRRPERKSMVLS 388  
Db 361 NOEKMIYLLLDKRYPCEDQDLPPRNDVDPKRVDSFMLSRRHGRKRRPERKSMVLS 420  
Qy 389 ITDAGGGSPVPTRRALMAQHSORSVSAGSTGLSSSLSSPSRSPVFSPEPGAGDE 448  
Db 421 ITDAGGGSPVPTRRALMAQHSORSVSAGSTGLSSSLSSPSRSPVFSPEPGAGDE 480  
Qy 449 ARGGSPTSQTQLPSRGRGGGAGEOPPPPSARSTPLPGPPSPRSSGGTPLHSLHTP 508  
Db 481 ARGGSPTSQTQLPSRGRGGGAGEOPPPPSARSTPLPGPPSPRSSGGTPLHSLHTP 540  
Qy 509 RASPTGPTTTPPPSGGVGGAARSLRNSIRNSFLGSPFRHRRKQVPTAEEMSLTP 568  
Db 541 RASPTGPTTTPPPSGGVGGAARSLRNSIRNSFLGSPFRHRRKQVPTAEEMSLTP 600  
Qy 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLTSLSHSVLSQTSF 628  
Db 601 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLTSLSHSVLSQTSF 660  
Qy 629 RAEYKASGSPVFOKPVRFQVDISSSEGPSPRRDGGGGGGIYVTFLLISGSPRRFKR 688  
Db 661 RAEYKASGSPVFOKPVRFQVDISSSEGPSPRRDGGGGGGIYVTFLLISGSPRRFKR 720  
Qy 689 VVETIQALLSTHDQPSVQALADEKNGAQTTPAGAPRRSLQPPRGRDPPELSSSPRRGPP 748  
Db 721 VVETIQALLSTHDQPSVQALADEKNGAQTTPAGAPRRSLQPPRGRDPPELSSSPRRGPP 780  
Qy 749 KDKKLLATNGTPLP 762  
Db 781 KDKKLLATNGTPLP 794

RESULT 11  
US-10-479-532-1  
; Sequence 1, Application US/10479532  
; Publication No. US20040151713A1  
; GENERAL INFORMATION:  
; APPLICANT: TAIHO PHARMACEUTICAL CO., LTD  
; TITLE OF INVENTION: CELL CYCLE REGULATORY FACTOR  
; FILE REFERENCE: 44B00JP  
; CURRENT APPLICATION NUMBER: US/10/479,532  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: JP 2001-168792  
; PRIOR FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 754  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7477486CD1  
US-10-479-532-1

Query Match 82.9%; Score 3362; DB 16; Length 754;  
Best Local Similarity 95.4%; Pred. No. 1.7e-167; Indels 24; Gaps 1;  
Matches 643; Conservative 1; Mismatches 6;  
QY 89 FRYLVLEHVSGLDFYLVKKGRLTPKEARKFPRQIVSALDFCHSYISICHRDLKPENLLL 148  
Db 105 YLVLEHVSGLDFYLVKKGRLTPKEARKFPRQIVVCGAGLCHSYISICHRDLKPENLLL 164  
QY 149 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADWSCGVILFAL 208  
Db 165 DEKNIRIADFGMASLQVGSLLTSCGSPHYACPEVIKGEKYDGRADWSCGVILFAL 224  
QY 209 LVGALPDDNLRQLLEKVKRGVFMHPFIPPCQSLRGMIEVBEPEKLSLEQIOKHPW 268  
Db 225 LVGALPDDNLRQLLEKVKRGVFMHPFIPPCQSLRGMIEVBEPEKLSLEQIOKHPW 284  
QY 269 YLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLMSASLFCFRDRERLHRELSEEE 328  
Db 285 YLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLMSASLFCFRDRERLHRELSEEE 344  
QY 329 NOEKMIYLLLDKRYPCSDQDLPFRNDVDPKRKVDSPMLSRHGKRPERKSMVLS 388  
Db 345 NOEKMIYLLLDKRYPCSDQDLPFRNDVDPKRKVDSPMLSRHGKRPERKSMVLS 404  
QY 389 ITDAGGGSPVPTRRALMAQHSORSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 448  
Db 405 ITDAGGGSPVPTRRALMAQHSORSVSGASTGLSSPLSSPRSPVFSPEPGAGDE 464  
QY 449 ARGGGSPSTKTQTLPSRGRGGAGQPPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 508  
Db 465 ARGGGSPSTKTQTLPSRGRGGAGQPPPPSARSTPLPGPGSPRSSGGTPLHSLHTP 500  
QY 509 RASPTGTPTTPPSPGGVGGAWSRLNSIRNSFLGSPRHRKMOVPTAEEMSLTP 568  
Db 501 RASPTGTPTTPPSPGGVGGAWSRLNSIRNSFLGSPRHRKMOVPTAEEMSLTP 560  
QY 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSISHSVLSQTSF 628  
Db 561 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLPSISHSVLSQTSF 620  
QY 629 RAEYKASGGSPVQKPVRFQVDISSESEGPSPRRDGGGGGIYSVTFTLISGSRFRKR 688  
Db 621 RAEYKASGGSPVQKPVRFQVDISSESEGPSPRRDGGGGGIYSVTFTLISGSRFRKR 680  
QY 689 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPPSLQPPPPGPP 748  
Db 681 VVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPPSLQPPPPGPP 740  
QY 749 KDKLLATNGTLP 762  
Db 741 KDKLLATNGTLP 754  
RESULT 12  
US-10-425-114-54189  
; Sequence 54189, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 54189  
; LENGTH: 506  
; TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:  
; OTHER INFORMATION: Clone ID: LIF4653-002-E1\_FLI.pep  
US-10-425-114-54189  
Query Match 65.4%; Score 2654; DB 15; Length 506;  
Best Local Similarity 99.8%; Pred. No. 9.9e-131; Indels 0; Gaps 0;  
Matches 505; Conservative 0; Mismatches 1;  
QY 257 RLSLBQIOKHPWYLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLMSASLGCFRDR 316  
Db 1 RLSLBQIOKHPWYLGKKEHPDPCLEPAPGRRVAMRSLPSNGELDPDVLMSASLGCFRDR 60  
QY 317 ERLHRELSEENOEKMIYLLLDKRYPCSDQDLPFRNDVDPKRKVDSPMLSRHGK 376  
Db 61 ERLHRELSEENOEKMIYLLLDKRYPCSDQDLPFRNDVDPKRKVDSPMLSRHGK 120  
QY 377 RPERKSMVLSITDAGGGSPVPTRRALMAQHSORSVSGASTGLSSPLSSPRSPV 436  
Db 121 RPERKSMVLSITDAGGGSPVPTRRALMAQHSORSVSGASTGLSSPLSSPRSPV 180  
QY 437 FSPSPGAGDEARGGGSPSTKTQTLPSRGRGGAGQPPPPSARSTPLPGPGSPRSS 496  
Db 181 FSPSPGAGDEARGGGSPSTKTQTLPSRGRGGAGQPPPPSARSTPLPGPGSPRSS 240  
QY 497 GGTPLHSLHTPRASPTGTPTTPPSPGGVGGAWSRLNSIRNSFLGSPRHRKMO 556  
Db 241 GGTPLHSLHTPRASPTGTPTTPPSPGGVGGAWSRLNSIRNSFLGSPRHRKMO 300  
QY 557 VPTAEEMSLTPESPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLIP 616  
Db 301 VPTAEEMSLTPESPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLIP 360  
QY 617 SLSHSVLSQTSFRAEYKASGGSPVQKPVRFQVDISSESEGPSPRRDGGGGGIYSVTF 676  
Db 361 SLSHSVLSQTSFRAEYKASGGSPVQKPVRFQVDISSESEGPSPRRDGGGGGIYSVTF 420  
QY 677 TLISGSRFRKRVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPPSLQPPPPGPP 736  
Db 421 TLISGSRFRKRVETIQALLSTHDQPSVQALADEKNGAQTRPAGAPPSLQPPPPGPP 480  
QY 737 PELSSSPRRGPPKDKLLATNGTLP 762  
Db 481 PELSSSPRRGPPKDKLLATNGTLP 506  
RESULT 13  
US-10-195-072-4  
; Sequence 4, Application US/10195072  
; Publication No. US20030092036A1  
; GENERAL INFORMATION:  
; APPLICANT: Origene Technologies  
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas  
; FILE REFERENCE: 16U 101 C2  
; CURRENT APPLICATION NUMBER: US/10/195,072  
; CURRENT FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: US 09/930,181  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-195-072-4  
Query Match 58.9%; Score 2390.5; DB 14; Length 585;  
Best Local Similarity 74.4%; Pred. No. 6.5e-117; Indels 65; Gaps 7;  
Matches 465; Conservative 51; Mismatches 44;  
QY 90 RYLVLHVHSGGELFDYLVKKGRLTPKEARKFPRQIVSALDFCHSYISICHRDLKPENLLLD 149  
Db 8 RYLVLHVHSGGELFDYLVKKGRLTPKEARKFPRQIVSALDFCHSYISICHRDLKPENLLLD 67

QY 150 EKNIRIADFGMASLQVDSLSLSTSCGSPHYACPEVTKGKYDGRADWMSGCVILFALL 209  
DB 68 EKNIRIADFGMASLQVDSLSLSTSCGSPHYACPEVTKGKYDGRADWMSGCVILFALL 127  
QY 210 VGLPFDNRLRLLEKVKRGVFMHPFIIPDQCOSLLRGMIEVEPEKRLSLEOIQKHPWY 269  
DB 128 VGLPFDNRLRLLEKVKRGVFMHPFIIPDQCOSLLRGMIEVEPEKRLSLEOIQKHPWY 187  
QY 270 LGGKHEPDPCLEAPGRVAMRSLPSNGELDPDVLMSASLGCFCFRDRERLHRELSEEN 329  
DB 188 IGGKNEPEP-EQPIP-RKVQIRSLPSLEDIPDVLDSMHLGCFRDRNKLQDLSEEN 245  
QY 330 QEKMIYLLDRKERYPSCDQDLPPRNDVPPKRVDSPLMRHGRKRRPERKSMVLSI 389  
DB 246 QEKMIYFLLLDRKERYPSCDQDLPPRNEIDPPKRVDSPLMRHGRKRRPERKSMVLSV 305  
QY 390 TDAGGCGSPVPTTRALMAHQSRSVSGASTGLSSPLSSPRSPVFSPEPGAGDEA 449  
DB 306 TD---GGSPVPARRAEMAQHQSRISGASSGLSTSPSSPR----- 346  
QY 450 RGGGSPSTKTQTLPSRPGCGGAGEQPPPPSARSTPLPGPPGSPRSSGGTPLHSPHTPR 509  
DB 347 -----VTPHSPRGSPPLTPKG-----TPVHTPK 370  
QY 510 ASPTGTPTTTPPPSPGGVGAARSLNIRNSFLGSPFRHRRKMQVPTAEEMSSLTPE 569  
DB 371 ESPAGTNPPTPPSSP--SVGGVPMRRLNSIKNSFLGSPFRHRRKMQVPTAEEMSSLTPE 428  
QY 570 SSPELAKRSWFGNFIPLDKEEQIFVLVKDPLSSIKADIHAFSLISPSLSHVSLSQTSFR 629  
DB 429 SSPELAKRSWFGNFIPLDKEEQIFVVIKDKPLSSIKADIHAFSLISPSLSHVSLSQTSFR 488  
QY 630 AEYKASGSPVFKPVRQVDIISSEGEPEPSPRRDGSGGGGIYSVTFTLISGSPRRKRV 689  
DB 489 AEYKATGGAFAVQKPVAFQVDITTEGEAQKE-----NGIYSVTFTLISGSPRRKRV 542  
QY 690 VETIQALLSTHDPSPVQALADEKN 714  
DB 543 VETIQALLSTHDPSPVQALADEKN 567

## RESULT 14

US-10-195-071-4  
; Sequence 4, Application US/10195071  
; Publication No. US20030096271A1  
; GENERAL INFORMATION:  
; APPLICANT: Origene Technologies  
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas  
; FILE REFERENCE: 16U 101 C1  
; CURRENT APPLICATION NUMBER: US/10/195,071  
; CURRENT FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: US 09/930,181  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-195-071-4

Query Match 58.9%; Score 2390.5; DB 14; Length 585;  
Best Local Similarity 74.4%; Pred. No. 6.5e-117; Indels 65; Gaps 7;  
Matches 465; Conservative 51; Mismatches 44

QY 90 RYLVLHVSGGELFDYLVKKGRLTPKEARFQIVSALDFCHSYISCHRDLPENLLLD 149  
DB 8 RYLVLHVSGGELFDYLVKKGRLTPKEARFQIISALDFCHSHISCHRDLPENLLLD 67  
QY 150 EKNIRIADFGMASLQVDSLSLSTSCGSPHYACPEVTKGKYDGRADWMSGCVILFALL 209  
DB 68 EKNIRIADFGMASLQVDSLSLSTSCGSPHYACPEVTKGKYDGRADWMSGCVILFALL 127

QY 210 VGLPFDNRLRLLEKVKRGVFMHPFIIPDQCOSLLRGMIEVEPEKRLSLEOIQKHPWY 269  
DB 128 VGLPFDNRLRLLEKVKRGVFMHPFIIPDQCOSLLRGMIEVEPEKRLSLEOIQKHPWY 187  
QY 270 LGGKHEPDPCLEAPGRVAMRSLPSNGELDPDVLMSASLGCFCFRDRERLHRELSEEN 329  
DB 188 IGGKNEPEP-EQPIP-RKVQIRSLPSLEDIPDVLDSMHLGCFRDRNKLQDLSEEN 245  
QY 330 QEKMIYLLDRKERYPSCDQDLPPRNDVPPKRVDSPLMRHGRKRRPERKSMVLSI 389  
DB 246 QEKMIYFLLLDRKERYPSCDQDLPPRNEIDPPKRVDSPLMRHGRKRRPERKSMVLSV 305  
QY 390 TDAGGCGSPVPTTRALMAHQSRSVSGASTGLSSPLSSPRSPVFSPEPGAGDEA 449  
DB 306 TD---GGSPVPARRAEMAQHQSRISGASSGLSTSPSSPR----- 346  
QY 450 RGGGSPSTKTQTLPSRPGCGGAGEQPPPPSARSTPLPGPPGSPRSSGGTPLHSPHTPR 509  
DB 347 -----VTPHSPRGSPPLTPKG-----TPVHTPK 370  
QY 510 ASPTGTPTTTPPPSPGGVGAARSLNIRNSFLGSPFRHRRKMQVPTAEEMSSLTPE 569  
DB 371 ESPAGTNPPTPPSSP--SVGGVPMRRLNSIKNSFLGSPFRHRRKMQVPTAEEMSSLTPE 428  
QY 570 SSPELAKRSWFGNFIPLDKEEQIFVLVKDPLSSIKADIHAFSLISPSLSHVSLSQTSFR 629  
DB 429 SSPELAKRSWFGNFIPLDKEEQIFVVIKDKPLSSIKADIHAFSLISPSLSHVSLSQTSFR 488  
QY 630 AEYKASGSPVFKPVRQVDIISSEGEPEPSPRRDGSGGGGIYSVTFTLISGSPRRKRV 689  
DB 489 AEYKATGGAFAVQKPVAFQVDITTEGEAQKE-----NGIYSVTFTLISGSPRRKRV 542  
QY 690 VETIQALLSTHDPSPVQALADEKN 714  
DB 543 VETIQALLSTHDPSPVQALADEKN 567

## RESULT 15

US-10-283-247-2  
; Sequence 2, Application US/10283247  
; Publication No. US20030119037A1  
; GENERAL INFORMATION:  
; APPLICANT: NEELAM, Beena et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001304  
; CURRENT APPLICATION NUMBER: US/10/283,247  
; CURRENT FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-283-247-2

Query Match 58.9%; Score 2387.5; DB 14; Length 674;  
Best Local Similarity 71.9%; Pred. No. 1.1e-116; Indels 85; Gaps 9;  
Matches 469; Conservative 53; Mismatches 45

QY 89 FRYLVLEHVSGBELFDYLVKKGRLTPKEARFQIVSALDFCHSYISCHRDLPENLLLD 148  
DB 90 YLYLVLEHVSGBELFDYLVKKGRLTPKEARFQIISALDFCHSHISCHRDLPENLLLD 149  
QY 149 DEKNIRIADFGMASLQVDSLSLSTSCGSPHYACPEVTKGKYDGRADWMSGCVILFALL 208  
DB 150 DEKNIRIADFGMASLQVDSLSLSTSCGSPHYACPEVTKGKYDGRADWMSGCVILFALL 209  
QY 209 LVGALPDDNRLRLLEKVKRGVFMHPFIIPDQCOSLLRGMIEVEPEKRLSLEOIQKHPW 268  
DB 210 LVGALPDDNRLRLLEKVKRGVFMHPFIIPDQCOSLLRGMIEVEPEKRLSLEOIQKHPW 269

```

QY 269 YLGKHEPDCLEPAGRRVAMSLPSNGELDPDVLSEMASLGCFRDRERLHRELSEEE 328
Db 270 YIGKNEPEP-EQIP-RKQIRSLPSLEIDPDVLDSMHSGLGCFRDRNKLQDLLSEEE 327
QY 329 NOEKMIYLLLDKRYPSCEDQDLPDRNDVDPKRKVDSPMLSRHGKRPERKSMEVLS 388
Db 328 NOEKMIYLLLDKRYPSQEDDLPDRNEIDPDRKVDSPMLNRHGKRPERKSMEVLS 387
QY 389 ITDAGGGSPVPTFRALMAOHSORSVSGASTGLSSPLSSPRSPVPSPEPGAGDE 448
Db 388 VTD---GGSPVARRALEMAHQGRSISGASGLSTSLSSPR----- 429
QY 449 ARGGGSPSTKTOTLPSRGRGGAGQQPPPSARSTPLPGPPGSPRSSGGTPLHSPHTP 508
Db 430 -----VTPHPSRGSPLTPKG-----TPVHTP 452
QY 509 RASPTGTPTTPPSPGGVGGAAWRSLNSIRNSFLGSPRFHRRKQVPTAEEMSLTP 568
Db 453 KESPAGTPTNTPPSSP--SVGGVFWARLNSIKNSFLGSPRFHRRKLQVPTPEEMSLTP 510
QY 569 ESSPELAKRSWFGNFISLDKEEQIFVLVKDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
Db 511 ESSPELAKRSWFGNFISLEKEEQIFVVKDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 570
QY 629 RAEYKASGSPSVFQKPVRFQVDISSESEGPSPRRDGGGGGIYSVTFTLISGSPRRFKR 688
Db 571 RAEYKATGGPAVFQKPVKFQVDITYTEGGEAQKE-----NGIYSVTFTLLSGSPRRFKR 624
QY 689 VVETIQALLSTHDQPSVQALADEKGAQTRPAGAPPRSLQPPGPRDPDELS 740
Db 625 VVETIQALLSTHDPPAAQHLS-----EPPP--PAPGLS 656

```

Search completed: February 17, 2005, 11:15:50  
Job time : 147 secs





```
QY 475 -----QPPPSARSTPLPGPPGSRSSGGTPLHSLPLHTPRASPTGTP 516
Db 489 SRKESKDRSDKASASSCKNDASTSSVPHKYSPSPVMSSESVVSSSTWNSTNSLSLI 548
QY 517 GTTPPPSGGVGGAWRSLNIRNSFLGSPRFRHRKQVPTAEEMSSLTPR-SSPELA 575
Db 549 AGNSQTSIGSTSG--PWRSKLNNIKNSFLGTPRFRHRKMSNGTAESDSDSDSQMIDTDLV 606
QY 576 KRSWFGNF--ISLDKEEQFLVLKOKPLSSIKADIVHAFSLSPSLSHSVLSQTSFRAEY 632
Db 607 KKSWMFGSLASMSVERDDTHCVFQGGKTLNLSKAEILRAFLQIHELHSHSVGQNCFRVEY 666
QY 633 K--ASGGPSVQKPVRFQVQDISSEGEPEPRRDG-SGGGGIYSTFTTLISGSPRRFRKV 689
Db 667 KRGTTCVGSVFRGKKNVDII-----PSPQQVVIAGETPTTVVQVLLAGPVRRFKRL 720
QY 690 VETIQALLSHDQPSVQALADEKNKA--QTRP 720
Db 721 VEHLISAIL-----QNSTQQRADRQQAALMVPR 748

RESULT 2
S37928
probable purine nucleotide-binding protein YKL101w - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKL453
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Aug-2004
C;Accession: S37928; S39084
R;Cheret, G.; Fukuhara, H.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Pallier, C.; Puzos
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37920
A;Accession: S37928
A;Molecule type: DNA
A;Residues: 1-1518 <CHR>
A;Cross-references: UNIPROT:P34244; EMBL:Z28101; NID:9486168; PIDN:CAA91941.1; PID:94861
A;Experimental source: strain S288C
R;Pallier, C.; Valens, M.; Puzos, V.; Fukuhara, H.; Cheret, G.; Sor, F.; Bolotin-Fukuhara
Yeast 9, 1149-1155, 1993
A;Title: DNA sequence analysis of a 17 kb fragment of yeast chromosome XI physically loc
protein kinases.
A;Reference number: S39084; MUID:94078677; PMID:8256524
A;Accession: S39084
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-1518 <PAL>
A;Cross-references: EMBL:X71133; NID:9431205; PIDN:CAA50456.1; PID:9431215
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:HSL1
A;Cross-references: SGD:S0001584; MIPS:YKL101w
A;Map position: 11L
C;Superfamily: protein kinase homology
C;Keywords: ATP; P-loop; purine nucleotide binding; serine/threonine-specific protein ki
F;79-369/Domain: protein kinase homology <kin>
F;79-86/Region: nucleotide-binding motif A (P-loop)
F;87-95/Region: protein kinase ATP-binding motif
F;85/Binding site: ATP/GTP (Lys) #status predicted

Query Match 16.7%; Score 677; DB 2; Length 1518;
Best Local Similarity 27.5%; Pred. No. 7.1e-17;
Matches 216; Conservative 120; Mismatches 240; Indels 210; Gaps 27;

QY 91 YLVLEHVS GGELFDYLVKGR LTPKEARKFRQIVSALDFCHSY SICHRLDKPENLLDDE 150
Db 190 YLVLEVVG GELFDYLVSKGLP REAETHYFKQIVGVSYCHSFNICHRLDKPENLLDDE 249
QY 151 KN-NIRIADFGMASIQVDSLSLETSCGSPHYACPEVKEKYGVDGRADMSGCVILFALL 209
Db 250 KURRIKIADFGMAELPNKLLKTS CGSPHYASPEIVMGRPVHGGPSDVMSCGIVLFA 309
QY 210 VCALEPDDNLEQLLEKVKRGVFNHPHTPPDCQLLRGMIVREPEKLSLEQIOKHPW- 268
Db 310 TGHLPFDNDNIKKLLLLKQSGYQMPNSLSEARLDISKILVIDPEKRITTEILKHLPI 369
```

```
QY 269 -----YLGKKHEPPCPEAPGRVAMRSLPSNGELDDPVLESMA 309
Db 370 KKYDDLPMVKLRKMRKONMARGKNSD--LHLLNNVSPSIVTLHSKGEIDSLRSLOI 427
QY 310 LCFDRDRRLHRELSEENOEKMIYYLLLDKERY-----PSCEDQDLPPNDVDPKPK 364
Db 428 LWHGVSRLEITAKLQKPMSEBKJFYLLQYKQHSISLSSSENKKSKATSESSVNEPRI 487
QY 365 RYDPSMLSRHGKRRPERKSMELVSLITDAGGGGSPVPTTRALEMAQHSQ-----RSRSVS 418
Db 488 EVASKTANNYGLR-----SENNDVKTLHSLLEI--HSEDTSTVNQNNAIT 529
QY 419 GASTGL-----SSSPSSPRS-----PVFSPSPPGAGDEARGG 453
Db 530 GVNTEINAPVLAQKQFSINTLSQSPESDKAEAEAVTLPPAIPFNAS-----SSRIFR 582
QY 454 SPISKQTQTLPSRPGGAGEQPPPSARST-----PLPGPPGSP-----RSGGTP 500
Db 583 NSYTSISRSRSLRLSLNSLSASTSRETVDHNMPLPQLPKSPRSYLSERRAIHASP 642
QY 501 ----LHSPHLTPRASPTGTPPTPPSPGGVGGAARSLNSI--RNSFLGSPRFRHRKM 555
Db 643 STKSIHKSLSRKNIAAT-----VAARRTLQNSASKRSLYSLSQISKRSL 686
QY 556 QV-----PTAEMSSLTPESSPE-----LAKRSWFGNFIS--LDKEEQIF 593
Db 687 NLNDLLVFDPLPSPKPKPASENVKNSPHELSDSDFEILCDQILFGNALDRILEEED-- 744
QY 594 LVLLKDK-----PLSSIKADIVHAFSLSPSLSHSVLSQTSFRAEYKA 634
Db 745 ---NEKERTQQRQNDTKSSADTFTTIGSVTNKENGEPYP----TKTEKQCFNMSYKP 797
QY 635 SGGPS-----VFQKPVRFQVDISSEGEPEPRRDGSGGGIYSTFTTLISGSPSRFRKR 688
Db 798 SENMGLSFPPIFEK-----ENTLSSSYLEEQPKR-----AALSDITNSFNKMKQEGMR 848
QY 689 VETIQ-AQLLSTHDQPSVQALADEKNKAQTRPAGAPPSLQ-----PGRDDEL 739
Db 849 IEKKIQREQLQKNDRPS-----PLKPIQHQLRVLNSLPNDQKPSL 890
QY 740 SSSPRR 745
Db 891 SLDPRR 896

RESULT 3
G01025
serine/threonine protein kinase - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C;Accession: G01025
R;Navarro, E.
submitted to the EMBL Data Library, April 1996
A;Reference number: H00564
A;Accession: G01025
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-745 <NAV>
A;Cross-references: UNIPROT:Q15524; UNIPROT:Q96HB3; EMBL:X97630; NID:g1310674
C;Superfamily: protein kinase homology
F;18-271/Domain: protein kinase homology <kin>

Query Match 15.7%; Score 637; DB 2; Length 745;
Best Local Similarity 29.4%; Pred. No. 9.3e-16;
Matches 211; Conservative 92; Mismatches 238; Indels 176; Gaps 28;

QY 91 YLVLEHVS GGELFDYLVKGR LTPKEARKFRQIVSALDFCHSY SICHRLDKPENLLDDE 150
Db 93 YLVMEYASGEVFDYLVHGRMKKEARKFRQIVSAVQYCHQKFIVRDLKAENLLDA 152
QY 151 KNRIADFGMASIQVDSLSLETSCGSPHYACPEVKEKYGVDGRADMSGCVILFALLV 210
```

Db 153 DMNIKIADFGSNEFTFCGLKLDTCGSPPYAAPLFGQKKYDGPVDVWSLGVILYTLVS 212  
Qy 211 GALTDDNNLRQLLEKVKRGVHHPHFIPPCQSLRLRMIEVEPEKRLSLBQIKQHPWYL 270  
Db 213 GSLPFDGONLKELRERVLGRYRIPFYFMSTDCENLLKKFLILNPSKRGTLQEIIMKDRWN 272  
Qy 271 GKGHEPD---PCLRPAPGRRVAMRSLPSNGELDPDLVLESMAISGCFRDRRLHRLRSEE 327  
Db 273 VG-HEDDELKYPVPLPYK-----DPRTLMVSMG--YTREBIQSLVGQR 317  
Qy 328 ENQEMIIYLLDRKERYPSCEDODLPPRNDV-----DPRTLMVSMG--YTREBIQSLVGQR 317  
Db 367 ENQEMIIYLLDRKERYPSCEDODLPPRNDV-----PPRKVD 367  
Db 318 YN-EWATYLLLVGYSSELEGDTITLKPSPADLTNSSAQFPKHQVRSVANPKQRFS 376  
Qy 368 S-----PMLSRHGK-----RRRP-----RSM----- 384  
Db 377 DQAGPAIPTSNSYSKKTOSNNAENKRPEDRESGRKASTAKVPASPPLGLERKKTTP 436  
Qy 385 ---EVLSTTDAGGSGSPVTRALEMA--QHSORSRSVSG--ASTGLSSPLSSPRSPVF 437  
Db 437 STNSVLSTSTWRSNPLERASLQASIQNGKDSLTMPGGRASTASAGVSAAR----- 492  
Qy 438 SFSPEPGADGARGGSGSPTQTLPSPRGPGGAGEQPPPSARSTPLPGPGSP----- 493  
Db 493 ---PRQHOKSMGSHVHPNKASGLP---PTESNC-EVPRESTA---PQVPVSPSAHN 540  
Qy 494 -RSGGCTP-----LHSPHTPR-----ASPTGPTGTPPPSPGGVGAARSLN 538  
Db 541 ISSGGGAPDRTNFPRGVSSRSTFHAGQLQRVDQONLPGYVTPASPSPGHSQGR--RGASG 598  
Qy 539 SIRNSFELGSPFHRKQVPTAEE-MSSLTP-----ESSPELAKRSW-P 580  
Db 599 SIFSKP--TSKVFARNLMEPSKORVETLRPHVVGSGNDKEKEFEAKPRSLRFTWSM 656  
Qy 581 GNFTSLDKEQIFVLKDKPLSSIKADIVHAFSLSPSLSHSVLSGTSFRAEYKASGGSPV 640  
Db 657 KTTSSMEPNEMREIRKVDANSQSELHEKYMLL--CMHTGPGHEP----- 702  
Qy 641 FQKPVRFQVDISSEGPSPRRDGGGGGYSYVTFLLISGPRFRFRVETIQAL 697  
Db 703 ---VQWEMEYCK-----LPRLSLNG-----VRFKRISGTSMAFKNIASKIANEL 743

## RESULT 4

JC1446  
serine/threonine-specific protein kinase (EC 2.7.1.1.) AK21 - Arabidopsis thaliana  
N;Alternate names: protein kinase SNF1 homolog  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: JCI446; S58266; S66334  
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.  
Gene 120, 249-254, 1992  
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein  
A;Reference number: JC1446; MUID:93013041; PMID:1339373  
A;Accession: JC1446  
A;Molecule type: DNA  
A;Residues: 1-512 <LEG>  
A;Cross-references: UNIPROT:Q39997; GB:M93023; NID:g166599; PIDN:AAA32736.1; PID:g166600  
R;Thummler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.  
submitted to the EMBL Data Library, May 1995  
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase genes  
A;Reference number: S58266  
A;Accession: S58266  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 144-198 <THU>  
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910  
R;Thummler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.  
Plant Mol. Biol. 29, 551-565, 1995  
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes  
A;Reference number: S66334; MUID:96123233; PMID:8534852  
A;Accession: S66334  
A;Molecule type: DNA

A;Residues: 144-198 <TH2>  
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910  
C;Comment: This enzyme plays an important role in a signal transduction cascade regulati  
C;Genetics:  
A;Gene: AKin10; AK21  
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
C;Superfamily: AMP-activated protein kinase; protein kinase homology  
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase  
F;17-271/Domain: protein kinase homology <KIN>  
F;25-33/Region: protein kinase ATP-binding motif  
F;48, 67, 142, 144/Active site: Lys, Glu, Asp, Lys #status predicted  
F;147, 151/Binding site: magnesium (Asn, Asp) #status predicted  
Query Match 15.4%; Score 624; DB 1; Length 512;  
Best Local Similarity 42.5%; Pred. No. 1.9e-15;  
Matches 122; Conservative 59; Mismatches 92; Indels 14; Gaps 4;  
Qy 91 YLVLEHVSGLPEFYLKVKRLTPKEARKFPRQIVSALDFCHSYSIHRDLKPNLLDDE 150  
Db 93 YLVMEYVNSGELFYIIVEKRLQDEARNFFQIISGVEYCHRMVVRDLKPNLLDDE 152  
Qy 151 KNNIRIADFGWASLOVGSLSLETSCGSPHYACPEVIGKEYDGRADWMSGCVILFALLV 210  
Db 153 KNNIRIADFGWASLOVGSLSLETSCGSPHYACPEVIGKEYDGRADWMSGCVILFALLV 212  
Qy 211 GALTDDNNLRQLLEKVKRGVHHPHFIPPCQSLRLRMIEVEPEKRLSLBQIKQHPWYL 270  
Db 213 GALTDDNNLRQLLEKVKRGVHHPHFIPPCQSLRLRMIEVEPEKRLSLBQIKQHPWYL 272  
Qy 271 GKGHEPDCLPEAPGRRVAMRSLPSNGELDPDLVLESMAISGCFRDRRLHRLRSEE 330  
Db 273 A--HLPRYLAVPPPD-----TVQAKKIDEEILQEVINMGF--DRNHLIESLRNRTQND 322  
Qy 331 EKMIYLLDRKER-----YFSCEDODLPPRNDVDPKRKVDSPMLSR 373  
Db 323 GTVTYLLDRFRASSGYLGAEPQETMEGTTPRMHPAESVASPVSHR 369  
RESULT 5  
T38929  
changed division response protein [validated] - fission yeast (Schizosaccharomyces pombe  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T38929; T50476  
R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, April 1997  
A;Reference number: Z21818  
A;Accession: T38929  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-775 <BAD>  
A;Cross-references: UNIPROT:P87050; EMBL:Z94864; PIDN:CAB08165.1; GSPDB:GN000066; SPDB:SP  
R;Breeding, C.S.; Hudson, J.; Balasubramanian, M.K.; Hemminge, S.M.; Young, P.G.; Goul.  
Mol. Biol. Cell 9, 3399-3415, 1998  
A;Title: The cdr2(+) gene encodes a regulator of G2/M progression and cytokinesis in Sch  
A;Reference number: Z25082; MUID:99060136; PMID:9843577  
A;Accession: T50476  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-775 <BRE>  
A;Cross-references: EMBL:AF092508; NID:g3859527; PIDN:AAC72832.1; PID:g3859528  
C;Genetics:  
A;Gene: SPDB:SPAC57A10.02; cdr2+  
A;Map position: 1  
C;Function:  
A;Description: acts as a mitotic inducer; important for the completion of cytokinesis at  
Query Match 15.4%; Score 623.5; DB 2; Length 775;  
Best Local Similarity 27.8%; Pred. No. 2.8e-15;

Matches	220;	Conservative	109;	Mismatches	263;	Indels	199;	Gaps	30;
Qy	34	GNWSFLP-ETHGWSLFLPRINGIVLCHQBPVEVGDALMSSTCFQPSA-----	84						
Db	8	GPWELGLSLGSGPNSRLAKHRETGLAVVKPI-VG-----WSELTSSQOARIEGELVLL	62						
Qy	85	-----PSI-----SFRVLVLEHVSQGLFDVLVKKGRITPKKARKFRQIVSALD	129						
Db	63	RLTEHNVLIQDIVISAQEQLFVVVEYMPGEGELFDCLMRKSGSTEQDTAKFLWQLCGLE	122						
Qy	130	FCHSYSTICHRDLKPNLLDKNNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGE	189						
Db	123	YCHKLHICHRDLKPNLYLDAHSGIKIGEGMASIQPGKLLQTSQSGSPHYASPEIIMGR	182						
Qy	190	KYDGRADMSQGVLPALLVGAALPFDDNLRLLEKVKVGVFHMHPFIPDCQSLRGM	249						
Db	183	SYDGCASDIWSCGIFFALLTGKLPFDDNIRSLLLKVCQCGPEMPSNISPQOHLLYRM	242						
Qy	250	IEVEPEKRLSLEIQKHFWYLGKGHEPDCLEPAPGRVAMRSLPSNGELDDPVLESMS	309						
Db	243	LDVDSSTRTWEQREHPFLSCFVH-----PNISIFIISAPIQ-PIDPLIVQHLSL	292						
Qy	310	L-GCFRDRERLHRELSEENQERMIYLLLDKRYPSCEDQDLPRNDVDPKRVDS	368						
Db	293	VFRCSDDPMPLYEKLASQSLVAKTLYTL--SRHLHP-----PSSAAVDRNRAVDD	343						
Qy	369	PM--LSRHGKRPRPKMEVLSI-----TDAGGSGSPVETRALEM	407						
Db	344	LLGTAASNGOQMDEREEOAINIPTLAPYPISYAAESVPRPATYSASPLTPVTITSGFNY	403						
Qy	408	AQHS-----QRSRSVSGA-----STGLS-----SSPLSSPSRSPVFSFSP-----	441						
Db	404	SFNAINPOSILQRPATYSSAVPOLPKSVTPCLAYPHDSSMLSSNYRPPSALSPRNFVSI	463						
Qy	442	-EPG-----ACDEARGGSPKSTQTILPSRGPGGGAGEQPPPPSARSTPLPG	488						
Db	464	NDPEVQLSRRATSLDMSNDFRMNENDPSIVGNLAASNFPFTGMG-----PPRKRYTSMSE	518						
Qy	489	PPGS-----PRSSGGTLP-----HSPHTPRASPT-----GTPGTPP	520						
Db	519	HTGNRWSPFRGSAFNPRVTFNVGNQFNSNINNNYNNQYANATWNSRRLTPS---	575						
Qy	521	PPSPGGGGAARSLRSLIRNSF--LGSPRFRHRKQVPTAEEMSSITPESSPELAKRS	578						
Db	576	-----GERSRADLSQSPASYDSLNVPKHRRRQSLFSPSTKXKLS--GSPFPKRS	625						
Qy	579	W-----FGNFISLDXEEQIFLVLDKPLSSIK-ADIVHAFSLIPSLSHVL	623						
Db	626	FLRLFSSEPSCKCVYASLVALEHEILEVLRWQLGIGIADIYDSVS-ASISARIK	684						
Qy	624	SQTSFRAEYKASGSPSVFKPVRFOVDISSEGEPEPPRRDGGGGGIYSVTFTLISGPS	683						
Db	685	QNSLNL-----KPVRFKRSIVIA-----EPPGS-----QAVFVLESQSS	718						
Qy	684	RRFKRWETIQ	694						
Db	719	TTFDHLATEFQ	729						

RESULT 6

T10449  
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber  
N/Alternate names: SNF1-related protein kinase  
C/Species: Cucumis sativus (cucumber)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C/Accession: T10449  
R/Gumpel, N.J.  
submitted to the EMBL Data Library, December 1996  
A/Reference number: Z17020  
A/Accession: T10449  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-504 <GUM>

A/Cross-references: UNIPROT:P93113; EMBL:Y10036  
A/Experimental source: cv. Masterpiece; cotyledon

C/Function:  
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine  
C/Superfamily: AMP-activated protein kinase; protein kinase homology  
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F/6-260/Domain: protein kinase homology <KIN>

Query Match	15.2%;	Score	618;	DB	2;	Length	504;
Best Local Similarity	44.7%;	Pred. No.	3e-15;				
Matches	115;	Conservative	55;	Mismatches	77;	Indels	10;
Gaps	3;						
Qy	91	YLVLEHVSQGLFDVLVKKGRITPKKARKFRQIVSALDFCHSYICHRDLKPNLLDDE	150				
Db	82	YVMEYKSGELFDYIVKGRLEQDEARNFFQQIISGVYCHRNVMVHRDLKPNLLDLS	141				
Qy	151	KNNIRIADFGMASLQVDSLLTSCGSPHYACPEVIKGEKVDGRRADWMSQGVILFALLIV	210				
Db	142	KCNVKIADFGSLNIMRDGHFLTKSCGSPNYAAPEVISGKLYAGPEVDVWSCGVILYALLC	201				
Qy	211	GALPPDDNLRQLLEKVKRGVFMHPFIPDCQSLLRGMIEVEPEKRLSLEIQKHFWYL	270				
Db	202	GTLFPDDENIPNLFKKIGIYTLPSHSSGARELIPSLMLVVDPMKRTITPEIRQHPMFQ	261				
Qy	271	GKGHEPDCLEPAPGRVAMRSLPSNGELDDPVLESMAISLGCFRDRERLHRELSEENQ	330				
Db	262	A--HLPRYLAIVPPP-----TMQAKKIDEDILQEVVWKGFF--DRNQLVESLRNRIQNE	311				
Qy	331	EKMIYVLLADRKERYPS	347				
Db	312	ATVAYVLLLDNRFRVSS	328				

RESULT 7

T18611  
probable serine/threonine-specific protein kinase (EC 2.7.1.-), long splice form - Caenor  
N/Contains: probable serine/threonine kinase, short splice form  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T18611; T18610; T23144; T23143  
R/McMurray, A.  
submitted to the EMBL Data Library, October 1996

A/Reference number: Z18997  
A/Accession: T18611  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1192 <WIL1>  
A/Cross-references: UNIPROT:Q9TW45; EMBL:Z81027; PIDN:CAB54179.1; GSPDB:GN00023; CESP:H3;  
A/Experimental source: clone AH10  
A/Accession: T18610  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-487,536-1192 <WIL2>  
A/Cross-references: EMBL:Z81027; PIDN:CAB54178.1; GSPDB:GN00023; CESP:H3E23.1b  
A/Experimental source: clone AH10  
R/McMurray, A.  
submitted to the EMBL Data Library, June 1997  
A/Reference number: Z19696  
A/Accession: T23144  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1192 <WIL3>  
A/Cross-references: EMBL:Z96102; PIDN:CAB54263.1; GSPDB:GN00023; CESP:H3E23.1a  
A/Experimental source: clone H39E23  
A/Accession: T23143  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-487,536-1192 <WIL4>  
A/Cross-references: EMBL:Z96102; PIDN:CAB54262.1; GSPDB:GN00023; CESP:H3E23.1b  
A/Experimental source: clone H39E23  
C/Genetics:  
A/Gene: CESP:H39E23.1a; CESP:H39E23.1b  
A/Map position: 5

A;Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 992/3  
C;Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific protein kinase; long splice form #8  
F;1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #8  
F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splice form #8

Query Match 15.2%; Score 616; DB 2; Length 1192;  
Best Local Similarity 27.3%; Pred. No. 7.5e-15;  
Matches 208; Conservative 106; Mismatches 281; Indels 168; Gaps 23;

```
Qy 91 YLVLEHVGSGELFDYLVKKGLRTPKEARKFPRQIVSALDFCHSYISICHRDLKPNLLDDE 150
Db 243 YLVLEASGGEVFDYLVAGHGMKEKARAKFRQIVSAVQLHSHKNIITHRDLKAENLLDQ 302
Qy 151 KNNIRIADFGWASLQVGDLSLETSCGSPHYACPEVIKGEKVDGRRADWMSGCVILFALLV 210
Db 303 DMNIIKADFGSNTFSLGKLDITFCGSPPYAAPLFFGKKYDGEVDVWSLGVLYLYTVLS 362
Qy 211 GALPFDNDNLRLQLEKVKRGVFMHPHFIIPDCQSLLRGMIEVEPEKRLSLEQIQHPWYL 270
Db 363 GSLPFDQNLKELRERVLKGYRIPFYMSTDCENLLKFLVINPQRSSLDNIMKORWMN 422
Qy 271 GKGHEPD---PCLEPAPGRVAMRSLPSNGELDPDVLESMAISLGCFR---DRELRHRELRS 325
Db 423 VGYEDDELKPEIE-----PPKQDIDEQRIEKLIIQI--FOLGFNKAALLESVEK 468
Qy 326 EENQERKMIYVLLDRKERVPSCE---DQDLPFRNDVDPKRVDSPLMRSHGKRRPERK 382
Db 469 EKFDIHATVLLGLERKSDMDASEITMAQSLSHSSINV-----SSSLGQHPAGVITRE 522
Qy 383 SMEVLSITDAGGGSPVPTRRALMAHQSRSVSGASTGLSS---SPLSSPSRSPVPSF 439
Db 523 --HVTSSAGSSASP-----SRYRSATATGASITAGSALASANAQAQHQSSA 571
Qy 440 SPEPAGDEARGGSPSTKQ---TLPSRGRGGGAGEGPPPPSARST-PLPGPPGSPRS 495
Db 572 APSSGSSSRSSQNDAAATAAGGTVMVMSGTRHGGVQVMAQPTSRQATISILQPPSYKPS 631
Qy 496 SGGT-----PLHPLHTPRAS---PTGPTGTTTPPSPGG-----GVGGAARSLN 538
Db 632 SNTTQIAQIPLFRNRNSTSSAAQPTGTITGTRKIDPKRIPLNSTAVQGHRTGAV 691
Qy 539 SIRNSFLGSPFRHRRKM---QVPTAEEMSSL---TP-----SSSSSSSSSSSSSSSSSS 568
Db 692 AANNGGIPSHRDHAQQOQYQNMQLTSWTMSKLNKTPAAGTAATSSSSSSSSSSSSSSSSSS 751
Qy 569 -----ESSPELAKRSWFGNF-----TP-----SSSSSSSSSSSSSSSSSSSSSSSS 590
Db 752 KSGSQISHAPTEPVIREDDDDNNSENQNVPLIGGVGQPTSPAVQVPTEDATSSSDKEQ 811
Qy 591 QIFVLVKDPLSSIKADIVHAFSLIPSLSHSVLSQTSFRARYKASGGPSVFPQVRVQVD 650
Db 812 QOKKASSETPKES-KPSMIHQSPSPMPSPQMMTAMESLKLSESGQTGGPTV-----SS 860
Qy 651 ISSSEGPEPSRRDGGSGGGIYVTFTLISGSPRRFRKRVVETIIQAQLSLTHDQPSVALA 710
Db 861 --ATGGP---PQR-----ATSQMSRSATTNSANNGSGGGGAAASAA 898
Qy 711 DEKNGAQTFRPAGAPRPSLQPPGRDPDELSSSPRRGPPKDKKL 753
Db 899 TNQLSGAPSTGASSQQYHPKA---PSSSSSSSTNPPHQHQL 937
```

RESULT 8  
S27966  
N;Accession: S27966  
N;Alternate names: protein p78  
C;Species: Homo sapiens (man)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004  
C;Accession: S27966  
R;Maheshwari, K.K.; Som, S.; Parsa, I.  
submitted to the EMBL Data Library, January 1992  
A;Description: Sequence of a cDNA encoding 78kD marker protein lost in chemically induced  
A;Reference number: S27966

A;Accession: S27966  
A;Molecule type: mRNA  
A;Residues: 1-713 <WAH>  
A;Cross-references: UNIPROT:P27448; EMBL:M80359; NID:g189511; PID:AAAS9991.1; PID:g18951  
C;Superfamily: protein kinase homology  
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F;54-307/Domain: protein kinase homology <KIN>  
F;62-70/Region: protein kinase ATP-binding motif

Query Match 15.0%; Score 608; DB 2; Length 713;  
Best Local Similarity 30.4%; Pred. No. 9.1e-15;  
Matches 202; Conservative 90; Mismatches 234; Indels 138; Gaps 28;

```
Qy 91 YLVLEHVGSGELFDYLVKKGLRTPKEARKFPRQIVSALDFCHSYISICHRDLKPNLLDDE 150
Db 129 YLIMEASGGEVFDYLVAGHGMKEKARAKFRQIVSAVQYCHQKRIVHRLDKAENLLD 188
Qy 151 KNNIRIADFGWASLQVGDLSLETSCGSPHYACPEVIKGEKVDGRRADWMSGCVILFALLV 210
Db 189 DMNIIKADFGSNEFTVGGKLDITFCGSPPYAAPLFFGKKYDGEVDVWSLGVLYLYTVLS 248
Qy 211 GALPFDNDNLRLQLEKVKRGVFMHPHFIIPDCQSLLRGMIEVEPEKRLSLEQIQHPWYL 270
Db 249 GSLPFDQNLKELRERVLKGYRIPFYMSTDCENLLKFLVINPDKGTLEQIMKDRWIN 308
Qy 271 GKGHEPD---PCLEPAPGRVAMRSLPSNGEL---DPDVLESMAISLGCFRDRERLHREL 324
Db 309 AG-HEEDELKPFVEP-----ELDISDQKRIDIMVGMG-----Y 340
Qy 325 SEENQERKMIYVLLDRKERVPSCE---DQDLPFRNDVDPKRVDSPLMRSHGKRRPERK 370
Db 341 SQSEIQESLSKMKYDELTATYLLGRK-----SSEVRPSSDLNNTGSPHKKVQSV 393
Qy 371 LSRHGKRRPERKSMELVSIITDAGGGSP---VPTRRALMAHQSR---SRSVSGAS 421
Db 394 SSSQKQRR-----YSDHAGPGIPSVVAYPKRSQTSADSLKEDGISSRKSTGSA 443
Qy 422 TGLSSPSPLSPRSPVPSFSPGAGDEARGGSPSTKQTLPSRGRGGGAGEGPPPPPSA 481
Db 444 VGGKG---IAPASPMILGNASNPNKADIPE-----RKKSSTVPSSNTASGGM-----TR 488
Qy 482 RSTPLPCGPPSPSSGGTPLHSPHTPRASPTGPTGTPPPSPCGGVGGGAARSL----- 537
Db 489 RNTYV---CSERTTDDR---HSVIQNGKENST-IPQORTPVASTHSSISAAATPDRIAPPR 541
Qy 538 -NIRNSFLGSPFRHRRKMVPTAEEMSSITPSSPELAKRS-----WFGNFIIS-LDKEE 590
Db 542 GTASRSTFHQQR-ERRATYNGPPASPSLSHEATPLSQTSRSGSTTLFSLKLSKLTISR 600
Qy 591 QIFVLVKD-----KPLS-----ADIVHAFSLIPSLSHSVLSQTSFRARYK 633
Db 601 NVSAKQKDEKAKPRSLRFTWMKTTSSMDPGDMREIRKVLDDANNCDYEQRE-RFLLF 659
Qy 634 ASGGPSVFPQVRVQVDISSESEGPSPRRDGGGGIYVTFTLISGSPRRFRKRVVETI 693
Db 660 CVHGDGHAENLVQWMEVCK-----LPLRSLNG-----VRPKRISGTSIAFKNIASKI 707
Qy 694 QAQL 697
Db 708 ANEL 711
```

RESULT 9  
S59359  
N;Accession: S59359  
N;Alternate names: protein YDR507c  
C;Species: Saccharomyces cerevisiae  
C;Date: 30-Nov-1995 #sequence\_revision 01-Mar-1996 #text\_change 16-Aug-2004  
C;Accession: S59359; S69565  
R;Longline, M.S.; Pringle, J.R.  
submitted to the EMBL Data Library, August 1995  
A;Reference number: S59359  
A;Accession: S59359

A;Molecule type: DNA  
A;Residues: 1-1142 <LON>  
A;Cross-references: UNIPROT:Q12263; EMBL:U331140; NID:g992650; PIDN:AAA75513.1; PID:g992650  
R;Dietrich, F.S.  
Submitted to the EMBL Data Library, August 1995  
A;Description: The sequence of S. cerevisiae cosmids 8166, 9787, 9717, and lambda 3073.  
A;Reference number: S69553  
A;Molecule type: DNA  
A;Residues: 1-1142 <DIE>  
A;Cross-references: EMBL:U33057; NID:g927764; PIDN:AA64949.1; PID:g927777; MIPS:YDR5070  
C;Genetics:  
A;Gene: SGD:GIN4  
A;Cross-references: SGD:S0002915; MIPS:YDR5070  
A;Map position: 4R  
C;Superfamily: protein kinase homology  
C;Keywords: Atp  
F;17-289/Domain: protein kinase homology <KIN>  
F;25-33/Region: protein kinase ATP-binding motif

Query Match 14.9%; Score 604; DB 2; Length 1142;  
Best Local Similarity 39.0%; Pred. No. 1.9e-14;  
Matches 152; Conservative 54; Mismatches 118; Indels 66; Gaps 12;

QY 91 YLVLEHVSGLGELFDYLVKKGRLTPKEARKFQIVSALDFCHSYISCHRDLPENLLDE 150  
DB 107 YLVLEYAEKGLFLLVVERGELPEHEAIRFRQIIIGVSYCHALGIVHRDLKPEENLLDH 166

QY 151 KNNIRIADFGMASLQVGDLSLETSCGSPHYACPVIRKGVKGYDGRADWMSGCVILFALLV 210  
DB 167 KYNKIADFGMALETGKLLTSCGSPHYAAPVIRKGVKGYDGRADWMSGCVILFALLV 226

QY 211 GALPPD--DDNLRLLEKVGKGVFHP--HPIPPDCQSLRGMIKVEPEKRLSLEQIKH 266  
DB 227 GRLPDEEDGNIRTLKLVKQGEFMPDSDISREAOQLIRKILTVDPERRIKTRDILKH 286

QY 267 PWYLGKHEPDPCLPAPGR--VAMRSLP-----SNGELPDVLESMAISGCF 313  
DB 287 -----PQQKYSIRDSKIRGLPREDIYVPLSESNSSIDATILQNLVILMHG 335

QY 314 RDRERLHRELSEENQEMKIYLLDRKERYPSC-----DQDLPPRDVD----PP 362  
DB 336 RDEGIGKEKLRPGANAEKTLVALLYRFK-----CDTQKELIKQVKKQSISSVSP 390

QY 363 RKRVDSPMLSRHGKRPKRKMEVLSITDAGGGSPVTRRALEMAQHSQRSSVSGAST 422  
DB 391 SKKV-----STPQRRNRRESU--ISVTSS-----RKKPIFNKFTASSSSNLT 435

QY 423 GLSSSPGSPRSP-----VFSFSPPCA 445  
DB 436 PGSSKRLSKNFSSKKLSTIVNQSSPTPAS 465

RESULT 10  
T07788  
Probable serine/threonine-specific protein kinase (EC 2.7.1.1-) SNF1 - potato  
N;Alternate names: StubSNF1 protein  
C;Species: Solanum tuberosum (potato)  
C;Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C;Accession: T07788  
R;Lakatos, L.; Banfalvi, Z.  
Submitted to the EMBL Data Library, January 1997  
A;Reference number: Z16133  
A;Accession: T07788  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-512 <LAK>  
A;Cross-references: UNIPROT:O04122; EMBL:U83797; NID:g1935915; PIDN:AA52224.1; PID:g1935915  
C;Genetics:  
A;Gene: SNF1  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
C;Superfamily: AMP-activated protein kinase; protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F;17-271/Domain: protein kinase homology <KIN>

Query Match 14.8%; Score 599; DB 2; Length 512;  
Best Local Similarity 43.6%; Pred. No. 1.4e-14;  
Matches 116; Conservative 53; Mismatches 83; Indels 14; Gaps 4;

QY 91 YLVLEHVSGLGELFDYLVKKGRLTPKEARKFQIVSALDFCHSYISCHRDLPENLLDE 150  
DB 93 YVMEYVKSGLGELFDYIVKGRQLQDEARNFQQIISGVYCHINMVVHRLKPEENLLDS 152

QY 151 KNNIRIADFGMASLQVGDLSLETSCGSPHYACPVIRKGVKGYDGRADWMSGCVILFALLV 210  
DB 153 KWNVKIADFGLSNIMRDGHFLKTSCTSPNYAAPVIRKGVKGYDGRADWMSGCVILYALLC 212

QY 211 GALPPDDNLRLLEKVGKGVFHPHPIPPDCQSLRGMIKVEPEKRLSLEQIKH 270  
DB 213 GTLPDDDENIPNLFKIKGGYITLPSHLSAGARDLIPRLMIVDPKMTIPEIRLHFWFQ 272

QY 271 GQKHEPDPCLPAPGRVAMRSLPSNGELDPDVLESMAISGCFDRERLHRELSEENQ 330  
DB 273 A--HLPRYLAVPPD-----TMOQAKKIDEEILQEVVVMGF--DRNNLTESLRNVQNE 322

QY 331 EKMIVYLLDRKER-----YPSCEDQD 352  
DB 323 GTVPYTYLLDNRHVRVSTGYLGAEPQ 348

RESULT 11  
G89287  
protein H39E23.1 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C;Accession: G89287  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology,  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: G89287  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1246 <STO>  
A;Cross-references: GB:chr\_V; PIDN:CAB09532.1; PID:g3878100; GSPDB:GN00023; CESP:H39E23.1  
C;Genetics:  
A;Gene: H39E23.1  
A;Map position: 5

Query Match 14.7%; Score 598; DB 2; Length 1246;  
Best Local Similarity 28.2%; Pred. No. 3.3e-14;  
Matches 204; Conservative 103; Mismatches 268; Indels 148; Gaps 24;

QY 91 YLVLEHVSGLGELFDYLVKKGRLTPKEARKFQIVSALDFCHSYISCHRDLPENLLDE 150  
DB 133 YLVLEASGGEVFDYLVHGRMKEKARAKFRQIVSAVQYLSKNTIHRDLKAENLLDQ 192

QY 151 KNNIRIADFGMASLQVGDLSLETSCGSPHYACPVIRKGVKGYDGRADWMSGCVILFALLV 210  
DB 193 DMNIKIADFGSFTSNGNKLDTFCGSPYAAPVIRKGVKGYDGRADWMSGCVILYTVLS 252

QY 211 GALPPDDNLRLLEKVGKGVFHPHPIPPDCQSLRGMIKVEPEKRLSLEQIKH 270  
DB 253 GSLPFDQNLKELRERVLKRYRIPFVMTSDCNLLKKFLVINPQRSSLDNMDRWMN 312

QY 271 GQKHEPDPCLPAPGRVAMRSLPSNGELDPDVLESMAISGCF--DRELRHRLRS 325  
DB 313 VGYEDBLKPFIE-----PPDQIDBQRIEKLQI--FQGFNKAAILSEVEX 358

QY 326 EENQERKMIVYLLDRKERYPSCB---DQDLPPRDVDPPRKRVDSPMLSRHGKRPKR 382  
DB 359 EKFDIATYLLIGERSKSDMDASEITWQASLLSHSSINV-----SSSLQHPAGVITRE 412





Db 91 YVMEYVKSGLFDYIVKGRLOQEDARKIFQOI IAGVEYCHKNMVVHRDLKPNLLIDA 150  
Qy 151 KNNIRIADFGWASLQVGSLLTSCGSPHYACPEVKGKYGDRADMMWSCGVILFALLV 210  
Db 151 RNNVKIADFGNIMRDGHFLKTKSCGSPNVAAPVGVSGKLYAGPEVDVWSCGVILYALLC 210  
Qy 211 GALPFDNDNLRLQLEKVKRGVFMHPIPPDCQSLRGMIEVEPEKRLSLEQIQKHPWYL 270  
Db 211 GTLPFDNDENIPNFKIKSGVYTLPSHLSPALDLIPRLMILVDPMKRISVPIRQHWPF- 269  
Qy 271 GKGHEPDCLEPAPGRVAMRSLPSNGELDPDVLESWASLGCFDRERLHRLRSEENQ 330  
Db 270 -KIHLPYLA VPPDARQHLK-----KLDDEILQQVSRMGL---DRDQLDLSLQKRIQDD 320  
Qy 331 EKMIYLLDRKERYPS-----CEDODLPFRNDVDPKRVDPSPMLSRHGKR 378  
Db 321 ATVAYILLYDNRSWASSGVLGAEGFQESVDCVSPGLFPNLDL-----QLSTGNGVSESLRR 376  
Qy 379 PERK 382  
Db 377 PERK 380  
RESULT 14  
T29858  
hypothetical protein T01C8.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29858  
R:Wohlmann, P.; Hawkins, J.  
A:Submitted to the EMBL Data Library, May 1996  
A:Description: The sequence of C. elegans cosmid T01C8.  
A:Reference number: 220699  
A:Accession: T29858  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-562 <WOH>  
A:Cross-references: UNIPROT:Q22068; EMBL:U58726; PIDN:AAB00579.1; GSPDB:IGN00028; CESP:TQ  
A:Experimental source: strain Bristol N2; clone T01C8  
C:Genetics:  
A:Gene: CESP:T01C8.1  
A:Map position: X  
A:Introns: 41/1; 197/2; 237/1; 272/2; 307/3; 375/1; 479/1; 529/3  
C:Superfamily: AMP-activated protein kinase; protein kinase homology  
Query Match 14.7%; Score 595; DB 2; Length 562;  
Best Local Similarity 31.0%; Pred. No. 2.1e-14;  
Matches 161; Conservative 65; Mismatches 146; Indels 148; Gaps 15;  
Qy 83 SAPSISFRVLVLEHVSGLGELFDYLVKKGRLTPKEARKFQIIVSALDFCHSYSTICHRDLK 142  
Db 93 STPSDIF--MIMHVSGLGELFDYIVKHGRLKTAERARFQOIISGVYCHRMVVRDLK 150  
Qy 143 PENLLDKNIRIADFGWASLQVGSLLTSCGSPHYACPEVKGKYGDRADMMWSCG 202  
Db 151 PENLLDQNNVKIADFGLSNIMTDCGLRSCGSPNVAAPVSGKLYAGPEVDVWSCG 210  
Qy 203 VILFALLVGLPDDNLRLQLEKVKRGVFMHPIPPDCQSLRGMIEVEPEKRLSLEQ 262  
Db 211 VILYALLCGTLPDDDEHVPSPFLFKIKSGVYTPDFLERIVNLLHMLCVDPMKATIKD 270  
Qy 263 IQKHPWYLGKGHEPDCLEPAPGRVAMRSLPSNGELDPDVLESWASLGCFDR-RELRHR 321  
Db 271 VIAHEWF-----QKDLFN--YLFPPISEASIVDIEAVREVTFR 308  
Qy 322 ELRSEENQEKMI-----YVILLDRKERYSCEDQDLPPRNDVDPKRVDPSPM 370  
Db 309 YHVAEEVTSALLGDDPHHLSLAYNLIVDNKGIADETAKLSIEEFYQVTP--NKGPGV 366  
Qy 371 LSRHGKRRP-----KSMVLSITDAGGG- 396  
Db 367 -----HRHPRIASVSSKITPTILDNTEASGANENKRAKWHLGIQSQRPEIMPEVFRA 421

Qy 397 -----SPV--PTRRALEWAQHSQRS-----RVSGASTGLSS 426  
Db 422 MKQLDMKVKVLPVHVIRRKPDAPAADPPKMSLQLYQVDQSYLLDFKSLADEESGAS 481  
Qy 427 SPLSSPSRPFVSPFEPGAGDEARGGSPKTKQTLPSRGRGGGAGEQPPPSARSTPL 486  
Db 482 A--SSSRHASMPQKPA-----GIRG-----TRTSSM 507  
Qy 487 PGPGSPRSGGTPLHSPHLPFRASPTGTGTGTTTPPPSPGG 526  
Db 508 FOAMSMEASIEKMEVHD-----FSDMSCDVTTPPPSPGG 540  
RESULT 15  
S59941  
serine/threonine-specific protein kinase (EC 2.7.1.1-) BKN2 - barley (fragment)  
C:Species: Hordeum vulgare (barley)  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C:Accession: S59941  
R:Hannappel, U.; Vicente-Carbajosa, J.; Barker, J.H.A.; Shewry, P.R.; Halford, N.G.  
A:Plant Mol. Biol. 27, 1235-1240, 1995  
A:Title: Differential expression of two barley SNF1-related protein kinase genes.  
A:Reference number: S59941; MUID:95284374; PMID:7766906  
A:Accession: S59941  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-473 <HAN>  
A:Cross-references: UNIPROT:Q43475; EMBL:X82548  
C:Genetics:  
A:Gene: BKN2  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine  
C:Superfamily: AMP-activated protein kinase; protein kinase homology  
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase  
F:1-244/Domain; protein kinase homology (fragment) <KIN>  
F:21,40,115,117/Active site: Lys, Glu, Asp, Lys #status predicted  
F:120,124/Binding site: magnesium (Asn, Asp) #status predicted  
Query Match 14.7%; Score 594.5; DB 1; Length 473;  
Best Local Similarity 38.6%; Pred. No. 1.9e-14;  
Matches 127; Conservative 60; Mismatches 103; Indels 39; Gaps 7;  
Qy 91 YLVLEHVSGLGELFDYLVKKGRLTPKEARKFQIIVSALDFCHSYSTICHRDLKPNLLD 150  
Db 66 YVMEYVKSGLFDYIVKGRLOQEDARKIFQOIISGVYCHRMVVRDLKPNLLD 125  
Qy 151 KNNIRIADFGWASLQVGSLLTSCGSPHYACPEVKGKYGDRADMMWSCGVILFALLV 210  
Db 126 KCVKIADFGLSNIMRDGHFLKTKSCGSPNVAAPVSGKLYAGPEVDVWSCGVILYALLC 185  
Qy 211 GALPFDNDNLRLQLEKVKRGVFMHPIPPDCQSLRGMIEVEPEKRLSLEQIQKHPWYL 270  
Db 186 GTLPFDNDENIPNFKIKSGIYTLPSHLSPALDLIPRLMILVDPMKRIITRIRHSWFK 245  
Qy 271 GKGHEPDCLEPAPGRVAMRSLPSNGELDPDVLESWASLGCFDRERLHRLRSEENQ 330  
Db 246 A--RLPRLAVPPDPTAQVK-----KLDDTLNDVIMKGF--DKNQLTESLQKQLONE 295  
Qy 331 EKMIYLLDRKRR-----YPSCEDQDLPPRNDVDPKRVDPSPMLSRHGKRRERKSMEV 386  
Db 296 ATVAYILLYDNKRLTTSYGILGAEO-----SMDSSFSOISPETFS--- 336  
Qy 387 LSITDAGGSPVPTRRALEWAQHSQRS 415  
Db 337 -SASEARQYGGSP-----GFGIRQHFAAER 359  
Search completed: February 17, 2005, 11:03:26  
Job time : 49 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2005, 10:30:05 ; Search time 179 Seconds  
(without alignments)  
2179.913 Million cell updates/sec

Title: US-10-803-277-4

Perfect score: 4056

Sequence: 1 MGLEFGLEAGNWSHPLPG.....PRRGPPKXKLLATNGTLP 762

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3545	87.4	794	1 K111_HUMAN	Q8tdc3 homo sapien
2	3518	86.7	776	2 Q699J6	Q699J6 mus musculu
3	2405	59.3	719	2 Q699J3	Q699J3 mus musculu
4	2400	59.2	766	2 Q6ZM04	Q6ZM04 homo sapien
5	2397	59.1	705	2 Q69298	Q69298 mus musculu
6	2390.5	58.9	675	2 Q699J4	Q699J4 mus musculu
7	2386	58.8	736	1 ST29_HUMAN	Q8iwd3 homo sapien
8	2379.5	58.7	653	2 Q6DMN7	Q6dmn7 mus musculu
9	2188.5	54.0	523	2 Q6PHM0	Q6phm0 mus musculu
10	1588	39.2	861	2 Q9VUV4	Q9vuv4 drosophila
11	1571.5	38.7	696	2 Q7PV95	Q7pv95 anopheles g
12	1438	35.5	698	2 Q61298	Q61298 halocynthia
13	1383	34.1	914	2 Q19469	Q19469 caenorhabdi
14	1228	30.3	701	2 Q95T92	Q95t92 drosophila
15	731	18.0	1058	2 Q6C6T2	Q6c6t2 yarrowia li
16	693	17.1	1425	2 Q75D01	Q75dd1 ashbya goss
17	677	16.7	1518	1 KKK1_YEAST	P34264 saccharomyc
18	658	16.2	833	2 Q76P07	Q76p07 dictyosteli
19	651.5	16.1	1311	2 Q6P4S6	Q6p4s6 mus musculu
20	647	16.0	1314	2 Q6BPT2	Q6bpt2 debaryomyce
21	646.5	15.9	1267	2 Q6CK49	Q6ck49 kluyveromyc
22	646.5	15.9	1267	2 Q72865	Q72865 kluyveromyc
23	643.5	15.9	764	2 Q6ZNL8	Q6znl8 homo sapien
24	643.5	15.9	783	2 Q86YJ2	Q86yj2 homo sapien
25	643	15.9	1531	2 Q6B1J25	Q6b1j25 debaryomyce
26	637	15.7	691	2 Q96RG0	Q96rg0 homo sapien
27	636	15.7	745	2 Q15524	Q15524 homo sapien
28	636	15.7	755	2 Q7KZ17	Q7kz17 homo sapien
29	636	15.7	778	2 Q96HB3	Q96hb3 homo sapien
30	632.5	15.6	1187	2 Q6NSH8	Q6nsh8 brachydanio
31	632	15.6	722	2 Q6PDR4	Q6pdr4 mus musculu

#### RESULT 1

ID	K111_HUMAN	STANDARD;	PRT;	794 AA.
AC	Q8TDC3; Q8NDD0; Q8NDR4; Q8TDC2; Q96AV4; Q96JL4;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	03-JUL-2004 (Rel. 44, Last annotation update)			
DE	Probable serine/threonine-protein kinase KIAA1811 (EC 2.7.1.37).			
GN	Name=KIAA1811;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Brain;			
RA	She X.Y., Yu L., Guo J.H.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 51-794 FROM N.A.			
RC	TISSUE=Brain;			
RA	Koehler K., Beyer A., Bloecker H., Boecher M., Brandt P., Mewes H.-W.,			
RL	Weil B., Wiemann S.;			
RN	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 80-794 FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=212451130; PubMed=11347906;			
RA	Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XX.			
RT	The complete sequences of 100 new cDNA clones from brain which code			
RL	for large proteins in vitro.";			
RN	DNA Res. 8:85-95(2001).			
RN	[4]			
RP	SEQUENCE OF 303-794 FROM N.A.			
RC	TISSUE=Lymph;			
RX	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			

Q96L34 homo sapien  
Q8ng37 homo sapien  
Q8phv1 brachydanio  
Q08679 rattus norv  
Q8br95 mus musculu  
Q6fmf3 candida gla  
Q9y2k2 homo sapien  
P57059 homo sapien  
Q88a18 homo sapien  
Q38997 arabidopsis  
P87050 schizosacch  
Q6v8y5 physcomitre  
Q8qgv3 xenopus lae  
Q80t81 mus musculu

#### ALIGNMENTS

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
-1- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Name=1;  
IsoId=Q8TRDC3-1; Sequence=Displayed;  
Name=2;  
IsoId=Q8TRDC3-2; Sequence=VSP\_008158;  
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
-1- SIMILARITY: Contains 1 USA domain.  
-1- CAUTION: Ref.2 (CAD38950) sequence differs from that shown due to a frameshift in position 781.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; AF479826; AAL87697.1; --  
EMBL; AF479827; AAL87698.1; --  
EMBL; AL834275; CAD38950.1; ALT\_FRAME.  
EMBL; AL831945; CAD38595.1; --  
EMBL; AB058714; BAB47440.1; --  
EMBL; BC016681; AAH16681.1; ALT\_INIT.  
HSP; Q63450; 1A06.  
InterPro; IPR011009; Kinase like.  
InterPro; IPR000719; Prot\_kinase.  
InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
InterPro; IPR002290; Ser\_thr\_pkinase.  
InterPro; IPR000449; USA.  
Pfam; PF00069; Pkinase; 1.  
ProDom; PD000001; Prot\_kinase; 1.  
SMART; SM00220; S\_TKC; 1.  
PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
PROSITE; PS00030; USA; 1.  
KW Alternative splicing; ATP-binding; Serine/threonine-protein kinase;  
KW Transferrase.  
FT DOMAIN 50 301 Protein kinase.  
FT DOMAIN 330 372 USA.  
FT DOMAIN 508 556 Pro-rich.  
FT NP\_BIND 56 64 ATP (By similarity).  
FT BINDING 79 79 ATP (By similarity).  
FT ACT\_SITE 172 172 Proton acceptor (By similarity).  
FT VARSPPLIC 1 42 MVAGLTGKGPSPDGVSPKDKVAGGGGEAEABERG  
R -> MSSGAKGGGSPAYHLPHPPPPQ (in isoform 2). 008158.  
/FTID=VSP\_008158.  
FT CONFLICT 778 778 G -> A (in Ref. 4).  
FT SEQUENCE 794 AA; 86753 MW; 5DD395B0E61AEF77 CRC64;  
Query Match 87.4%; Score 3545; DB 1; Length 794;  
Best Local Similarity 99.7%; Pred. No. 5e-130; 1; Indels 0; Gaps 0;  
Matches 672; Conservative 1; Mismatches 0;  
QY 89 FRYLVLEHVS GGELFDYLVKKGRLTPKEARKFRQIVSALDFCHSYSI CHRLDKPENLLL 148  
DB 121 YLYLVLEHVS GGELFDYLVKKGRLTPKEARKFRQIVSALDFCHSYSI CHRLDKPENLLL 180  
QY 149 DEKNRIADFGMASLVGSLLETSCGSPHYACPEVIKGEKYDGRADWMSGVILFAL 208  
DB 181 DEKNRIADFGMASLVGSLLETSCGSPHYACPEVIKGEKYDGRADWMSGVILFAL 240  
QY 209 LVGALPDDNNLRQLLEKVRGVFHPHFIPPDQCSSLRGMI EVEPEKRLSLQIQKHPW 268  
DB 241 LVGALPDDNNLRQLLEKVRGVFHPHFIPPDQCSSLRGMI EVEPEKRLSLQIQKHPW 300

QY 269 YLGKHEPDCLEPAPGRVAMESLPSNGELDDVLESMAISLGCFFDRDRRLHRELSEEE 328  
DB 301 YLGKHEPDCLEPAPGRVAMESLPSNGELDDVLESMAISLGCFFDRDRRLHRELSEEE 360  
QY 329 NQEKMIYLLLDLDRKERYPSCEDQDLPRNDVDPKRKVDSPMLSRHGKRPERKSMEVLS 388  
DB 361 NQEKMIYLLLDLDRKERYPSCEDQDLPRNDVDPKRKVDSPMLSRHGKRPERKSMEVLS 420  
QY 389 ITDAGGGSPVPTRRALMAHQSRVSVCAGSTGLSSSLSPSPRSPVFSFSPGAGDE 448  
DB 421 ITDAGGGSPVPTRRALMAHQSRVSVCAGSTGLSSSLSPSPRSPVFSFSPGAGDE 480  
QY 449 ARGGSPTSXTQTLPSPRGPGGAGEOPPPPSAASSTPLPGPGSPRSSGGTGLHSLHTP 508  
DB 481 ARGGSPTSXTQTLPSPRGPGGAGEOPPPPSAASSTPLPGPGSPRSSGGTGLHSLHTP 540  
QY 509 RASPTGPTGTPPPSPGGVCGAAWRSLNIRNSFLGSPFRHRRKMQVPTAEEMSLTP 568  
DB 541 RASPTGPTGTPPPSPGGVCGAAWRSLNIRNSFLGSPFRHRRKMQVPTAEEMSLTP 600  
QY 569 ESSPELAKRSWFGNFISLDKEEQIFVLKDKPLSSIKADIVHAFSLSPSLSHSVLSQTSF 628  
DB 601 ESSPELAKRSWFGNFISLDKEEQIFVLKDKPLSSIKADIVHAFSLSPSLSHSVLSQTSF 660  
QY 629 RAEYKASGSPVFPKPVRFQVDISSSEGPSPRRDGGGGIYSVTFTLISGSPRRFKR 688  
DB 661 RAEYKASGSPVFPKPVRFQVDISSSEGPSPRRDGGGGIYSVTFTLISGSPRRFKR 720  
QY 689 VVETIQALLSHDQPSVQALADENKGAQTRPAGAPPSRLOPPGPRDPPELSSSPRGPP 748  
DB 721 VVETIQALLSHDQPSVQALADENKGAQTRPAGAPPSRLOPPGPRDPPELSSSPRGPP 780  
QY 749 KDKKLLATNGTLP 762  
DB 781 KDKKLLATNGTLP 794  
RESULT 2  
Q699J6 PRELIMINARY; PRT; 776 AA.  
ID AC Q699J6  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Putative serine/threonine kinase SADB.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kishi M., Sanes J.R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC EMBL; AY533671; AAT0846.1; --  
DR GO; GO:000524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR InterPro; IPR000449; USA.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00030; USA; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase;  
SQ SEQUENCE 776 AA; 84920 MW; EAC59E8740C159D8 CRC64;  
Query Match 86.7%; Score 3518; DB 2; Length 776;  
Best Local Similarity 99.0%; Pred. No. 5.5e-129;  
Matches 667; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 89 FRYLVLEHVS GGLFDYLVKKGR LTPKEARK FFRQIVSALDFCHSY SICH RD LK P EN L L L 148  
DB 103 YLVLEHVS GGLFDYLVKKGR LTPKEARK FFRQIVSALDFCHSY SICH RD LK P EN L L L 162  
QY 149 DEKNIRIADFG MASLQVGS LLETSCGSPHYACPEV IKG EYDGRAD MWSCGVILFAL 208  
DB 163 DEKNIRIADFG MASLQVGS LLETSCGSPHYACPEV IKG EYDGRAD MWSCGVILFAL 222  
QY 209 LVGALPDDDN LRLLEKVKRGV FHPHFIPPCQSL LRGMIEVEPKRLSL EGIQKHPW 268  
DB 223 LVGALPDDDN LRLLEKVKRGV FHPHFIPPCQSL LRGMIEVEPKRLSL EGIQKHPW 282  
QY 269 YLGCKHEPDPCL PAPGRRVAMRSLPSNGELDPDVL ESMASLGC FRDRERLHRELSEEE 328  
DB 283 YLGCKHEPDPCL PAPGRRVAMRSLPSNGELDPDVL ESMASLGC FRDRERLHRELSEEE 342  
QY 329 NQEKMIYLL LDRKERYPS CEDQDLP PRNDVDP PRKRVDS PMLSRHGKRRPERKSM E V L S 368  
DB 343 NQEKMIYLL LDRKERYPS CEDQDLP PRNDVDP PRKRVDS PMLSRHGKRRPERKSM E V L S 402  
QY 389 ITDAGGGSPVPTRRAL EMAHQSRSVSGASTGLSS PLSPSPRS PVFSP EPGAGDE 448  
DB 403 ITDAGGGSPVPTRRAL EMAHQSRSVSGASTGLSS PLSPSPRS PVFSP EPGAGDE 462  
QY 449 ARGGSPTS KTQTLPSRGRPGGAG EOPPPSARSTPLPGPGSPRSSGGTPLHSLPHT 508  
DB 463 ARGGSPTS KTQTLPSRGRPGGAG EOPPPSARSTPLPGPGSPRSSGGTPLHSLPHT 522  
QY 509 RASPTGTPTGTTPTPPSPGGVGGAAWRSLRNSIRNS FLGSPFRHRRKMQVPTAEEMSLTP 568  
DB 523 RASPTGTPTGTTPTPPSPGGVGGAAWRSLRNSIRNS FLGSPFRHRRKMQVPTAEEMSLTP 582  
QY 569 ESSPELAKRSWFGNFISLDKEEQIFLV LKDKPLSSIKADIVHAPLSIPSLSHSVLSQTSF 628  
DB 583 ESSPELAKRSWFGNFISLDKEEQIFLV LKDKPLSSIKADIVHAPLSIPSLSHSVLSQTSF 642  
QY 629 RAEYKASGGSPVFOKPVRFQVDI SSSGEGPEPSRRDGS GGGGIYVTFLLISGSPRRFKR 688  
DB 643 RAEYKASGGSPVFOKPVRFQVDI SSSGEGPEPSRRDGS GGGGIYVTFLLISGSPRRFKR 702  
QY 689 VVETIQALLSTHDQPSVQALAD EKNAGQTRPAGAPRSLOPPGRDPBELSSSPRGPP 748  
DB 703 VVETIQALLSTHDQPSVQALAD EKNAGQTRPAGAPRSLOPPGRDPBELSSSPRGPP 762  
QY 749 KDKLLATNGT TPL 762  
DB 763 KDKLLATNGT TPL 776

## RESULT 3

Q699J3 PRELIMINARY; PRT; 719 AA.  
ID Q699J3  
AC Q699J3  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Putative serine/threonine kinase SADA gamma.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kishi M., Sanes J.R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL: AV533674; AAT08449.1; --  
DR GO: 0005524; P-ATP binding; IEA.  
DR GO: 0004674; P-protein serine/threonine kinase activity; IEA.  
DR GO: 0004713; P-protein-tyrosine kinase activity; IEA.  
DR GO: 0006468; P-protein amino acid phosphorylation; IEA.  
DR InterPro: IPR011009; Kinase like.  
DR InterPro: IPR000719; Prot kinase.  
DR InterPro: IPR002290; Ser Thr\_kinase.  
DR InterPro: IPR008271; Ser Thr\_kin\_As.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR ProDom: PD000001; Prot kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR SMART: SM00219; Tyr\_Kc; 1.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN 1.  
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.  
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 719 AA; 79938 MW; 4C2ABA57205974AB CRC64;  
Query Match 59.3%; Score 2405; DB 2; Length 719;  
Best Local Similarity 69.3%; Pred. No. 6.9e-86;  
Matches 481; Conservative 55; Mismatches 64; Indels 94; Gaps 11;  
QY 89 FRYLVLEHVS GGLFDYLVKKGR LTPKEARK FFRQIVSALDFCHSY SICH RD LK P EN L L L 148  
DB 91 YLVLEHVS GGLFDYLVKKGR LTPKEARK FFRQIVSALDFCHSY SICH RD LK P EN L L L 150  
QY 149 DEKNIRIADFG MASLQVGS LLETSCGSPHYACPEV IKG EYDGRAD MWSCGVILFAL 208  
DB 151 DEKNIRIADFG MASLQVGS LLETSCGSPHYACPEV IKG EYDGRAD MWSCGVILFAL 210  
QY 209 LVGALPDDDN LRLLEKVKRGV FHPHFIPPCQSL LRGMIEVEPKRLSL EGIQKHPW 268  
DB 211 LVGALPDDDN LRLLEKVKRGV FHPHFIPPCQSL LRGMIEVEPKRLSL EGIQKHPW 270  
QY 269 YLGCKHEPDPCL PAPGRRVAMRSLPSNGELDPDVL ESMASLGC FRDRERLHRELSEEE 328  
DB 271 YLGCKHEPDPCL PAPGRRVAMRSLPSNGELDPDVL ESMASLGC FRDRERLHRELSEEE 328  
QY 329 NQEKMIYLL LDRKERYPS CEDQDLP PRNDVDP PRKRVDS PMLSRHGKRRPERKSM E V L S 388  
DB 329 NQEKMIYLL LDRKERYPS CEDQDLP PRNDVDP PRKRVDS PMLSRHGKRRPERKSM E V L S 388  
QY 389 ITDAGGGSPVPTRRAL EMAHQSRSVSGASTGLSS PLSPSPRS PVFSP EPGAGDE 448  
DB 389 VTD---GGSPVARRA IEMAHQSRSVSGASTGLSS PLSPSPRS PVFSP EPGAGDE 430  
QY 449 ARGGSPTS KTQTLPSRGRPGGAG EOPPPSARSTPLPGPGSPRSSGGTPLHSLPHT 508  
DB 431 -----VTTPSPRGSP LPTPKG-----TPVHTP 453  
QY 509 RASPTGTPTGTTPTPPSPGGVGGAAWRSLRNSIRNS FLGSPFRHRRKMQVPTAEEMSLTP 568  
DB 454 KESPACTPNPTPPSP--SVGGVPWRTRLNSIKNS FLGSPFRHRRKMQVPTAEEMSLTP 511  
QY 569 ESSPELAKRSWFGNFISLDKEEQIFLV LKDKPLSSIKADIVHAPLSIPSLSHSVLSQTSF 628  
DB 512 ESSPELAKRSWFGNFISLDKEEQIFLV LKDKPLSSIKADIVHAPLSIPSLSHSVLSQTSF 571  
QY 629 RAEYKASGGSPVFOKPVRFQVDI SSSGEGPEPSRRDGS GGGGIYVTFLLISGSPRRFKR 688  
DB 572 RAEYKATGGGPAVFOKPVRFQVDI TEGGEAQKE-----NGIYSVTFLLISGSPRRFKR 625  
QY 689 VVETIQALLSTHDQPSVQALA-----DEKNAGQTRPAGAPRSLOPP 731  
DB 626 VVETIQALLSTHDQPSVQALSTTNCMEVMTGRLSKCKDEKNAGQAAQAPSTPAKRSAGHP 685  
QY 732 PGRDPBELSSSPRRGPPKDK-----KLLATNGTP 760  
DB 686 -----LGDAAAAGPGGDT EYPMGKDMAKMGPP 712

## RESULT 4

Q6ZMQ4	PRELIMINARY;	PRT;	766 AA.	
ID	Q6ZMQ4			
AC	Q6ZMQ4			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DE	Hypothetical protein FLJ16763.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=AmvGdala;			
RA	Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,			
RA	Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,			
RA	Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,			
RA	Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,			
RA	Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,			
RA	Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,			
RA	Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,			
RA	Suzuki Y., Sugano S., Nagahari K., Masuho Y., Negai K., Isogai T.,			
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
DR	EMBL; AK131534; BAD18671.1; -.			
DR	HSSP; Q63450; 1A06.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR011009; Kinase like.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR002290; Ser_thr_pkinase.			
DR	InterPro; IPR001245; Tyr_pkinase.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00220; S_TKc; 1.			
DR	SMART; SM00219; TyrKc; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; Serine/threonine-protein kinase; Transferase.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
SEQUENCE	766 AA; 84831 MW; B05187AF729E947 CRC64;			
Query Match	59.2%; Score 2400; DB 2; Length 766;			
Best Local Similarity	68.5%; Pred. No. 1.1e-85;			
Matches	475; Conservative 59; Mismatches 65; Indels 94; Gaps 10;			
QY	89 FRYLVLEHVS GGE LFDYLVKKGR LTPKEAR KFFRQIVSALDFCHSYSTCHRDLPENLLL 148			
Db	136 YLYLVLEHVS GGE LFDYLVKKGR LTPKEAR KFFRQIVSALDFCHSYSTCHRDLPENLLL 195			
QY	149 DEKNRIADFGMASLQVDSLETSCGSPHYACVEIKGKYDGRADMWSCGVILFAL 208			
Db	196 DEKNRIADFGMASLQVDSLETSCGSPHYACVEIKGKYDGRADMWSCGVILFAL 255			
QY	209 LVGALPFDDNLRQLLEKVKRGVFMHPHPIPPDCQSLLRGLMEVPEKRLSLEQIQHPW 268			
Db	256 LVGALPFDDNLRQLLEKVKRGVFMHPHPIPPDCQSLLRGLMEVPEKRLSLEQIQHPW 315			
QY	269 YLGKGEHPDCLPEAPGRRVMSLPSNGELPDVLEWASLGCFDRRLHRLRSEEE 328			
Db	316 YIGKNEPEP-EQIP-RKQVIRSLPSLEDIDPDVLDMSHISGCFDRNRKLQDLSLEE 373			
QY	329 NQEKMYILLDRKEYVPSCEDLPPRNDVDPKRVDS PMLSRHGKRRPKRSMEVLS 388			
Db	374 NQEKMYILLDRKEYVPSCEDLPPRNDVDPKRVDS PMLSRHGKRRPKRSMEVLS 433			
QY	389 ITDAGGSGSPVPTRRALMAQHSQRGRSVSGASTGLSSSPLSPSPVPSFSPCAGDE 448			
Db	434 VTD---GGSPVARRALMAHQGRGRSISGASSGLSTSPSSPR----- 475			
QY	449 ARGGGSPTSQTQLPSRPGGGNGEGQPPPPSARSTPLPGPGSPRSSGGTPLHSPHTP 508			

RESULT 5

Q6Z998

ID Q6Z998 PRELIMINARY; PRT; 705 AA.

AC Q6Z998;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE MKIAA1811 protein (fragment).

GN Name=MKIAA1811;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,

RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,

RA Nagase T., Ohara O., Koga H.;

RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:

RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous

RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones

RT Randomly Sampled from Size-Fractionated Libraries."

RL DNA Res. 11:205-218 (2004).

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; AK173268; BAD32546.1; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_pkinase.

DR InterPro; IPR008271; Ser\_thr\_pkinase.

DR InterPro; IPR001245; Tyr\_pkinase.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00220; S\_TKc; 1.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

FT NON\_TER 1

SEQUENCE 705 AA; 78577 MW; 8DFF00585E981DFC CRC64;

Query Match 59.1%; Score 2397; DB 2; Length 705;

Best Local Similarity 67.7%; Pred. No. 1.4e-85;

Matches 481; Conservative 55; Mismatches 64; Indels 110; Gaps 11;

QY

89 FRYLVLEHVS GGE LFDYLVKKGR LTPKEAR KFFRQIVSALDFCHSYSTCHRDLPENLLL 148

```

Db 61 YLVLEHVSGBGLFDYLVKKGRLLTPKEARKFFRQIIISALDFCHSHSICHRLDKPENLLL 120
Qy 149 DEKNIRIADFGMASLQVDSLLTSCSGSPHYACPEVIGKGYDGRADMMSCGVILFAL 208
Db 121 DERNIRIADFGMASLQVDSLLTSCSGSPHYACPEVIRGEKYDGRADMMSCGVILFAL 180
Qy 209 LVGALPDDDDNLRLLEKVKRGVFMHPHFIPDQCSSLRGMIIEVEPEKRLSLEOIQKHPW 268
Db 181 LVGALPDDDDNLRLLEKVKRGVFMHPHFIPDQCSSLRGMIIEVEADAARRLTLEHIQHIW 240
Qy 269 YLGKHEPDPCLPAPGRVAMRSLPSNGELDDPVLESMAISLGCGRDRERLHRLSEEE 328
Db 241 YIGGKNEPEP-EQIP-RKQVIRSLPSLEDDPDVLSMHSGLGCFRDRNKLQDLSSEEE 298
Qy 329 NOEKMIYLLLDKRYPCEDQDLPDRNDVDPKRKVDSPMLRHGKRPERKSMVLS 388
Db 299 NOEKMIYLLLDKRYPCEDQDLPDRNEIDPPRKVDSPMLRHGKRPERKSMVLS 358
Qy 389 ITDAGGGSPVPTRRALMAHQSRSSVSGASTGLSSPLSSPSRSPVFSPPGAGDE 448
Db 359 VTD---GGSPVPARRALEMAHQSRSSISGASGLSTSPSSPR----- 400
Qy 449 ARGGGSPTKTQTLPSRGRGGAGEQPPPSARSTPLPGPGSPRSGGTPLHSLPHTP 508
Db 401 -----VTPHSPRGSPLTPKG-----TPVHTP 423
Qy 509 RASPTGTPGTPPPSPGGVGAARSLRNSIRNSIFLGSPPRFRHRKQVPTAEMSLTP 568
Db 424 KESPAQTGTPNTPPSSP--SVGGVPWRTRLNSIKNSIFLGSPPRFRHRKQVPTAEMSLTP 481
Qy 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLTSPSLSHSVLSQTSF 628
Db 482 ESSPELAKRSWFGNFIINLEKEEQIFVVKDKPLSSIKADIVHAFSLTSPSLSHSVLSQTSF 541
Qy 629 RAEYKASGGSPVFOKPVRFQVDISSSEGPSPRRDGGGGIYSVFTTILSGSPRRFKR 688
Db 542 RAEYKATGGPAVFQKPVKQVDITYTEGGAQKE-----NGIYSVFTTILSGSPRRFKR 595
Qy 689 VVETIOALLSTHDQPSVQAL-----ADEKNG- 715
Db 596 VVETIOALLSTHDQPSAQLSDTTNCMEVMTGRLSKGTPLSNFFDVIKQLFSDENNGQ 655
Qy 716 AQTTPAGAPRSLQPPGRDPPELSSSPRGPDK-----KLLATNGTP 760
Db 656 AAQAPSTPAKRSAGHP-----LGDSAAAGPGGDTBYPWGMKQWKGPP 698

RESULT 6
Q699J4 ID Q699J4 PRELIMINARY; PRT; 675 AA.
AC Q699J4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative serine/threonine kinase SADA beta.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kishi M., Sanes J.R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AY533673; AAT08448.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_kin_AS.

```

```

DR InterPro: IPR001245; Tyr_kinase.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE: PS00108; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 675 AA; 75361 MW; B01DBD8F9C24C71F CRC64;

Query Match 58.9%; Score 2390.5; DB 2; Length 675;
Best Local Similarity 71.9%; Pred. No. 2.4e-85;
Matches 469; Conservative 54; Mismatches 44; Indels 85; Gaps 9;

Qy 89 FRYLVLEHVSGBGLFDYLVKKGRLLTPKEARKFFRQIIISALDFCHSHSICHRLDKPENLLL 148
Db 91 YLVLEHVSGBGLFDYLVKKGRLLTPKEARKFFRQIIISALDFCHSHSICHRLDKPENLLL 150
Qy 149 DEKNIRIADFGMASLQVDSLLTSCSGSPHYACPEVIGKGYDGRADMMSCGVILFAL 208
Db 151 DERNIRIADFGMASLQVDSLLTSCSGSPHYACPEVIRGEKYDGRADMMSCGVILFAL 210
Qy 209 LVGALPDDDDNLRLLEKVKRGVFMHPHFIPDQCSSLRGMIIEVEPEKRLSLEOIQKHPW 268
Db 211 LVGALPDDDDNLRLLEKVKRGVFMHPHFIPDQCSSLRGMIIEVEADAARRLTLEHIQHIW 270
Qy 269 YLGKHEPDPCLPAPGRVAMRSLPSNGELDDPVLESMAISLGCGRDRERLHRLSEEE 328
Db 271 YIGGKNEPEP-EQIP-RKQVIRSLPSLEDDPDVLSMHSGLGCFRDRNKLQDLSSEEE 328
Qy 329 NOEKMIYLLLDKRYPCEDQDLPDRNDVDPKRKVDSPMLRHGKRPERKSMVLS 388
Db 329 NOEKMIYLLLDKRYPCEDQDLPDRNEIDPPRKVDSPMLRHGKRPERKSMVLS 388
Qy 389 ITDAGGGSPVPTRRALMAHQSRSSVSGASTGLSSPLSSPSRSPVFSPPGAGDE 448
Db 389 VTD---GGSPVPARRALEMAHQSRSSISGASGLSTSPSSPR----- 430
Qy 449 ARGGGSPTKTQTLPSRGRGGAGEQPPPSARSTPLPGPGSPRSGGTPLHSLPHTP 508
Db 431 -----VTPHSPRGSPLTPKG-----TPVHTP 453
Qy 509 RASPTGTPGTPPPSPGGVGAARSLRNSIRNSIFLGSPPRFRHRKQVPTAEMSLTP 568
Db 454 KESPAQTGTPNTPPSSP--SVGGVPWRTRLNSIKNSIFLGSPPRFRHRKQVPTAEMSLTP 511
Qy 569 ESSPELAKRSWFGNFIISLDKEEQIFLVLDKPLSSIKADIVHAFSLTSPSLSHSVLSQTSF 628
Db 512 ESSPELAKRSWFGNFIINLEKEEQIFVVKDKPLSSIKADIVHAFSLTSPSLSHSVLSQTSF 571
Qy 629 RAEYKASGGSPVFOKPVRFQVDISSSEGPSPRRDGGGGIYSVFTTILSGSPRRFKR 688
Db 572 RAEYKATGGPAVFQKPVKQVDITYTEGGAQKE-----NGIYSVFTTILSGSPRRFKR 625
Qy 689 VVETIOALLSTHDQPSVQALADEKNGAQTTPAGAPRSLQPPGRDPPELS 740
Db 626 VVETIOALLSTHDQPSAQLS-----EPPP--PAPGLS 657

RESULT 7
ST29 HUMAN ID ST29 HUMAN STANDARD; PRT; 736 AA.
AC Q61W03; Q60843; Q95099; Q8TB60;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase 29 (EC 2.7.1.37) (BRSK2) (HUSSY-12).
GN Name=STK29; Synonyms=PEN11B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).	DR	EMBL; AF020089; AAD09654.1; ALT_SEQ.
RC	TISSUE=Brain;	DR	HSP; O63450; 1A06.
RA	Guo J.H., Yu L.;	DR	Genew; HGNC:11405; STK29.
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	DR	InterPro; IPR011009; Kinase like.
RN	[2]	DR	InterPro; IPR000719; Prot_kinase.
RP	SEQUENCE OF 72-736 FROM N.A. (ISOFORM 2).	DR	InterPro; IPR008271; Ser_thr_pkin_AS.
RC	TISSUE=Brain;	DR	InterPro; IPR002290; Ser_thr_kinase.
RA	DOI=10.1002/1097-0061(200101)18:1<69:;AID-YEA647>3.3.CO;2-8;	DR	Pfam; PF00069; kinase; 1.
RX	Stanchi F., Bertocco E., Toppi S., Dioguardi R., Simonati B.,	DR	ProDom; PD000001; Prot_kinase; 1.
RA	Canata N., Zimbello R., Lanfranchi G., Valle G.;	DR	SMART; SM00220; S_TKC_1.
RL	"Characterization of 16 novel human genes showing high similarity to	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
RT	yeast sequences.";	DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
RN	Yeast 18:69-80(2001).	DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
RP	SEQUENCE OF 454-736 FROM N.A. (ISOFORM 2).	KW	Alternative splicing; ATP-binding; Serine/threonine-protein kinase;
RC	TISSUE=EYE;	KW	Transferase.
RA	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;	FT	DOMAIN 19 270 Protein kinase.
RL	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	FT	DOMAIN 424 468 Pro-rich.
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	FT	NP_BIND 25 33 ATP (By similarity).
RL	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	FT	BINDING 48 48 ATP (By similarity).
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,	FT	ACT_SITE 141 141 Proton acceptor (By similarity). EPPPPAPGL
RL	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,	FT	VARSPLIC 647 674 DTTCNMWMTGRLSKCGSLNFFDVIK -> EPPPPAPGL
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	FT	Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J.,
RL	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	FT	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RL	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	FT	Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.;
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	FT	Schmerch A., Schen J.E., Jones S.J.M., Marra M.A.;
RL	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,	FT	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RL	Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RT	"Generation and initial analysis of more than 15,000 full-length human	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RL	and mouse cDNA sequences.";	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RP	SEQUENCE OF 463-736 FROM N.A. (ISOFORM 3).	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RC	TISSUE=Brain, and Testis;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Mura K., Jinno Y.;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RL	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	-1- ALTERNATIVE PRODUCTS.	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	Event-Alternative splicing; Named isoforms=3;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	Name=1;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	isoId=Q81WQ3-1; Sequences=VSP_008154, VSP_008155;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	Name=2;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	isoId=Q81WQ3-2; Sequences=VSP_008154, VSP_008155;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	Name=3;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	isoId=Q81WQ3-3; Sequences=VSP_008156, VSP_008157;	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	-1- CAUTION: Ref.4 (AAD09654) sequence, isoform 3, differs from that	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	shown due to a stop codon in position 663 which was translated as	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	Gly to extend the sequence.	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	the European Bioinformatics Institute. There are no restrictions on its	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	use by non-profit institutions as long as its content is in no way	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	modified and this statement is not removed. Usage by and for commercial	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC	-----	FT	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
DR	EMBL; AV166857; AAN87839.1; -	DR	EMBL; AV166857; AAN87839.1; -
DR	EMBL; AF533876; AAP97723.1; -	DR	EMBL; AF533876; AAP97723.1; -
DR	EMBL; AF533877; AAP97724.1; -	DR	EMBL; AF533877; AAP97724.1; -
DR	EMBL; AF533878; AAP97725.1; -	DR	EMBL; AF533878; AAP97725.1; -
DR	EMBL; AF533879; AAP97726.1; -	DR	EMBL; AF533879; AAP97726.1; -
DR	EMBL; AF533880; AAP97727.1; -	DR	EMBL; AF533880; AAP97727.1; -
DR	EMBL; AJ006701; CAA07196.1; -	DR	EMBL; AJ006701; CAA07196.1; -
DR	EMBL; BC024291; AAN24291.1; ALT_INIT.	DR	EMBL; BC024291; AAN24291.1; ALT_INIT.



```

Db 571 RAEYKATGPAVFOKPVKFOVDITYTEGGEAQKE-----NGIYSVTFTLLSGSPRRFKR 624
Qy 689 VVEITQALLSTHDQPSVQAL-----ADENKGA 716
Db 625 VVEITQALLSTHDQPSVQAL-----ADENKGA 684
Qy 717 QTRPAGAPPR-----SLOPPPG- -RPDPELSSSPRGPDKK 752
Db 685 AAQAPSTPAKSAHGPLGDSAAAGPGGDAEYPTGKDTAKGPPPTARR 733

RESULT 8
Q6DMN7
ID Q6DMN7 PRELIMINARY; PRT; 653 AA.
AC Q6DMN7
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Brain-selective kinase 2 (Putative serine/threonine kinase SADA
DE alpha).
GN Name=Brsk2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang W.W., Shan Y.X.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kishi M., Sanes J.R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY660739; AAT74618.1; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR002719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 653 AA; 73149 MW; 8A23B94D71850E9A CRC64;

Query Match 58.7%; Score 2379.5; DB 2; Length 653;
Best Local Similarity 74.3%; Pred. No. 6.2e-85;
Matches 462; Conservative 53; Mismatches 42; Indels 65; Gaps 7;

Qy 89 FRYLVLEHVSQGLFDYLVKKGRLTPKEARFFQIVSALDFCHSYSTCHRDLPENLL 148
Db 91 YLYLVLEHVSQGLFDYLVKKGRLTPKEARFFQIVSALDFCHSYSTCHRDLPENLL 150
Qy 149 DEKNRIADFGMASLQVSDSLSTSCGSPHYACPEVIKGYDGRADWMSCGVILFAL 208
Db 151 DEKNRIADFGMASLQVSDSLSTSCGSPHYACPEVIKGYDGRADWMSCGVILFAL 210
Qy 209 LVGALPDDDLNRLLEKVKGVFMHPHIFPPDCQSLLRGMIEVEPEKRLSLEIOKHPW 268
Db 211 LVGALPDDDLNRLLEKVKGVFMHPHIFPPDCQSLLRGMIEVEPEKRLSLEIOKHPW 270
Qy 269 YLGGKHPDCLPEAPGRVAVRSI.PSNGELDDPVLSMASLGCGRFRRLHRLSEEE 328
Db 271 YLGGKHPDCLPEAPGRVAVRSI.PSNGELDDPVLSMASLGCGRFRRLHRLSEEE 328

```

```

Qy 329 NOEKMIYILLDRKERYPCEDQDLPPRNDVDPPKXVDSFMLSRHGRKRRPERKSMVLS 388
Db 329 NOEKMIYILLDRKERYPCEDQDLPPRNDVDPPKXVDSFMLSRHGRKRRPERKSMVLS 388
Qy 389 ITDAGGGGVPVPTRRALMAHQSRSSVSGASTGLSSSSPLSSSPRSVPVSPSPGAGDE 448
Db 389 VTD---GGSPVARRALEMAHQSRSSVSGASTGLSSSSPLSSSPRSVPVSPSPGAGDE 430
Qy 449 ARGGSPTSXTQTLPSRGRGGGAGEQPPPSARSTPLPGPPGSPRSRGGTPLHSLHTP 508
Db 431 -----VTPHPSRGSPLTPKG-----TPVHTP 453
Qy 509 RASPTGTPTTPPPSPGGVGGAAWRSIRNSIFLGSFRFRRKQVQVPTAEMSLTTP 568
Db 454 KESPGAGTNPPTPPSP--SVGGVPTWRLNLSIKNSIFLGSFRFRRKQVQVPTAEMSLTTP 511
Qy 569 ESSPELAKRWFNGFNISLDEKQIFLVLDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 628
Db 512 ESSPELAKRWFNGFNINLEKEQIFVVIKDKPLSSIKADIVHAFSLPSLSHVSLSQTSF 571
Qy 629 RAEYKASGSPSVFQKPVRFQVDISSSESGPEPSRRDGGGGGGIYSVTFTLLSGSPRRFKR 688
Db 572 RAEYKATGPAVFOKPVKFOVDITYTEGGEAQKE-----NGIYSVTFTLLSGSPRRFKR 625
Qy 689 VVEITQALLSTHDQPSVQALA 710
Db 626 VVEITQALLSTHDQPSVQALS 647

RESULT 9
Q6PHMO
ID Q6PHMO PRELIMINARY; PRT; 523 AA.
AC Q6PHMO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 4832424K13Rik protein (Fragment).
GN Name=4832424K13Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

```







```

269 Y-LGCKHPD---PCLBAPGRRVAMRSLPSNGELDPDVLESMASJGCFDRERLHREL 324
257 VTAGKGGELELPMNEV-----VQTHVFNASAVTDVNLNAICSLGCFKDKLIQELL 311
325 SEENOQKMIYYLLLDKRYFSCEDQD---LPPRNDV-----DPRKRVDSFMLSRHKKR 378
312 SPHNTKVIYFLLLDKRRRPAIEDEBDVLRPRNDIIEIADPPKRLDTCRIN----- 365
379 PERKNEVLISITDAGGGGSPVTPTRALEMAQHSORSESVGASTGLSSPLSSPRSPVFS 438
366 -GSSLSLYQISE-----GSLTSSRQTQFNNGHRSHSGSTSG---GSRSSSVVPLSRSSY 417
439 FSPGECAGDEARGGSGPTSKTQTLPSRPGCGAG-----BOPPPPSARSTPLP 487
418 QSPTRGV---VNNSSQPLSKSDVPR-----DFGRTLSVLFLLDQLHFPSPNAASNR 469
488 GPPGSPRSS-----GGTPLHSLHTPRASPTGTGP-----TTPPSPG 526
470 HSNYSRPSSTKQVDDSSSPVH---HRANGPAVTVGLFSETDNNMTSSINAIPGSPIL 526
527 G-----VGAARSRSLNSIRNSFLGSPREHRKMOPVTAEMSSSLTPESPSELAKR 577
527 GSPQQLQAVTTSQMLKTKLTNKSFLGSPKFRHRKMQISTE--VHLTPESPSELTKX 584
578 SWFGNFTSLDKBOEIFVLKDKPLXSIIKADIHAFSLSPSLSHSVLSQTSFRAFYKAG- 636
585 SWFGNLMTEKEDBTFFVIVKGFLATVKAHLIHAFLSMTELSHSVLSVSPMSRVEYKRG 644
637 GPSVFOKPRVFOVDISSSEGPSPRRDGGGGGYSVTFFLISGSPRRFKVVEITQA 695
645 GPTMFGRHVRIQVDINTI-----CKQGDVGDMFLFAITFTLISGNIRRRFRICEHTQA 696

RESULT 12
O61298 PRELIMINARY; PRT; 698 AA.
ID O61298
AC O61298;
DT 01-AUG-1998 (TREWBLrel. 07, Created)
DT 01-AUG-1998 (TREWBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREWBLrel. 26, Last annotation update)
DE HrPOPK-1 protein.
GN Name=HrPOPK-1;
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OC NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
PT TISSUE=Egg;

```

RC	TSISUB=Eggs;
RE	MEDLINE=98440280; PubMed=9767157; DOI=10.1016/S0925-4773(98)00100-2;
RF	Sasakura Y., Ogasawara M., Makabe K.W.;
RG	"Maternally localized RNA encoding a serine/threonine protein kinase
RH	in the ascidian, <i>Halocynthia roretzi</i> .";
RI	Mech. Dev. 76:161-163(1998).
RJ	-L- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
RK	EMBL; AB014885; BAA28663.1; -.
RL	HSP; Q63450; IA06.
RM	GO: GO:0005524; F:ATP binding; IEA.
RN	GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
RO	GO: GO:0016740; F:transferase activity; IEA.
RP	GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
RQ	InterPro; IPR011003; kinase_like.
RR	InterPro; IPR000719; prot_kinase.
RS	InterPro; IPR002290; Ser thr_pkin.
RT	InterPro; IPR008271; Ser thr_pkin_AS.
RU	Pfam; PF00069; Kinase; 1.
RV	SMART; SM00220; S_TKC; 1.
RW	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
RX	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
RY	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
RZ	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferrase.
SA	SEQUENCE 698 AA; 78607 MW; B29B1751E932D00BF CRC64;

Query Match	35.5%;	Score 1438;	DB 2;	Length 698;
Best Local Similarity	48.4%;	Pred. No. 2e-48;		
Matches 312;	Conservative	103;	Mismatches 112;	Indels 118; Gaps 21;
QY	89	FRLVLEHVSGGFLDYLVKKGRLLPKTGARKPFRIOIVSALDFCHYSICHKDLKPENLLL	148	
Db	85	YLVLILEVSGGFLDYLVOKGRLLPREARRFROIISAVDYNCHNNVCHRDLKPENLLL	144	
QY	149	DEKNIRIADFGWASLOVGDSLLETSCGSPHYACPEVKIKGYDCRRADMWSCGVILFAL	208	
Db	145	DEKNIKIADFGWASIQPGFLLTETSCGSPHYACEVIGERYDGRTADVWSCGVILFAL	204	
QY	209	LVGALPPDDNLRLQLLEKVKRGVFYHMHPHIPDPDQCSLLRGMIEVEPEKRLSLQIQKHWP	268	
Db	205	LVGALPPDDNLRLQLLEKVKRGVYTHPEVPDPAQNLLRGMIDVRPDKLSLQQVLOHPW	264	
QY	269	YLQKGHE-----PD----PCLEPAPGRVAMRS.LPSNGELDPDVLESMAISLGCFPRDRER	318	
Db	265	MRPGNSVEGVLVTPDPVWEVIDCVP-----LPBESVDPDVLASMTSLGCFCNKEK	316	
QY	319	LHRELRESEENOEKMIYYILLDRKERYPSCEDQ-DLPPRDNDVPPRKRV--SPMLSRHG	375	
Db	317	LLKLNIITEEQNTKVVYMLLRKKRYPSFDDADSLLCKHPDAKRKRVDTSSLSSSNG	376	
QY	376	-----KRPPEK-SMEVLSTITDAGGGGSVPVTRALEMAHQSRSVSGASTGLSSSPL	429	
Db	377	DWCVNPIPTQRKMSAESLCITDS-----SSPLLRSK--KSTETHQRSOSL-----TGESNEL	427	
QY	430	SSPSPVSFSPGADGEARGGSPTSKTQTLPSPRGCGGAGEOPPPPSARSTPLPGP	489	
Db	428	-----VCNISDQTKASKRINGTPVRGTTCSS-----NQVPV-----	461	
QY	490	PGSPRSSGGTFLHSPLHTPRASPFTGTPTPPSPGGVGAWRSLNRSLNSFLGSPR	549	
Db	462	-----QINTPAS-----PNP-----WRORLASLKMTFMGSPR	488	
QY	550	FHRKXOVPTAEEMSSLTPESSPELAKSRWGFNFISLD-----KEEQIFLVFKDKPLS	602	
Db	489	FHRKXOVQAPSEDVEN-CGNSSSELKSRLFWMFSMSSRYSTSEHCDELPAIYAKNURLN	547	
QY	603	SIAKDVIHAFISIPSLSHSVLSOTSFAEYKASG--GPSVF-QKPYRFQVDI-----S	652	
Db	548	SVKSELVHAFLSIPLNTHSMVSPTRFCRDYRSSTGTTSTVFHORSIKFQVDIIQHSSLR	607	
QY	653	SESGEPSPRRDGGGGGIYVTFTLLSGPEREKRVTETIQAL	697	
Db	608	QENGKKPSSQTGVS-----FTIASLSGPIRRKYRVELLQWQM	647	

RESULT 13	
Q19469	PRELIMINARY;
ID	PRT; 914 AA.
AC	Q19469; Q9ENN6;
AT	01-NOV-1996 (T-EMBLrel. 01, Created)
CT	01-NOV-1996 (T-EMBLrel. 18, Last sequence update)
DT	01-OCT-2001 (T-EMBLrel. 28, Last annotation update)
DT	25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE	Hypothetical protein F15A2.6 (Serine/threonine kinase SAD-1).
DE	Name=sad-1; ORFNames=F15A2.6;
GN	Caenorhabditis elegans.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabdi-
OC	Rhabditidae; Pelodierinae; Caenorhabditis.
OX	NCBI_TaxId=6239;
NCBI	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=Bristol N2;
RC	MEDLINE=39065613; PubMed=9851916;
RX	RA none;
RA	"Genome sequence of the nematode C.elegans: A platform for
RT	investigating biology.";
RT	Science 282:2012-2018(1998).
RL	[2]
RP	SEQUENCE FROM N.A.



285 ANAIRPSSPAACRTHSTYGDRLDRSGHSSVSRTPSHSSQKSTEGDVVVVVREPRIERRDS 344  
 448 --EARGGSGTSTKTQ-LPSRGRGGAGGQPPPSARSTFLPGPGSPRSSGGTTLHSP 504  
 345 LRQERGGSPRRDGDGIPPGSGGNSGTSAPSVMHRANGP-----TIAISMFWHDP 399  
 505 LHTPRASPTGTP---GTPP--PPSPGGVGGAARSLRSLRNSIRNSFLSGSPRFRHRKMQVPT 559  
 400 DSNVSNVNPSPMNNSSPMPGSPCNTPGQLWKRLTNKSLFSGSPRFRHRKMQV-S 458  
 560 AEEMSSITPSSPELAKRSGWFGNFIKDEEQIFLVKOKPLSIIKADIIVHAFSLSPSL 619  
 459 ADEV-HLTPSSPELTKRSNFGNLTITKDETEFTLVKGRPIATVKAHLHAFSLMAELS 517  
 620 HSVLSQTSFRAEYKASG-GPSVQKPVRFQVDLSSSEGGPPSPRRDGGSGGGIYSVTFTL 678  
 518 HSVVSPSTSFVEYKRNNGSPVQKRVKQVDISAI-----CKQGDIAIDLMLFAITFTL 570  
 679 ISGSPRRFRKRWETIQALLS 699  
 571 LSGNIRFRACEHQVQCS 591

RESULT 15  
 Q6C6T2 PRELIMINARY; PRT; 1058 AA.  
 ID Q6C6T2  
 AC Q6C6T2  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Similar to sp|P34244 Saccharomyces cerevisiae YKL101w HSL1 ser/thr protein kinase.  
 DE ORFNames=YAL10E06523g;  
 OS Yarrowia lipolytica CLIB99.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Dipodascaceae; Yarrowia.  
 OX NCBI\_TaxID=284591;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CLIB99;  
 RG Genolevures;  
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
 RA Goffard N., Franguel L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
 RA Boismare A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.L.;  
 RT "Genome evolution in yeasts."  
 RL Nature 430:35-44(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CLIB99;  
 RG Genoscope;  
 RA Genoscope;  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; CR392131; CAG79212.1; -  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein-serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000719; Prot.kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR001245; Tyr\_kinase.

DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR SMART; SM00219; TyKc; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1058 AA; 117047 MW; D999B29BC20B8AC0 CRC64;

Query Match 18.0%; Score 731; DB 2; Length 1058;  
 Best Local Similarity 26.5%; Pred. No. 7, 4e-21;  
 Matches 233; Conservative 111; Mismatches 258; Indels 276; Gaps 26;

QY 87 ISFRYLVLHVGSGGELFDYLVKGRITPKARKFPQIVSALDFCHSVISICHRDLKPEML 146  
 DB 1 MTFKVLVEYIEGGELFDYLVKGRLEEYEAASYFLQINGVDYCHRFNICHRLDKPEML 60  
 QY 147 LLDEKNIRIADFGASLQVGSLSLETSCGSHYACPEVIGKEKYDGRADWMSQGVILF 206  
 DB 61 LLDKNRNIXIADFGMALET-DRMLETSCGSHYASPEIVAGKTYHGAFSDIWSGCIILF 119  
 QY 207 ALLVAGALPFDDDNLRLEKVKRGVFMHPHFIPPCQSLLRGMIEVEPEKRLSLEIQKH 266  
 DB 120 ALLTGHLPFDDDNIRLLKLVQTKENMPSELSPYAKDLIWRMLRTDPTTRITMDEIFQH 179  
 QY 267 PW---YLGGKHBPDCLEPAPGRVRVAMSLPNEGELDPDVLSEMASLGCFRDRERLREL 323  
 DB 180 PFVRKYSGG---VTPTIHAPSVYEHVAREFVASVQDIDIEILKNLQILMHGEDAIIIMQKL 236  
 QY 324 RSEENQEKMIYLLLDLDRKERYPSCEDQLPP-----RNDVDPKRKYDVSFMLSRRGKR 377  
 DB 237 LSPDANPEKTFYCLLMKRYRHHAAVAATAPPTLQQQSQEQEMQPMHKHSHSSRKQHKR 296  
 QY 378 RPERKMEVLISITDAGGGSPVPTERRA-----LEMAQHSQRS-RSVSGASTG----- 423  
 DB 297 KTSNHSRL-----CSRGLSVSVSAHKRGVSFTVHKRSQOSIRSMGSAASNVASVP 350  
 QY 424 ---LSSSLSSPRSPV-----FSFSPGAGDEARGGSGTSTKTQTLPSRGRGGGAGEQ 475  
 DB 351 RKQTASAPVSAGTAPIPFNVNVPYTEAPATAPAAPTAAATSTATRAPAQPLAPTQAVOS 410  
 QY 476 PP-----PPSARSTPLGPPG---SPRSSG----- 497  
 DB 411 PPQSPVHQOQPTSRRAFISSAPSWLTSPPASKDADFEALDSAFNKPVTKSYGSL 470  
 QY 498 -GTFLHS-----PLHTPRASPTGTPGTT----- 525  
 DB 471 LGSFVDARRHVTDPANTSIASTRAGATAANTSKRAVTWAYNDEFEFERPMSLDFREVG 530  
 QY 526 GGVGGGAARW----- 538  
 DB 531 GDTGRAQQPSVSRAQTISHTHRSERVANAHSDDTPNPLPMIFEEGDRFADAEIEEFHLN 590  
 QY 539 SIENS-----FLGSPR-----PHRRKMQVP 558  
 DB 591 ISDNTLSAPSTNHTTLMGDRKSSWENLFDTERGDQVVVGEDSLDLSIFHR-----D 645  
 QY 559 TABEMSSLTP-----ESSPELAKRSGWFGNFIKDEEQIFLVKOKPLSIIKADI----- 608  
 DB 646 NANEATPVAPAATHVGRSTELYKDLQFPEIPVVDRE---TAVESMPRTQSKMKISGQM 702  
 QY 609 -VIAFLSIPS-----LSHSVLSQTSFRAEYKA-----SGGPSVQKPVRFQVD 650  
 DB 703 QTDNFMKRPSSINLNGHLSQSNLSRQTSASQRRLVSRDMNTHAASPRRAKPVK----- 758  
 QY 651 ISSSEGPSPRRDGGSGGGIYSVTFTLISGSPRRFRKRVVETIQAQLLSTHDQFSQALA 710  
 DB 759 -----QLQAAELHERRPVEVLQKQ-----QPQQQQQH 786  
 QY 711 DEKNQATRPAGAPRRSLQPPGPPDPPELSSSPRRGPP 748  
 DB 787 HHQQQQQQTQ-----HQLQAPVPFREKPVVSAPRRPAP 818

Search completed: February 17, 2005, 10:47:32  
Job time : 185 secs

This Page Blank (uspto)



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 09:15:18 ; Search time 6692 Seconds  
(without alignments)  
13019.891 Million cell updates/sec

Title: US-10-803-277-3  
Perfect score: 2289  
Sequence: 1 atgggacttgagtttggttt.....acgggacccctctgcctga 2289

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_est3.\*
- 4: gb\_est4.\*
- 5: gb\_est5.\*
- 6: gb\_est6.\*
- 7: gb\_est7.\*
- 8: gb\_gss1.\*
- 9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2009.2	87.8	2720	3	HSM805307	AL834275 Homo sapi
2	723.6	31.6	881	5	BQ717903	BQ717903 AGRNCOURT
3	671	29.3	671	7	CN365650	CN365650 170005325
4	657	28.7	950	5	BUS20742	BUS20742 AGRNCOURT
5	653.2	28.5	831	2	BF529743	BF529743 602044002
6	652	28.5	868	6	CA984329	CA984329 AGRNCOURT
7	602.2	26.3	658	4	BG818795	BG818795 602781839
8	601.8	26.3	693	6	CB056707	CB056707 NISC fj19
9	600	26.2	770	7	CO568702	CO568702 AGRNCOURT
10	595.8	26.0	615	7	CV023843	CV023843 878 Full
11	592.4	25.9	698	5	EM948524	EM948524 UI-M-EGOP
12	579.8	25.3	693	7	CO393904	CO393904 AGRNCOURT
13	574.8	25.1	742	5	BM944329	BM944329 UI-M-EHOP
14	571.4	25.0	686	6	CA319620	CA319620 UI-M-FW0-
15	570	24.9	596	5	BP251302	BP251302 BP251302
16	556	24.3	556	7	CK819107	CK819107 if08a12.y
17	548.6	24.0	840	7	CO400752	CO400752 AGRNCOURT
18	547.6	23.9	889	5	BQ434571	BQ434571 AGRNCOURT
19	547	23.9	689	7	CK356951	CK356951 AGRNCOURT
20	543.2	23.7	692	6	CD354865	CD354865 UI-M-GM0-
21	543	23.7	671	5	B0178547	B0178547 UI-M-EV0-
22	540.4	23.6	658	5	BQ573641	BQ573641 UI-M-FD0-
23	527.8	23.1	857	7	CO393564	CO393564 AGRNCOURT
24	522.4	22.8	936	2	BF529630	BF529630 602043855

25	510	22.3	510	5	BQ086295	BQ086295 ij20h01.y
26	493.2	21.5	554	6	CB613769	CB613769 AMGNNUC:N
27	492.8	21.5	898	2	BF529174	BF529174 602042051
28	487.8	21.3	753	2	BF796285	BF796285 602258590
29	476.2	20.8	614	5	BM944236	BM944236 UI-M-EHOP
30	465.8	20.3	790	6	CB849097	CB849097 MRA-0761
31	459.6	20.1	759	7	CF535475	CF535475 UI-M-GH0-
32	454.2	19.8	625	7	CO882466	CO882466 BovGen_10
33	450	19.4	600	5	BQ444032	BQ444032 UI-M-EW0-
34	444	19.4	492	2	BF686432	BF686432 IL3-ET011
35	439	19.2	463	2	BF364892	BF364892 QV0-NN114
36	429.4	18.8	733	5	BQ178695	BQ178695 UI-M-EV0-
37	426.6	18.6	508	5	BM950539	BM950539 UI-M-EHOP
38	421.4	18.4	520	9	CG514077	CG514077 OST67749
39	415.4	18.1	521	5	BQ442731	BQ442731 UI-M-EV0-
40	410	17.9	791	5	BQ611869	BQ611869 UI-M-F10-
41	406.4	17.8	693	5	BQ443644	BQ443644 UI-M-EW0-
42	406	17.7	961	7	W41136	W41136 mc38f03.r1
43	397.2	17.4	467	5	BX528055	BX528055 BX528055
44	392.6	17.2	731	7	CF723220	CF723220 UI-M-GV0-
45	383.8	16.8	610	6	CB580741	CB580741 AMGNNUC:N

ALIGNMENTS

RESULT 1  
HSM805307 2720 bp mRNA linear HTC 22-SEP-2004  
LOCUS Homo sapiens mRNA; cDNA DKFp547E1613 (from clone DKFp547E1613).  
DEFINITION  
ACCESSION AL834275.1 GI:21739846  
VERSION  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2720)  
AUTHORS Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,  
Fobo,G., Han,M. and Wiemann,S.  
CONSRM The German cDNA Consortium  
TITLE Direct Submission  
JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuherberg, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Sequenced by BMFZ (Biomedical Research Center at the  
Heinrich-Heine-University, Dueseldorf/Germany) within the cDNA  
sequencing consortium of the German Genome Project. This clone  
(DKFp547E1613) is available at the RZPD Deutsches  
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.  
Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFp547E1613  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.

FEATURES  
source

Location/Qualifiers  
1..2720  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="RZPD:DKFp547E1613"  
/db\_xref="taxon:9606"  
/clone="DKFp547E1613"  
/tissue\_type="brain"  
/clone\_lib="547 (synonym: hfbri). Vector pSport1; host  
DH10B; sites NotI + SalI"  
/dev\_stage="fetal"  
/note="hypothetical protein, N-terminus truncated"  
join(3..2192,2194..2238)  
/gene="DKFp547E1613"  
join(<3..2192,2194..2238)  
/gene="DKFp547E1613"  
/codon\_start=1  
/product="hypothetical protein"

/protein_id="CAD38950.2" /db_xref="UniProt/Swiss-Prot:O8TDC3" /translation="RLEKTLGKGTGLVGLVGHVCIITGOKVAIKIVNREKLSBSLMKV ERIALILKLEHPSVLIKLDVYENKKYLIYLVLEHVGSGELFDYLVKKGLTPEAKRF FRQIVSALDFCHSYISICHRDLKPEENLULDEKNIRIADFGMASIQVSDLSLSCSP HYACPEVIKERYDGRADMWSCGVILFALLVGLPDDNQLLEKLEKRVGFHMPH FIPDQSLRLRMIYEVPEKRLSLEQTKHPWYLGKHEPDPCLPEPAPGRVAMRSLP SNGLDPLVSMASLPCFRDLRHLRLEAREENOBKMIYLLLDKERYPSCEQD LPRNDVDPRKVDSPMLSRHGRKRPERSMEVLSITDAGGGSPVPTRRALEMAQH SQRSRSVSGASTGLSSPLSSPSPVSPSPERPGADGDEAGGSPSKCTPLSPRPR GGAGGEPFPSPARSPTLPFPSPSSGSGTPLHSLHTPRASPTGPTGTPFPSPGG GVGGAWSRLSIRNSFLGSPRHRKMQVPTABEMSLTPPESSPELAKRPPGFNFI SLDKEQIFVLKXDLKSLIKADIYHAFILSPISLHVSILVSLPFAEYKASGSPSFQ KPVRFQVDISSSGPSPRRDGGGGIYSVFTLISGSPSRFRKRVETIQALLST HDQPSVQALADERKGAQTRPAGAPRSLQPPGPRPDELSSSPRGRPKDKLLATNG TLPD"									
ORIGIN									
Query Match 87.8%; Score 2009.2; DB 3; Length 2720; Best Local Similarity 99.8%; Pred. No. 0; Matches 2022; Conservative 0; Mismatches 3; Indels 1; Gaps 1;									
Qy	265	TTTAGTACCTGGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG	324						
Db	213	TATTTGTACCTGGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG	272						
Qy	325	AAGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCCGAGATTGTCTCGGCTG	384						
Db	273	AAGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCCGAGATTGTCTCGGCTG	332						
Qy	385	GACTTCTGCCACACTACTCCTATCGCCACAGACACTTAAGCCCGAGAACCTGCTTTTG	444						
Db	333	GACTTCTGCCACACTACTCCTATCGCCACAGACACTTAAGCCCGAGAACCTGCTTTTG	392						
Qy	445	GATGAGAAAAACAATCCGATTTGACAGATTGCGCATGCGGTCCCTGCGAGGTGGGGAC	504						
Db	393	GATGAGAAAAACAATCCGATTTGACAGATTGCGCATGCGGTCCCTGCGAGGTGGGGAC	452						
Qy	505	AGCCTCTGGAGACAGCTGGGGTCCGCCATTATGCTGTCCAGAGGTGATTAAAGGGG	564						
Db	453	AGCCTCTGGAGACAGCTGGGGTCCGCCATTATGCTGTCCAGAGGTGATTAAAGGGG	512						
Qy	565	GAATAATATGATGCGCGCGGACAGATGTGGAGCTGTGGAGTATCTCTTCGCGCTG	624						
Db	513	GAATAATATGATGCGCGCGGACAGATGTGGAGTATCTCTTCGCGCTG	572						
Qy	625	CTCGTGGGGCTCTGCCCTTTGATGACAACTCCGCGAGCTGTGGAGAGGTGAAA	684						
Db	573	CTCGTGGGGCTCTGCCCTTTGATGACAACTCCGCGAGCTGTGGAGAGGTGAAA	632						
Qy	685	CGGGCGTCTTCCACATGSCCCACTTCAATCTCCAGATTGCCAGAGCTCTCGAGGGGA	744						
Db	633	CGGGCGTCTTCCACATGSCCCACTTCAATCTCCAGATTGCCAGAGCTCTCGAGGGGA	692						
Qy	745	ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG	804						
Db	693	ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG	752						
Qy	805	TACCTAGCGGGAAACACAGAGCCAGACCCGCTGCTGAGCCAGCCCTTGGCGCGGGTA	864						
Db	753	TACCTAGCGGGAAACACAGAGCCAGACCCGCTGCTGAGCCAGCCCTTGGCGCGGGTA	812						
Qy	865	GCCATGCGGAGCTGCCATCAACCGAGAGTGGACCCCGAGCTCTTAGAGAGCATGGCA	924						
Db	813	GCCATGCGGAGCTGCCATCAACCGAGAGTGGACCCCGAGCTCTTAGAGAGCATGGCA	872						
Qy	925	TCACTGGGCTGCTTCAGGGACCGGAGAGGTGCAATCGCGAGCTCGCAGTGGAGAGAG	984						
Db	873	TCACTGGGCTGCTTCAGGGACCGGAGAGGTGCAATCGCGAGCTCGCAGTGGAGAGAG	932						
Qy	985	AACNAGAAAAAGATATATATCTGCTTTTGGATCGGAGGAGCGGTATCCAGCTGT	1044						

Db	933	AACCAAGAAAAAGATGATATATATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGT	992						
Qy	1045	GAGGACCAAGACCTGCTCCCGGAATGATGTGACCCCGGGAAGCGTGTGGAATCT	1104						
Db	993	GAGGACCAAGACCTGCTCCCGGAATGATGTGACCCCGGGAAGCGTGTGGAATCT	1052						
Qy	1105	CCCATGCTAGCGGTCA CGGGAAGCGGCAACAGAGCGGAAGTCCATGAAAGTCCCTGAGC	1164						
Db	1053	CCCATGCTAGCGGTCA CGGGAAGCGGCAACAGAGCGGAAGTCCATGAAAGTCCCTGAGC	1112						
Qy	1165	ATCACCGATGCGGGGGTGGTGGCTCCCTGCTATACCCACCGACGGGCTTTGAGATGGCC	1224						
Db	1113	ATCACCGATGCGGGGGTGGTGGCTCCCTGCTATACCCACCGACGGGCTTTGAGATGGCC	1172						
Qy	1225	CAGCACAGCCAGAGATPCCCGTACGTAGCTAGTGAGGCTTCA CGGGTGTGCTTCCAGCCCT	1284						
Db	1173	CAGCACAGCCAGAGATPCCCGTACGTAGCTAGTGAGGCTTCA CGGGTGTGCTTCCAGCCCT	1232						
Qy	1285	CTAAGCAGCCCAAGGAGTCCGGTCTTTTCTTTTACCGGAGCGGGGCTGGAGATGAG	1344						
Db	1233	CTAAGCAGCCCAAGGAGTCCGGTCTTTTCTTTTACCGGAGCGGGGCTGGAGATGAG	1292						
Qy	1345	GCTTCGAGGCGGGGCTCCCGACTTCCAAAAACGACAGCGTCTTCTCGGGGCCCCAGG	1404						
Db	1293	GCTTCGAGGCGGGGCTCCCGACTTCCAAAAACGACAGCGTCTTCTCGGGGCCCCAGG	1352						
Qy	1405	GCTGGGGGCGCGGGGAGCAGCCCCCGCCCGCAGTGCCGCTTCCACACCCCTGCGCGG	1464						
Db	1353	GCTGGGGGCGCGGGGAGCAGCCCCCGCCCGCAGTGCCGCTTCCACACCCCTGCGCGG	1412						
Qy	1465	CCCCGAGGCTCCCGCGCTCTCTGCGGGGACCCCTTGCACCTCGGCTCTGACACGCCC	1524						
Db	1413	CCCCGAGGCTCCCGCGCTCTCTCTGCGGGGACCCCTTGCACCTCGGCTCTGACACGCCC	1472						
Qy	1525	CGGGCAGTCCCAACCGGGACCCCGGGGACAAACACACCCCGAGCCCGCGGTGGCGTC	1584						
Db	1473	CGGGCAGTCCCAACCGGGACCCCGGGGACAAACACACCCCGAGCCCGCGGTGGCGTC	1532						
Qy	1585	GGGGGAGCCGCTTGGAGGAGTCTCTCAAATCGCAACAGCTTCTTGGGCTCCCT	1644						
Db	1533	GGGGGAGCCGCTTGGAGGAGTCTCTCAAATCGCAACAGCTTCTTGGGCTCCCT	1592						
Qy	1645	CGTTTTCACGGGCGAGATGAGGTCCCTACCGCTGAGGAGATGCCAGTTGAGCCCA	1704						
Db	1593	CGTTTTCACGGGCGAGATGAGGTCCCTACCGCTGAGGAGATGCCAGTTGAGCCCA	1652						
Qy	1705	GAGTCTCCCGGAGCTGGCAAAACGCTCTCGTTCGGGAACTTTCATCTCTTGGACAA	1764						
Db	1653	GAGTCTCCCGGAGCTGGCAAAACGCTCTCGTTCGGGAACTTTCATCTCTTGGACAA	1712						
Qy	1765	GAAGAAACAAATATTCCTGCTGCTAAAGGACAAACCTCTCAGAGCATCAAGCAGCATC	1824						
Db	1713	GAAGAAACAAATATTCCTGCTGCTAAAGGACAAACCTCTCAGAGCATCAAGCAGCATC	1772						
Qy	1825	GTCCATGCTTTTGTGTCATCCCGCTGAGTGCAGTGTGCTGTGTCACAGACAGCTTC	1884						
Db	1773	GTCCATGCTTTTGTGTCATCCCGCTGAGTGCAGTGTGCTGTGTCACAGACAGCTTC	1832						
Qy	1885	AGGCGCGAGTACAAAGGCGAGTGGCGGCCCTCCGCTTTCACAAAGCCCGCTTCCAG	1944						
Db	1833	AGGCGCGAGTACAAAGGCGAGTGGCGGCCCTCCGCTTTCACAAAGCCCGCTTCCAG	1892						
Qy	1945	GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGGACGGGAGGAGGT	2004						
Db	1893	GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGGACGGGAGGAGGT	1952						
Qy	2005	GTTGGCATCTACTCCGTCAGCTTCACTCTCATCTCGGGTCCCGCTTCCAGCGCA	2064						
Db	1953	GTTGGCATCTACTCCGTCAGCTTCACTCTCATCTCGGGTCCCGCTTCCAGCGCA	2012						
Qy	2065	GTGTGGAGACCATCCAGGACAGCTCTCTGAGCACTCATGACCAAGCCCTCCGTCAGGCC	2124						
Db	2013	GTGTGGAGACCATCCAGGACAGCTCTCTGAGCACTCATGACCAAGCCCTCCGTCAGGCC	2072						

```

QY 2125 CTGGCAGCAGAGACGGGGCCAGACCCGGGCTCTGGTGGCCCAACCCCGAGCCTG 2184
Db |||||||
QY 2073 CTGGCAGACGAGAGAACGGGGCCAGACCCGGGCTCTGGTGGCCCAACCCCGAGCCTG 2132
Db |||||||
QY 2185 CAGCCCCCACCAGCCGCCCCAGACCCAGAGCTGAGCAGCTCTCCCGCCCGAGG-CCCCCCC 2243
Db |||||||
QY 2133 CAGCCCCCACCAGCCGCCCCAGACCCAGAGCTGAGCAGCTCTCCCGCCCGAGGCCCCCCCC 2192
QY 2244 CAGGACAAGAAGCTCTGGCCACCAACGGGACCCCTCTGCCCTGA 2289
Db |||||||
QY 2193 CAAGGACAAGAAGCTCTGGCCACCAACGGGACCCCTCTGCCCTGA 2238

RESULT 2
BQ717903 881 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT 8241190 Lupski sympathetic_trunk Homo sapiens cDNA clone
INAGB:6186946 5', mRNA sequence.
ACCESSION BQ717903
VERSION BQ717903.1 GI:21856800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 881)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM3580 row: c column: 11
High quality sequence stop: 620.
FEATURES
source
1..881
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="INAGB:6186946"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski sympathetic trunk"
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors;
5'-TCGACCCACCGCTCCG-3' and
5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

ORIGIN
Query Match 31.6%; Score 723.6; DB 5; Length 881;
Best Local Similarity 95.3%; Pred. No. 8.9e-158;
Matches 753; Conservative 0; Mismatches 36; Indels 1; Gaps 1;

QY 437 TGCCTTTGGATGAGAAAAACAATCCGCATTGCGACTTCGGCATGCGCTCCCTGCAGG 496
Db |||||||
QY 1 TGCCTTTGGATGAGAAAAACAATCCGCATTGCGACTTCGGCATGCGCTCCCTGCAGG 60
QY 497 TGGGGGACAGCCTCTCTGGAGACCAGCTGCGGGTCCCCCCCAATTATGCGTGTCCAGAGGTGA 556

```

```

Db 61 TGGGGGACAGCCTCTCTGGAGACCAGCTGCGGGTCCCCCAATTATGCGTGTCCAGAGGTGA 120
QY 557 TTAAGGGGGGAAAAAATATGATGGCCGCGGCGAGACATGTGGAGCTGTGGAGTCAATCTCT 616
Db 121 TTAAGGGGGGAAAAAATATGATGGCCGCGGCGAGACATGTGGAGCTGTGGAGTCAATCTCT 180
QY 617 TCGCCCTTGTCTGTGGGGGCTCTGCCCTTTGATGACGACAACTCCCGCAGCTGTGAGAGA 676
Db 181 TCGCCCTTGTCTGTGGGGGCTCTGCCCTTTGATGACGACAACTCCCGCAGCTGTGAGAGA 240
QY 677 AGGTGAAACGGGGCGCTTCCACATGCCCACTTTCATTCTCCAGATTGCCAGAGCTCC 736
Db 241 AGGTGAAACGGGGCGCTTCCACATGCCCACTTTCATTCTCCAGATTGCCAGAGCTCC 300
QY 737 TGAGGGGAATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAC 796
Db 301 TGAGGGGAATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAC 360
QY 797 ATCTTTGGTACCTAGGCGGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGGCC 856
Db 361 ATCTTTGGTACCTAGGCGGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGGCC 420
QY 857 GCCGGGTAGCATGCGGAGCCTGCATCCAAACGAGAGCTGGACCCGAGCTCTAGAGA 916
Db 421 GCCGGGTAGCATGCGGAGCCTGCATCCAAACGAGAGCTGGACCCGAGCTCTAGAGA 480
QY 917 GCATGGCATCACTGGGCTGCTTCAGGGACCCGAGAGGCTGCATCGGAGCTGCGCAGTG 976
Db 481 GCATGGCATCACTGGGCTGCTTCAGGGACCCGAGAGGCTGCATCGGAGCTGCGCAGTG 540
QY 977 AGGAGGAAACCAAGAAAAGATATATATATATCTCTTTTGGATCGGAAGAGCGGTATC 1036
Db 541 AGGAGGAAACCAAGAAAAGATATATATATATCTCTTTTGGATCGGAAGAGCGGTATC 600
QY 1037 CCAGCTGTGAGGACCGAGGACCTGCTCCCGGGAATGATGTGACCCCGCCCGG-AAAGCGT 1095
Db 601 CCAGCTGTGAGGACCGAGGACCTGCTCCCGGGAATGATGTGACCCCGCCCGGNAAGCGT 660
QY 1096 GTGGATTCTCCCATGCTGAGCCGCTACGGAAGCGGCGACGAGCGGAAGTCCATGGAA 1155
Db 661 GTGGATTCTCCCATGCTGAGCCGCTACGGAAGCGGCGACGAGCGGAAGTCCATGGAA 720
QY 1156 GTCTGAGCATACCGATGCGGGGGTGGTGGCTTCCCTGTACCCACCGAGCGGCTTG 1215
Db 721 GTTCTGAGCATCCGATGCGGGGGGNGGGTTCCTCCCTGNCCTCCCGGAGGGG 780
QY 1216 GAGATGCCCCAG 1227
Db 781 GCCTTGGCAAG 792

RESULT 3
CN365650 671 bp mRNA linear EST 16-MAY-2004
LOCUS 1700053255282 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN365650
ACCESSION CN365650
VERSION CN365650.1 GI:47365584
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 671)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 671)
JOURNAL Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
L.Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
COMMENT Transcription characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation

```



```

Db      420 AAATATTCCTGCTGCTAAAGAGCAAACTCTCAGAGCATCAAGCGGACATTTGTCATG 479
Qy      1832 CTTTCTGTGTCATCCCGAGCTGAGTCACAGTGTGCTGTCTCAGACACGAGCTTTCAGGGCCG 1891
Db      480 CTTTCTGTGTCATCCCGAGCTGAGTCACAGTGTGCTGTCTCAGACACGAGCTTTCAGGGCCG 539
Qy      1892 AGTCAAGGCGCAGTGGCGGCCCTCCGTCTTCCAAAAGCCGTCGCTTCAGAGTGACACA 1951
Db      540 AATAAAGGCGCAGCGCGGCCCTCCGTCTTCCAAAAGCCCTGTCGCTTTTCAGGTGGACA 599
Qy      1952 TCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGACGCGGACGCGAGGGAGTGTGTCGCA 2011
Db      600 TCAGCTCTCTGAGGGTCCAGAACCTTCACCCGAGAGATGGCAGCATGGAGTGGCA 659
Qy      2012 TCTACTCGGTCACTTCACTCTCATCTCTGAGTCCGAGCCGTCGCTTCAAGCGAGTGGTG 2071
Db      660 TCTACTCAGTCACCTTACTCTCATCTCTGAGTCCGAGCCGTCGCTTCAAGCGTGGTAG 719
Qy      2072 AGACATCCAGGACAGCTCTGAGCACTCATGACACG-CCCTCGGTGCGGCCCT-GGC 2129
Db      720 AGACATCCAGGACAGTGTGAGTACTTCAAGCAACGAGCCCTCCGTCGAGGCCCTTGGGC 779
Qy      2130 AGACGAGAAGAAAGGGGCCCAAG-CCCGGCTGCTGGTG-CCCCACCCCGGAGGCTG 2184
Db      780 AGATGAGAAAGACGAGGACCCAGACCCGCGGCTGTGNGACCCACCCCGGAGGCTG 839
Qy      2185 CAGCCCCCACC 2196
Db      840 CAGCCCCCACC 851

```

```

RESULT 5
BF529743
LOCUS      602044002P1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181688
DEFINITION
5' mRNA sequence.
ACCESSION BF529743
VERSION    BF529743.1 GI:11617106
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
Plate: LLAM9495 row: c column: 01
High quality sequence stop: 736.
Location/Qualifiers
1. .831
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4181688"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SpOPE6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

```

## FEATURES

```

source
CA984329
LOCUS      CA984329
DEFINITION
AGENCYCOURT 11296377 NIH MGC 164 Mus musculus cDNA clone
IMAGE:30147920 5', mRNA sequence.
ACCESSION CA984329
VERSION    CA984329.1 GI:27516985
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 868)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.

```

## ORIGIN

```

Query Match      28.5%; Score 653.2; DB 2; Length 831;
Best Local Similarity 96.3%; Pred. No. 2.4e-141;
Matches 711; Conservative 0; Mismatches 23; Indels 4; Gaps 4;
Qy      268 AGGTACCTGGTTCGGAGCACGCTCTGGGGGTGAGCTATTTCGACTACCTGTTAAAGAG 327
Db      42 AGGTACCTGGTTCGGAGCACGCTCTGGGGGTGAGCTATTTCGACTACCTGTTAAAGAG 101
Qy      328 GGAGAGCTGACGGCCAA-GGAGGCCGAAAGATTCTTCGGCCAGATTGTCTGCGCTGGA 386
Db      102 GGAGAGCTGACGGCCAAAGGAGGAGCCGAAAGTTCTTCGGCCAGA-TGTGTCTGCGCTGGA 160
Qy      387 CTTCTGCCACAGCTACTTCCATCTGCCACAGAGACTTAAAGCCGAGAACCTGCTTTTGA 446
Db      161 CTTCTGCCACAGCTACTTCCATCTGCCACAGAGACTTAAAGCCGAGAACCTGCTTTTGA 220
Qy      447 TGAGAAAACAACATCCGCAATTCAGACTTTCGGCATGGCTCCCTGAGGTGGGGGACAG 506
Db      221 TGAGAAAACAACATCCGCAATTCAGACTTTCGGCATGGCTCCCTGAGGTGGGGGACAG 280
Qy      507 CTTCTCGAGACACAGCTGCGGCTCCCGCCATTATGCGTGTCCAGAGGTGATTAAGGGGA 566
Db      281 CTTCTCGAGACACAGCTGCGGCTCCCGCCATTATGCGTGTCCAGAGGTGATTAAGGGGA 340
Qy      567 AAAATATGATGGCGCGCGGACAGATGTGGAGCTGTGGAGTCACTCTTTCGCCCTGCT 626
Db      341 AAAATATGATGGCGCGCGGACAGATGTGGAGCTGTGGAGTCACTCTTTCGCCCTGCT 400
Qy      627 CGTGGGGGCTCTGCCCTTTGATGACGACAACCTCCCGCAGCTGCTGGAGAGGTGAAACG 686
Db      401 CGTGGGGGCTCTGCCCTTTGATGACGACAACCTCCCGCAGCTGCTGGAGAGGTGAAACG 460
Qy      687 GGGGCTCTCCACATGCCCACTTTCATCTCCAGATTGCGAGAGCTCTTCAGGGGAAT 746
Db      461 GGGGCTCTCCACATGCCCACTTTCATCTCCAGATTGCGAGAGCTCTTCAGGGGAAT 520
Qy      747 GATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGGTA 806
Db      521 GATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGGTA 580
Qy      807 CCTAGGCGGAAACACAGCCAGCCCGCTGCTGGAGCCAGCCCTGGCCCGCGGGTAGC 866
Db      581 CCTAGGCGGAAACACAGCCAGCCCGCTGCTGGAGCCAGCCCTGGCCCGCGGGTAGC 640
Qy      867 CATGCGG-AGCCTGCCATCCAAAGAGAGCTGGAACCCGACGCTCCTAGAGAGCATGGCAT 925
Db      641 CATGCGGAGCCTGCCATCCAAAGAGAGCTGGA-CCGAGCTCCTAGAGAGCATGGCAT 699
Qy      926 CACTGGGCTCTTTCAGGGACCGGAGAGGTGCAATCGAGCTGCGAGTGAGGAGGAGA 985
Db      700 CACTGGGCTTTCAGGGACCGGAGAGGTGCAATCGAGCTGCGAGTGAGGAGGAGAA 759
Qy      986 ACCAAGAAAGATGATAT 1003
Db      760 CCACAAAATGGTTTATAT 777

```

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Dr. David Rowe and Dr. Mina  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM0065 row: p column: 09  
High quality sequence start: 15  
High quality sequence stop: 649.  
High quality sequence stop: 649.  
Location/Qualifiers  
1. 868  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30147920"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_164"  
/note="vector: PCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;  
Non-normalized full-length enriched library from pooled  
mouse embryonic limb, maxilla and mandible, day 10.5 and  
11.5 (size selected for the 0.5-1 kb fragments) Cloned  
directionally, priming method: Oligo-dT. cDNA enrichment:  
>1k bp, Average insert size 1.8k bp. Priming sequence:  
5'-GACTAGTCTAGATCGAGCGCGCCCT(T) 3'. Tissue contributed  
by, David Rowe. Library constructed by ResGen, Invitrogen  
Corp."

source  
1. 868  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30147920"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_164"  
/note="vector: PCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;  
Non-normalized full-length enriched library from pooled  
mouse embryonic limb, maxilla and mandible, day 10.5 and  
11.5 (size selected for the 0.5-1 kb fragments) Cloned  
directionally, priming method: Oligo-dT. cDNA enrichment:  
>1k bp, Average insert size 1.8k bp. Priming sequence:  
5'-GACTAGTCTAGATCGAGCGCGCCCT(T) 3'. Tissue contributed  
by, David Rowe. Library constructed by ResGen, Invitrogen  
Corp."

Query Match 28.5%; Score 652; DB 6; Length 868;  
Best Local Similarity 92.0%; Pred. No. 4.5e-141;  
Matches 710; Conservative 0; Mismatches 60; Indels 2; Gaps 2;  
QY 1215 GGAGATGCCAGACAGCAGACAGATCCGAGGCTCAGTGGAGCTCCAGCGGTCTGTC 1274  
Db 1 GGAGATGCCAGACAGCAGATCAGATCCGAGGCTCAGTGGAGCTCCAGCGGTCTGTC 60  
QY 1275 CTCAGCGCTCTAAGCAGCCCAAGAGTCCGGTCTTTCTTTTTCACGGAGCGGGGC 1334  
Db 61 CTCAGCGCTCTGAGCAGCCCAAGAGTCCGGTCTTTCTTTCTCAGCGGAGCGGC 120  
QY 1335 TGGAGATGAGCTCGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCG 1394  
Db 121 TGGAGATGAGCTAGAGCGGAGGCTCCCGACTTCCAAACGAGAGCTGCTTCG 180  
QY 1395 GGGCCCCAGGGTGGGGGCGCGGGGAGCAGCCCCCGCCCGAGTGCCCGCTCCACCC 1454  
Db 181 GGGCCCCAGAGGTGGGGGCGCTGGAGAGAGCCACCCCCAGTGCCTTCCAGGCC 240  
QY 1455 CTTGCCCGCCCCCAGAGCTCCCGCTCTCTCTGGGGGAGCCCGCTTGACTGCTCT 1514  
Db 241 CTTGCTGGACCAACAGGCTCCCGCTCTCTCTGGGGGAGCCCGCTTGACTGCTCT 300  
QY 1515 GCACAGCCCCGGGCGAGTCCACCGGACCCCGGGGACAAACACACCCCGCCAGCCCGG 1574  
Db 301 GCACAGCGCTCGAGCGAGCCCTACCGGGACCCCGAGAGAGCGCCACCTCCAGGCCAG 360  
QY 1575 CGGTGGCTCGGGGAGCGCGCTGGAGGAGTCTTCAACTCCATCCGCAACAGTTCT 1634  
Db 361 CGGTGGCTCGGGGAGCGCGCTGGAGGAGTCTTCAACTCCATCCGCAACAGTTCT 420  
QY 1635 GGGCTCCCTCTCTTTCACCGCGGAGATGAGTCCCTACCGCTGAGGAGTCTCCAG 1694  
Db 421 GGGCTCCCTCTCTTTCACCGCGGAGATGAGTCCCTACCGCTGAGGAGTCTCCAG 480  
QY 1695 CTTGAGCCAGAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTCGGGAACTTCATCTC 1754  
Db 481 TTTGACACAGATCTCTCTCTGAGCTGGCAAAACGCTCTCTGGTTCGGGAACTTCATCTC 540

QY 1755 CTTGGACAAAGAGAAACAAATATTTCTCTGCTAAAGGACAAACCTCTCAGCAGCATCA 1814  
Db 541 CTTGGACAAAGAGAAACAAATATTTCTCTGCTAAAGGACAAACCTCTCAGCAGCATCA 600  
QY 1815 AGCAGACATCGTCCATGCTTCTCTGATCCCGAGCTGAGTACAGTGTCTGTCA 1874  
Db 601 AGCGGACATTTGCTTCTGATCCCGAGCTGAGTACAGTGTCTGTCA 660  
QY 1875 GACCAGCTTCAGGCGCGAGTACAAGGCCAGTGGCGG-CCCTTCCTGTTTCCAAAAGCCG 1933  
Db 661 GACCAGCTTCAGGCGCGAGTACAAGGCCAGTGGCGGCGCCCTTCCTGTTTCCAAAAGCCG 720  
QY 1934 TCCGTTCCAGTGGAGATCAGTCTCC-TCTGAGGTCAGAGCCCTTCCCGC 1984  
Db 721 TCCGTTCCAGTGGAGATCAGTCTCC-TCTGAGGTCAGAGCCCTTCCCGC 772

RESULT 7  
BG819795  
LOCUS 602781839F1 NCI CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:4932680  
DEFINITION 5', mRNA sequence.  
ACCESSION BG819795  
VERSION BG819795.1 GI:14167382  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 658)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL0858 row: n column: 09  
High quality sequence stop: 612.  
High quality sequence stop: 612.  
Location/Qualifiers  
1. 658  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4932680"  
/tissue\_type="anaplastic oligodendroglioma with 1p/19q  
loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI CGAP\_Brn67"  
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: this is a NCI CGAP library."

FEATURES  
source  
1. 658  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4932680"  
/tissue\_type="anaplastic oligodendroglioma with 1p/19q  
loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI CGAP\_Brn67"  
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: this is a NCI CGAP library."

ORIGIN  
Query Match 26.3%; Score 602.2; DB 4; Length 658;  
Best Local Similarity 98.4%; Pred. No. 1.8e-129;  
Matches 619; Conservative 0; Mismatches 8; Indels 2; Gaps 1;  
QY 811 GCGGGGAAACAGCAGCGAGACCCGCTGCTGAGCAGCCCGCTGGCCCGGGTAGCCATG 870  
Db 1 GCGGGGAAACAGCAGCGAGACCCGCTGCTGAGCAGCCCGCTGGCCCGGGTAGCCATG 60  
QY 871 CGGAGCTTCCATCCACGGAGAGCTGAGCCCGACCTCTAGAGAGATGGCATCTG 930  
Db 61 CGGAGCTTCCATCCACGGAGAGAGCTGAGCCCGACCTCTAGAGAGATGGCATCTG 120  
QY 931 GGCTGCTTCGGGACCGCGAGAGGCTGCATCGCGAGCTGCGAGTGGAGGAGGAGCA 990







```

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 770)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: dsgerha@nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM15535 row: o column: 22
High quality sequence stop: 665.

FEATURES
source
1..770
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7379280"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_249"
/notes="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-TGACTAGTCTTAGATCGGACGCGCCGCTT-25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.4 kb. This primary
library is normalized (primary library is NIH_MGC_248)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library".

ORIGIN
Query Match 26.2%; Score 600; DB 7; Length 770;
Best Local Similarity 90.6%; Pred. No. 6,1e-129;
Matches 662; Conservative 0; Mismatches 66; Indels 3; Gaps 2;

QY 1469 CAGGCTCCCGGCTCTCTGCGGGACCCCTTGCACTCGCTTCGACACGCGCCGGG 1528
DB 1 CAGGCTCCCGGCTCTCTGCGGGACCCCTTGCACTCGCTTCGACACGCGCTCGAG 60
QY 1529 CCAGTCCCAACCGGGACCCCGGGGACACACACCCCGCGCGGGTGGCGTGGGG 1588
DB 61 CCAGCGCTACCGGAGCTCCAGGAACTACACCACTCCAGCGCGGCGGTGGCGTGGGG 120
QY 1589 GAGCGCGTGGAGGAGTCTCTCACTCCATCCGCAACAGCTTCCTGGGCTCCCTCGCT 1648
DB 121 GAGCGCGTGGAGAGTCTCTCACTCCATCCGCAACAGCTTCCTGGGCTCCCTCGCT 180
QY 1649 TTACCGCGCGCAAGATGCAAGTCCCTACCGTGGAGAGATGTCAGCTTGAGCCAGAGT 1708
DB 181 TCCACCGCGCGCAAGATGCAAGTCCCTACCGTGGAGAGATGTCAGCTTGAGCCAGAGT 240
QY 1709 CTTCCCGGAGCTGGCAAAACGCTCTCTGTTGCGGAACTTCATCTCTTGGCAAGAG 1768
DB 241 CTTCTCCAGAGCTGGCAAAACGCTCTCTGTTGCGGAACTTCATCTCTTGGCAAGAG 300
QY 1769 AACAAATATTCCTCGTGCTAAAGGACAAACCTCTCAGCAGCATCAAGAGCAGCATCGTCC 1828
DB 301 AACAAATATTCCTCGTGCTAAAGGACAAACCTCTCAGCAGCATCAAGAGCAGCATGTGCC 360

EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 770)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: dsgerha@nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM15535 row: o column: 22
High quality sequence stop: 665.

FEATURES
source
1..770
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7379280"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_249"
/notes="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-TGACTAGTCTTAGATCGGACGCGCCGCTT-25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.4 kb. This primary
library is normalized (primary library is NIH_MGC_248)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library".

ORIGIN
Query Match 26.2%; Score 600; DB 7; Length 770;
Best Local Similarity 90.6%; Pred. No. 6,1e-129;
Matches 662; Conservative 0; Mismatches 66; Indels 3; Gaps 2;

QY 1469 CAGGCTCCCGGCTCTCTGCGGGACCCCTTGCACTCGCTTCGACACGCGCCGGG 1528
DB 1 CAGGCTCCCGGCTCTCTGCGGGACCCCTTGCACTCGCTTCGACACGCGCTCGAG 60
QY 1529 CCAGTCCCAACCGGGACCCCGGGGACACACACCCCGCGCGGGTGGCGTGGGG 1588
DB 61 CCAGCGCTACCGGAGCTCCAGGAACTACACCACTCCAGCGCGGCGGTGGCGTGGGG 120
QY 1589 GAGCGCGTGGAGGAGTCTCTCACTCCATCCGCAACAGCTTCCTGGGCTCCCTCGCT 1648
DB 121 GAGCGCGTGGAGAGTCTCTCACTCCATCCGCAACAGCTTCCTGGGCTCCCTCGCT 180
QY 1649 TTACCGCGCGCAAGATGCAAGTCCCTACCGTGGAGAGATGTCAGCTTGAGCCAGAGT 1708
DB 181 TCCACCGCGCGCAAGATGCAAGTCCCTACCGTGGAGAGATGTCAGCTTGAGCCAGAGT 240
QY 1709 CTTCCCGGAGCTGGCAAAACGCTCTCTGTTGCGGAACTTCATCTCTTGGCAAGAG 1768
DB 241 CTTCTCCAGAGCTGGCAAAACGCTCTCTGTTGCGGAACTTCATCTCTTGGCAAGAG 300
QY 1769 AACAAATATTCCTCGTGCTAAAGGACAAACCTCTCAGCAGCATCAAGAGCAGCATCGTCC 1828
DB 301 AACAAATATTCCTCGTGCTAAAGGACAAACCTCTCAGCAGCATCAAGAGCAGCATGTGCC 360

RESULT 10
CV023843
LOCUS
DEFINITION
878 Full length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC016681, mRNA sequence.
CV023843
VERSION
CV023843.1 GI:51481642
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 615)
Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingsmith,R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,B., Le Peuch,C.,
Vandenhaute,J., Cusick,M.E., Alabala,J.S., Hill,D.E. and Vidal,M.
Human ORFeome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers
FORWARD: ATGGGAGCGCTGCATCCAA
BACKWARD: CAGGCGAGGGGTCCCGTT
Insert length: 615 Std Error: 65.00
Plate: 11065 row: 12 column: A
Seq primer: ACTGCGGTCTTTTACACAGTCTGTGCTGGAAAC
High quality sequence start: 98
High quality sequence stop: 614
POLYA=No.
Location/Qualifiers
1..615
/organism="Homo sapiens"
/mol_type="mRNA"

1829 ATGCTTTCTCTCGATCCCGAGCGCTGAGTCACTGCTGTCTACAGACCGCTTCAGG 1888
361 ATGCTTTCTCTCGATCCCGAGCGCTGAGTCACTGCTGTCTACAGACCGCTTCAGG 420
1889 CCGAGTACAGCGCAGTGGCGCGCCCTCCGCTTCCAAAGCCCGTCCGCTTCAGGTTG 1948
421 CCGAATACAGCGCAGCGTGGCGCCCTCTGCTTCCAGAGCTGTCCGCTTCAGGTTG 480
1949 ACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGTTGGT 2008
481 ACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGGAGTGTAGCAGTGGAGTG 540
2009 GCATCTACTCCGTTCACTTCTCATCTCGGTCCTGAGCGCTGTGAGCGGTTCAGG 2068
541 GCATCTACTCAGTCACTTCTCATCTCGGTCCTGAGCGCTGTGAGCGGTTCAGG 600
2069 TGGAGACCATCCAGGACAGCTCTCTGAGCACTCATGACAGCCCTCCCTGAGGCGCT 2128
601 TAGAGACCATCCAGGACAGCTCTCTGAGCACTCATGACAGCCCTCCCTGAGGCG 660
2129 CAGACGAGAGAACGGGGCCAGACCCCGCTCTGCTGTGGTGGCCACCCGAGAGCT 2188
661 CAGATGAGAAGA--TGGAGCCAGACCGCGCTCTGCTGTGTAACCCA-CCGAGAG 717
2189 CCCACCCCGGC 2199
718 TTCCCCCAGGCC 728

CV023843 615 bp mRNA linear EST 20-AUG-2004
878 Full length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC016681, mRNA sequence.
CV023843
VERSION
CV023843.1 GI:51481642
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 615)
Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingsmith,R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,B., Le Peuch,C.,
Vandenhaute,J., Cusick,M.E., Alabala,J.S., Hill,D.E. and Vidal,M.
Human ORFeome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers
FORWARD: ATGGGAGCGCTGCATCCAA
BACKWARD: CAGGCGAGGGGTCCCGTT
Insert length: 615 Std Error: 65.00
Plate: 11065 row: 12 column: A
Seq primer: ACTGCGGTCTTTTACACAGTCTGTGCTGGAAAC
High quality sequence start: 98
High quality sequence stop: 614
POLYA=No.
Location/Qualifiers
1..615
/organism="Homo sapiens"
/mol_type="mRNA"

```

```
/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_lib="Full length cDNA from the Mammalian Gene
Collection"
/note="vector: mixed; The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
Donor vector. Reference : MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"

ORIGIN
Query Match 26.0%; Score 595.8; DB 7; Length 615;
Best Local Similarity 99.0%; Pred. No. 5.6e-128;
Matches 609; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

Qy 868 ATGGGAGCTCCATCCACGGAGAGCTGACCCGACGCTCTAGAGAGCATGGCATCA 927
Db 1 ATGGGAGCTCCATCCACGGAGAGCTGACCCGACGCTCTAGAGAGCATGGCATCA 60

Qy 928 CTGGGCTGCTTCAGGACCGCGAGAGGCTGCATCGGAGCTGCCAGTGGAGGAGAAC 987
Db 61 CTGGGCTGCTTCAGGACCGCGAGAGGCTGCATCGGAGCTGCCAGTGGAGGAGAAC 120

Qy 988 CAAGAAAGATGATATATTATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGTGAG 1047
Db 121 CAAGAAAGATGATATATTATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGTGAG 180

Qy 1048 GACGAGGACCTGCTCCCGGAATGATGTTGACCCCGGAGCGGTGCGATTCCTCC 1107
Db 181 GACGAGGACCTGCTCCCGGAATGATGTTGACCCCGGAGCGGTGCGATTCCTCC 240

Qy 1108 ATGTGAGCCCTCAGGGAAGCGGACGAGAGCGGAAGTCCATGGAAGTCTCTGAGCATC 1167
Db 241 ATGTGAGCTGTCAGGGAAGCGGACGAGAGCGGAAGTCCATGGAAGTCTCTGAGCATC 300

Qy 1168 ACCGATGCGGGGTGTTGCTCCCTGTATACCCAGCGGCTTGGAGATGGCCGAG 1227
Db 301 ACCGATGCGGGGTGTTGCTCCCTGTATACCCAGCGGCTTGGAGATGGCCGAG 360

Qy 1228 CACAGCAGAGATCCGTTAGGCTGAGTGGAGCTCCAGGGTCTGTCTCCAGCCCTTA 1287
Db 361 CACAGCAGAGATCCGTTAGGCTGAGTGGAGCTCCAGGGTCTGTCTCCAGCCCTTA 420

Qy 1288 AGCAGCCCAAGGAGTCCGCTCTTTTCTTTTACCGAGCGGGGCTGGAGATGAGGCT 1347
Db 421 AGCAGCCCAAGGAGTCCGCTCTTTTCTTTTACCGAGCGGGGCTGGAGATGAGGCT 480

Qy 1348 CGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCTTGGGGGCCCCAGGGGT 1407
Db 481 CGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCTTGGGGGCCCCAGGGGT 540

Qy 1408 GGGGG--CGCGGGGAGCAGCCCGCCCGCCAGTCCCGCTCCACACCCCTGCGCGCC 1465
Db 541 GNGGGGCGCGGGGAGCAGCCCGCCCGCCAGTCCCGCTCCACACCCCTGCGCGCC 600

Qy 1466 CCCAGGCTCCCGC 1480
Db 601 CCCAGGCTCCCGC 615

RESULT 11
BM948524
LOCUS
DEFINITION UI-M-EG0p-bve-1-10-0-UI.r1 NIH_BMAP_EG0p Mus musculus cDNA clone
IMAGE:5691033 5', mRNA sequence.
ACCESSION BM948524
VERSION BM948524.1 GI:19432115
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 698)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
Seq primer: pYX-5.  
Location/Qualifiers  
1..698  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5691033"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 18.5 dpc"  
/lab\_host="DH10B (TI phase resistant)"  
/clone\_lib="NIH\_BMAP\_EG0p"  
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured mRNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was size selected according to mRNA size fraction,  
ligated with EcoR I adaptor, digested with Not I, and then  
cloned directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA  
tail, is CAGCCACGAC. This library was created for the  
University of Iowa Mouse Brain Molecular Anatomy Project  
(BMAP): 'Gene Discovery in the Developing Mouse Nervous  
System', supported by National Institute of Mental Health  
(NIMH), Hemin Chin, Ph.D., program coordinator."

Query Match 25.9%; Score 592.4; DB 5; Length 698;  
Best Local Similarity 90.5%; Pred. No. 3.5e-127;  
Matches 632; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 284 AGCAGCTCTCGGGGTGAGCTATTCGACTACCTGGTAAAGAGGGGAGACTGACGCCA 343  
Db 1 AGCAGCTTCTGTTGTTGAGCTGTTTCGACTACCTGGTAAAGAGGGGAGACTGACGCCA 60

Qy 344 AGGAGGCCCGAAGTTCTTCGCCAGATTGTTCTGCGCTGGACTTCTGCCACAGCTACT 403  
Db 61 AGGAGGCCCGAAGTTCTTCGCCAGATTGTTCTGCGCTGGACTTCTGCCACAGCTACT 120

Qy 404 CCATCTGCACAGAGACTAAAGCCGAGAACCTGCTTTTGGATGAGAAAAACAACATCC 463  
Db 121 CCATCTGCACAGAGACTTGAAGCAGAGAACCTGCTTGGATGAGAAAAACAACATCC 180

Qy 464 GCATTGAGACTTCGGCATGCGCTCCCTGCGAGTGGGGGACAGCCTCTGTGAGACCACT 523  
Db 181 GCATCGCAGACTTTGGTATGGCGTCCCTGCAAGTGGGGGACAGCCTCTGTGAGACCACT 240

Qy 524 GCGGGTCCCCCATATTGCGTGTCCAGAGTGTATTAGGGGGGAAAAATATGATGGCCGC 583  
Db 241 GCGGGTCCCCCATATTGCGTGTCCAGAGTGTATTAGGGGGGAAAAATGATGATGGCCGC 300

Qy 584 GGGCAGACATGTGGAGCTGTGAGTGCATCTCTTTCGCCCTGCTGCTGGGGGCTCTGCCCT 643  
Db 301 GGGCAGACATGTGGAGCTGTGAGTGCATCTCTTTCGCCCTGCTGCTGGGGGCTCTGCCCT 360

ORIGIN



```

REFERENCE
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Tissue Procurement: Dr. James Lin, University of Iowa
              cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              This clone was contributed by the Brain Molecular Anatomy Project
              (BNAP)

FEATURES
source
Seq primer: pYX-5.
Location/Qualifiers
1. 742
   /organism="Mus musculus"
   /mol_type="mRNA"
   /strain="C57BL/6"
   /db_xref="taxon:10090"
   /clone="IMAGE:5695440"
   /tissue_type="whole brain"
   /dev_stage="embryo 18.5 dpc"
   /lab_host="DH10B (T1 phage resistant)"
   /clone_lib="NIH_BMAP_EH0p"
   /note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
   Site 2: Not I; The library was constructed according to
   Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
   1996. Denatured mRNA was size fractionated on a 1% agarose
   gel. First strand cDNA synthesis was primed with an
   oligo-dT primer containing a Not I site. Double stranded
   cDNA was size selected according to mRNA size fraction,
   ligated with EcoR I adaptor, digested with Not I, and then
   cloned directionally into pYX-Asc vector. The library tag
   sequence located between the Not I site and the polyA
   tail, is CHGCCACGAC. This library was created for the
   University of Iowa Mouse Brain Molecular Anatomy Project
   (BNAP): 'Gene Discovery in the Developing Mouse Nervous
   System', supported by National Institute of Mental Health
   (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Query Match      25.1%; Score 574.8; DB 5; Length 742;
Best Local Similarity 89.4%; Pred. No. 4.6e-123;
Matches 663; Conservative 0; Mismatches 74; Indels 5; Gaps 4;

394 CACAGCTACTCCATCTGCCACAGACCTTAAGCCCGAGACCTGTTTGATGAGAAA 453
    |||
2  CATAGCTACTCCATCTGTACAGAGACTTGAAGCCAGAGAACCTGCTGTTTGATGAGAAA 61
    |||
454 AACACATCCCATCTGCAGACTTCGGCATGCGCTCCCTGCAGGTGGGGACAGCTCTGTG 513
    |||
62 AACACATCCCATCTGCAGACTTGTGTATGCGTCCCTGCAAGTGGGGACAGCTCTGTG 121
    |||
514 GAGACCAAGTCGGGTCCCCCATTTATCGTGTCCAGAGGTGATTAAAGGGGAAAAATAT 573
    |||
122 GAGACCAAGTCGGGTCCCCCATTTAGCATGTCCAGAGGTGATCAAGGGGAAAAATAT 181
    |||
574 GATGGCCCGGGCAGACATGTGAGTGTGGAGTATCTCTTCGCGCTGCTCGTGGGG 633
    |||
182 GATGGCCCGGGCAGACATGTGAGTGTGGAGTATCTCTTATTTGCGCTGCTTGTGGGG 241
    |||
634 GCTCTGCCCTTTGATGACGACAACTCCGCGAGCTGTGGAGAGGTGCAACGGGGCGTC 693
    |||
242 GCACTGCCCTTCGATGACGACAACTCGCGCAGCTACTGTGGAGAGGTGAAACGTGGGGTC 301
    |||
694 TTCCACATGCCGCCACTTTCATTTCCAGATGCGCAGAGCTCTCCAGGGGAATGATCGAA 753
    |||
302 TTCCACATGCTCACTTCATCTCCAGACTGCCAGAGCTCTCTGAGAGGATGATGAA 361
    |||
754 GTGGAGGCCGAAAAAAGGCTCAGTCTGGAGCAAAATTACAGAAACATCTTGTA--CCTAG 811
    |||

```

```

Db 362 GTGAGGCCGAGAAAAGGCTCAGTCTGGAGCAAAATTAGAAAACATCTTTGGTATCNTGG 421
    |||
Qy 812 GCGGGAACACGAGCCAGACCCGTCCTCGGAGCCAGCCCTCGGCGCGGGTAGGCATGC 871
    |||
Db 422 GCGGGAACACGAGCCAGACCCCTTTCCTCGGAGCCAGCCCGCCAGAGTAGGCATGC 481
    |||
Qy 872 GGAGCCTGCCATCAACGAGAGAGCTGGACCCCGAGCTCTAGAGAGCATGCAATCATTGG 931
    |||
Db 482 GTAGCCTGCCCTTCAATGGCGAGCTGGACCCCTGACCTTCTGGAAGCATGCGCTCTCTGG 541
    |||
Qy 932 GCTCTTCAGGAGCCGCGAGAGGCTGCATCGCAGCTGCGCAGTGAGGAGGAGAACCAAG 991
    |||
Db 542 GCTCTTCAGAGACCCGAGCGGCTGCACAGAACTGCGAAGCGAGGAGGAACCAAG 601
    |||
Qy 992 AAAAGATGATATATTTATCTGC-TTTTGGATCGGAAGGAGCGGTATCCAGCTGTGAGGAC 1050
    |||
Db 602 AAAAGATGATCTATTTATTTGCTTTTGGATCGGAAGGAGCGGTATCTAGCTGTGAAGAC 661
    |||
Qy 1051 CAGGACCTGCTCCCGGAATGATGTTGACCC-CCCCGGGAAGCGTGTGGATTTCTCCCAT 1109
    |||
Db 662 CAGGA-CTGCTCTCTCGGAATGATGTTGACCCACCTCCGAGGCGTGTGGATTTCCCCCAT 720
    |||
Qy 1110 GCTGAGCCGCTCACGGGAGCGG 1131
    |||
Db 721 GCTGAGCANACACGGGAACGG 742
    |||

RESULT 14
LOCUS      CA319620
DEFINITION UI-M-FW0-cca-c-12-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
ACCESSION  CA319620
VERSION     CA319620.1 GI:24537744
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE   1 (bases 1 to 686)
            NIH-MGC http://mgc.nci.nih.gov/
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            This clone was contributed by the Brain Molecular Anatomy Project
            (BNAP)

FEATURES
source
Seq primer: pYX-5.
Location/Qualifiers
1. 686
   /organism="Mus musculus"
   /mol_type="mRNA"
   /strain="C57BL/6"
   /db_xref="taxon:10090"
   /clone="IMAGE:6816805"
   /tissue_type="whole brain"
   /dev_stage="embryo 13.5, 14.5, 16.5, 17.5dpc"
   /lab_host="DH10B (T1 phage resistant)"
   /clone_lib="NIH_BMAP_FW0"
   /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
   Site 2: Not I; The library was constructed according
   Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
   1996. Denatured RNA was size fractionated on a 1% agarose
   gel. First strand cDNA synthesis was primed with oligo-dT
   primer containing a Not I site. Double strand cDNA was

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.  
  
OM nucleic - nucleic search, using sw model  
  
Run on: February 19, 2005, 12:29:10 , Search time 1209 Seconds  
(without alignments)  
11190.344 Million cell updates/sec

Title: US-10-803-277-3  
Perfect score: 2289  
Sequence: 1 atgggaatttgattggttt.....acgggaccctctgcctga 2289

Scoring table: IDENTITY\_NUC  
, Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2289	100.0	2289	16 US-10-116-326-3	Sequence 3, Appli
2	2289	100.0	2289	18 US-10-803-277-3	Sequence 3, Appli
3	2020.2	88.3	2112	16 US-10-116-326-5	Sequence 5, Appli
4	2020.2	88.3	2112	18 US-10-803-277-5	Sequence 5, Appli
5	2020.2	88.3	2337	17 US-10-116-326-1	Sequence 1, Appli
6	2020.2	88.3	2337	17 US-10-423-543-12	Sequence 12, Appli
7	2020.2	88.3	2337	18 US-10-803-277-1	Sequence 1, Appli
8	2020.2	88.3	2337	17 US-10-311-034-43	Sequence 43, Appli
9	2020.2	88.3	2980	16 US-10-354-358-91	Sequence 91, Appli
10	2020.2	88.3	2980	17 US-10-423-543-10	Sequence 10, Appli
11	2020.2	88.3	2980	18 US-10-757-262-135	Sequence 135, Appli

12	1839	80.3	2799	18	US-10-479-532-2	Sequence 2, Appli
13	1518.8	66.4	1949	17	US-10-425-114-26847	Sequence 26847, A
14	980	42.8	1797	17	US-10-120-988-221	Sequence 221, App
15	800.8	35.0	1911	15	US-10-283-247-4	Sequence 4, Appli
16	800.8	35.0	3791	17	US-10-425-114-26842	Sequence 26842, A
17	780.4	34.1	3364	14	US-10-195-072-3	Sequence 3, Appli
18	780.4	34.1	3364	14	US-10-195-071-3	Sequence 3, Appli
19	778.8	34.0	2908	14	US-10-195-072-1	Sequence 1, Appli
20	778.8	34.0	2908	14	US-10-195-071-1	Sequence 1, Appli
21	777.2	34.0	1827	13	US-10-054-579-3	Sequence 3, Appli
22	777.2	34.0	2007	13	US-10-054-579-1	Sequence 1, Appli
23	777.2	34.0	2647	17	US-10-288-798-42	Sequence 42, Appli
24	777.2	34.0	2647	17	US-10-362-892-42	Sequence 42, Appli
25	774.8	33.8	2025	15	US-10-283-247-1	Sequence 1, Appli
26	774.8	33.8	3831	18	US-10-618-941-12	Sequence 12, Appli
27	773.2	33.8	2025	9	US-09-842-582-3	Sequence 3, Appli
28	773.2	33.8	2219	9	US-09-842-582-1	Sequence 1, Appli
29	614	26.8	614	17	US-10-276-774-700	Sequence 700, App
30	551	24.1	906	17	US-10-276-774-72	Sequence 72, Appli
31	512	22.4	512	9	US-09-960-253-87	Sequence 87, Appli
c 32	408.4	17.8	584	16	US-10-029-386-6329	Sequence 6329, Ap
c 33	408.4	17.8	19640	13	US-10-087-192-1084	Sequence 1084, Ap
34	365	15.9	700	18	US-10-723-860-7743	Sequence 7743, Ap
35	296.8	13.0	2173	16	US-10-102-548-1	Sequence 1, Appli
36	215	9.4	275	9	US-09-960-352-5086	Sequence 5086, Ap
37	204.4	8.9	1594	15	US-10-284-060-1	Sequence 1, Appli
38	204.4	8.9	1594	15	US-10-284-060-3	Sequence 3, Appli
39	202.2	8.8	3170	17	US-10-276-645-1	Sequence 1, Appli
40	202.2	8.8	3250	17	US-10-276-645-2	Sequence 2, Appli
41	202	8.8	515	16	US-10-029-386-6161	Sequence 6161, Ap
42	199.2	8.7	2086	16	US-10-161-565-4	Sequence 4, Appli
43	199.2	8.7	2112	9	US-09-919-585-4	Sequence 4, Appli
44	199.2	8.7	2112	16	US-10-161-565-7	Sequence 7, Appli
45	199.2	8.7	2222	9	US-09-919-585-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-10-116-326-3  
; Sequence 3, Application US/10116326  
; Publication No. US20030166889A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. US20030166889A1el Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0332-USA  
; CURRENT APPLICATION NUMBER: US/10/116.326  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/282,036  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2289  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-116-326-3

Query Match 100.0%; Score 2289; DB 16; Length 2289;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGACTTGAGTTTGGTTTCTTAGAGCTGGTGGAACTGGAGTCACTTCTCCAGGG	60
Db	1	ATGGGACTTGAGTTTGGTTTCTTAGAGCTGGTGGAACTGGAGTCACTTCTCCAGGG	60
Qy	61	AGTCATGGGAACCTGGAATCTCTCCAGAGATTAATGGAATGAGTCTCTCTC	120
Db	61	AGTCATGGGAACCTGGAATCTCTCTCCAGAGATTAATGGAATGAGTCTCTCTC	120



QY 121 CCAGGACCCATGGGAATTGGAGTCTCTTCTCCCAAGGATCATGGAAATTGGAGTTCTC 180  
DB 121 CCAGGACCCATGGGAATTGGAGTCTCTTCTCCCAAGGATCATGGGAATTGGAGTTCTC 180  
QY 181 TGGCACAGAGGACGAGTGGGAAGTGGAGACAGAGCCCTTTGGTCTCTCCAGATGCCCTTC 240  
DB 181 TGGCACAGAGGACGAGTGGGAAGTGGAGACAGAGCCCTTTGGTCTCTCCAGATGCCCTTC 240  
QY 241 CAGCCCTCTGCCCTCTATATCTTTAGTACTGGTCTCTGAGACAGCTCTCGGGGGGT 300  
DB 241 CAGCCCTCTGCCCTCTATATCTTTAGTACTGGTCTCTGAGACAGCTCTCGGGGGGT 300  
QY 301 GAGCTATTCCGACTACCTGTGTAAAGAGGGAGACTGACGCCCAAGAGAGGCCGGAAGTTTC 360  
DB 301 GAGCTATTCCGACTACCTGTGTAAAGAGGGAGACTGACGCCCAAGAGAGGCCGGAAGTTTC 360  
QY 361 TTCCGCCAGATTGTCTGGCTGGACTTTGTGCCACAGCTACTCTCATCTGCCACAGAGAC 420  
DB 361 TTCCGCCAGATTGTCTGGCTGGACTTTGTGCCACAGCTACTCTCATCTGCCACAGAGAC 420  
QY 421 CTAAAGCCCGAGACCTGCTTTGGATGAGAAACCAACATCCGCAATTGCAGACTTCGGC 480  
DB 421 CTAAAGCCCGAGACCTGCTTTGGATGAGAAACCAACATCCGCAATTGCAGACTTCGGC 480  
QY 481 ATGGCGTCCCTGCAGGTGGGGACAGCCTCTCTGGAGACCAAGCTGCGGGTCCCCCAATTAT 540  
DB 481 ATGGCGTCCCTGCAGGTGGGGACAGCCTCTCTGGAGACCAAGCTGCGGGTCCCCCAATTAT 540  
QY 541 GCCTGTCCAGAGTGTATTAAGGGGGAATAATATGATGCGCGCGCGGAGACATGTGAGC 600  
DB 541 GCCTGTCCAGAGTGTATTAAGGGGGAATAATATGATGCGCGCGCGGAGACATGTGAGC 600  
QY 601 TGTGGATCATCTCTTCGCCCTCTGCTGGGGGCTCTGCCCTTTGATGACGACCAACTC 660  
DB 601 TGTGGATCATCTCTCTTCGCCCTCTGCTGGGGGCTCTGCCCTTTGATGACGACCAACTC 660  
QY 661 CGCAGCTGCTGGAGAGGTGAACCGGGGCTCTTCCACATGCGCCCACTTCATCTCTCCA 720  
DB 661 CGCAGCTGCTGGAGAGGTGAACCGGGGCTCTTCCACATGCGCCCACTTCATCTCTCCA 720  
QY 721 GATTGCCAGAGCTCTGAGGGGAATGATCAAGTGGAGCCCGAAGAGGCTCAGTCTG 780  
DB 721 GATTGCCAGAGCTCTGAGGGGAATGATCAAGTGGAGCCCGAAGAGGCTCAGTCTG 780  
QY 781 GAGCAAAATTCAGAAACATCTTGTGTAACCTAGCGGGAAACAGAGCCAGACCCGTGCTG 840  
DB 781 GAGCAAAATTCAGAAACATCTTGTGTAACCTAGCGGGAAACAGAGCCAGACCCGTGCTG 840  
QY 841 GAGCCAGCCCTGGCCCGGGTAGCCATGCGGAGCTGCCATCCAAAGAGAGCTGGAC 900  
DB 841 GAGCCAGCCCTGGCCCGGGTAGCCATGCGGAGCTGCCATCCAAAGAGAGCTGGAC 900  
QY 901 CCGGAGCTCTAGAGAGATGGCATCACTGGGCTGCTTCAGGACCGGAGAGCTGCAT 960  
DB 901 CCGGAGCTCTAGAGAGATGGCATCACTGGGCTGCTTCAGGACCGGAGAGCTGCAT 960  
QY 961 GCGGAGCTGCGAGTGAGAGAGAACCAAGAAAGATGATATTAATCTGCTTTTGGAT 1020  
DB 961 GCGGAGCTGCGGAGTGAGAGAGAACCAAGAAAGATGATATTAATCTGCTTTTGGAT 1020  
QY 1021 CGGAAGGACGGTATCCAGCTGTGAGGACAGGACCTGCGCTCCCGGAATGATGTTGAC 1080  
DB 1021 CGGAAGGACGGTATCCAGCTGTGAGGACAGGACCTGCGCTCCCGGAATGATGTTGAC 1080  
QY 1081 CCCCCCGGAGAGCTGTGATTTCTCCATGCTGAGCGCTGACGGGAAGCGGACAGAG 1140  
DB 1081 CCCCCCGGAGAGCTGTGATTTCTCCATGCTGAGCGCTGACGGGAAGCGGACAGAG 1140  
QY 1141 CGGAAGTCCATGGAAGTCTGAGCATCACCGATGCGGGGGTGGTCTCCCTGTACCC 1200  
DB 1141 CGGAAGTCCATGGAAGTCTGAGCATCACCGATGCGGGGGTGGTCTCCCTGTACCC 1200  
QY 1201 ACCCGAGCGGGCCTTGAGATGGCCAGCAGCCAGAGATCCCGTAGCGTCAGTGGAGCC 1260

DB 1201 ACCCGAGCGGGCCTTGAGATGGCCAGCAGAGATCCCGTAGCGTCAGTGGAGCC 1260  
QY 1261 TCCACGGGTCTGTCTCTCAGAGCCCTTAAGCAGCCCAAGAGAGTCCGGTCTTTTCTTTTCA 1320  
DB 1261 TCCACGGGTCTGTCTCTCAGAGCCCTTAAGCAGCCCAAGAGAGTCCGGTCTTTTCTTTTCA 1320  
QY 1321 CCGGAGCCGGGGCTGGAGATGAGCTCAGAGCGGGGGTCCCGACTTCCAAAGAGCAG 1380  
DB 1321 CCGGAGCCGGGGCTGGAGATGAGCTCAGAGCGGGGGTCCCGACTTCCAAAGAGCAG 1380  
QY 1381 AGCTGCTCTTCTCGGGGCCCAAGGGGTGGGGGCGCGGGGAGCAGCCCGCCCGCCAGT 1440  
DB 1381 AGCTGCTCTTCTCGGGGCCCAAGGGGTGGGGGCGCGGGGAGCAGCCCGCCCGCCAGT 1440  
QY 1441 GCCCGCTCCACACCCCTGCGCCCGCCCGAGGCTCCCGCGCTCTCTGCGGGGACCCCC 1500  
DB 1441 GCCCGCTCCACACCCCTGCGCCCGCCCGAGGCTCCCGCGCTCTCTGCGGGGACCCCC 1500  
QY 1501 TTGCACTCGCTCTGCAACCGCCCGGGCAGTCCCAACCGGGACCCCGGGGACCAACCA 1560  
DB 1501 TTGCACTCGCTCTGCAACCGCCCGGGCAGTCCCAACCGGGACCCCGGGGACCAACCA 1560  
QY 1561 CCCCCAGCCCGGGGCTGGGCTCGGGGAGCGCCTGAGAGTCTCTCAACTCCATC 1620  
DB 1561 CCCCCAGCCCGGGGCTGGGCTCGGGGAGCGCCTGAGAGTCTCTCAACTCCATC 1620  
QY 1621 CGCAACAGCTTCTCGGGCTCCCTCGCTTTTACCGCGCAAGATGAGGTCCTACCGCT 1680  
DB 1621 CGCAACAGCTTCTCGGGCTCCCTCGCTTTTACCGCGCAAGATGAGGTCCTACCGCT 1680  
QY 1681 GAGGAGATGTCAGCTGTGAGCGCCAGAGTCTCTCCCGAGCTGGCAAAAGCTCTGGTTC 1740  
DB 1681 GAGGAGATGTCAGCTGTGAGCGCCAGAGTCTCTCCCGAGCTGGCAAAAGCTCTGGTTC 1740  
QY 1741 GGGAACTTCACTCTCTTGGACAAAGAAACAAATATTCCTGCTGCTAAAGAGCAAACT 1800  
DB 1741 GGGAACTTCACTCTCTTGGACAAAGAAACAAATATTCCTGCTGCTAAAGAGCAAACT 1800  
QY 1801 CTGAGCAGCATCAAGCAGACATCGTCCATGCTTCTGTCGATCTCCAGCGCTGAGTCAC 1860  
DB 1801 CTGAGCAGCATCAAGCAGACATCGTCCATGCTTCTGTCGATCTCCAGCGCTGAGTCAC 1860  
QY 1861 AGTGTGCTGTACAGACAGCTTTCAGGGCGGAGTACAAAGCCAGTGGCGGCCCTCGTC 1920  
DB 1861 AGTGTGCTGTACAGACAGCTTTCAGGGCGGAGTACAAAGCCAGTGGCGGCCCTCGTC 1920  
QY 1921 TTCCAAAGCCCGTCCGCTTCCAGGTGGAATCATGAGTCTCTTCTGAGGGTCCAGAGCCCTCC 1980  
DB 1921 TTCCAAAGCCCGTCCGCTTCCAGGTGGAATCATGAGTCTCTTCTGAGGGTCCAGAGCCCTCC 1980  
QY 1981 CCGCGACGGGACGGCAGAGGTGGATCTAATCTGCTCACTTCTCTCTCATCTCG 2040  
DB 1981 CCGCGACGGGACGGCAGAGGTGGATCTAATCTGCTCACTTCTCTCTCATCTCG 2040  
QY 2041 GGTCCAGCGCTCGGTTCAGCCAGGTGGTGGAGACCATCCAGGCAGAGCTCTGAGCACT 2100  
DB 2041 GGTCCAGCGCTCGGTTCAGCCAGGTGGTGGAGACCATCCAGGCAGAGCTCTGAGCACT 2100  
QY 2101 CATGACAGCCCTCGGTTCAGGGCCCTGGCAGAGAGAGAAACGGGGGCCAGACCCGGCT 2160  
DB 2101 CATGACAGCCCTCGGTTCAGGGCCCTGGCAGAGAGAGAAACGGGGGCCAGACCCGGCT 2160  
QY 2161 GCTGGTCCCAACCCCGAAGCTTGCAGCCCGCCAGCCCGCCAGACCCAGAGCTGAGC 2220  
DB 2161 GCTGGTCCCAACCCCGAAGCTTGCAGCCCGCCAGCCCGCCAGACCCAGAGCTGAGC 2220  
QY 2221 AGCTCTCCCGCGAGGCCCCCCCAAGAGCAAGAGTCTCTGGGCAACCAAGGAGCCCT 2280  
DB 2221 AGCTCTCCCGCGAGGCCCCCCCAAGAGCAAGAGTCTCTGGGCAACCAAGGAGCCCT 2280  
QY 2281 CTGCGCTGA 2289  
DB 2281 CTGCGCTGA 2289



```
Db      2281  CTGCCCTGA 2289

RESULT 2
US-10-803-277-3
; Sequence 3, Application US/10803277
; Publication No. US20040180416A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/803,277
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2289
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-277-3

Query Match      100.0%; Score 2289; DB 18; Length 2289;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGAGCTTGAGTTGGTTTCTAGAGCTGGTGGAAATCGAGTCACTTCTCCAGGG 60
Db
Qy      1  ATGGAGCTTGAGTTGGTTTCTAGAGCTGGTGGAAATCGAGTCACTTCTCCAGGG 60
Db
Qy      61  AGTCATGGGAACCTGAAATCTCTCCACAGAAATTAATGAAATCGAGTCTCTGTC 120
Db
Qy      61  AGTCATGGGAACCTGAAATCTCTCTCCACAGAAATTAATGAAATCGAGTCTCTGTC 120
Db
Qy      121  CCAGGGACCCATGGGAATGGAGTCTCTTTCTCCCAAGGATCATGGGAATGGAGTCTC 180
Db
Qy      121  CCAGGGACCCATGGGAATGGAGTCTCTTTCTCCCAAGGATCATGGGAATGGAGTCTC 180
Db
Qy      181  TGCCACAGGAGCCAGTGGGAATGGGAGACAGAGCCCTTTGGTCTCCACATGCCCTTC 240
Db
Qy      181  TGCCACAGGAGCCAGTGGGAATGGGAGACAGAGCCCTTTGGTCTCCACATGCCCTTC 240
Db
Qy      241  CAGCCCTCTGCCCTCTATATCTTTAGGTACCTGTTCTGGAGCAGTCTCGGGGGT 300
Db
Qy      241  CAGCCCTCTGCCCTCTATATCTTTAGGTACCTGTTCTGGAGCAGTCTCGGGGGT 300
Db
Qy      301  GAGCTATTTCGACTACCTGTTAAAGAGGGGAGACTGACGCCCAAGAGAGCCCGGAAATTC 360
Db
Qy      301  GAGCTATTTCGACTACCTGTTAAAGAGGGGAGACTGACGCCCAAGAGAGCCCGGAAATTC 360
Db
Qy      361  TTCCGCGAGATTGTCTGCGCTGGACTTCTGCGAGTCTGCGAGTCTGCGAGTCTGCGAG 420
Db
Qy      361  TTCCGCGAGATTGTCTGCGCTGGACTTCTGCGAGTCTGCGAGTCTGCGAGTCTGCGAG 420
Db
Qy      421  CTAAGCCCGAGAACCTGCTTTTGGATGAGAAACAAACATCCGATTCGAGACTTCGGC 480
Db
Qy      421  CTAAGCCCGAGAACCTGCTTTTGGATGAGAAACAAACATCCGATTCGAGACTTCGGC 480
Db
Qy      481  ATGGCGTCTCTGAGTGGGGGACAGCCTCTCTGGAGACAGTCTGGGTCTCCCATTTAT 540
Db
Qy      481  ATGGCGTCTCTGAGTGGGGGACAGCCTCTCTGGAGACAGTCTGGGTCTCCCATTTAT 540
Db
Qy      541  GCGTGTCCAGAGGTGATTAAAGGGGAAATATATATGATGCGCCCGGAGACATGTGGAGC 600
Db
Qy      541  GCGTGTCCAGAGGTGATTAAAGGGGAAATATATATGATGCGCCCGGAGACATGTGGAGC 600
Db
Qy      601  TGTGAGTCACTTCTTCCCTGCTCGTGGGGGCTCTGCCCTTTGATGACGACAACTC 660
Db

601  TGTGAGTCACTTCTTCCCTGCTCGTGGGGGCTCTGCCCTTTGATGACGACAACTC 660
661  CGCCAGCTGTGTGGAGAAAGGTGAAACGGGGCGCTCTTCCACATGCCCCCACTTCAATCTTCA 720
661  CGCCAGCTGTGTGGAGAAAGGTGAAACGGGGCGCTCTTCCACATGCCCCCACTTCAATCTTCA 720
721  GATTGCCAGAGCCTCTGTAGGGGGAATGATGAAAGTGGAGCCCGGAAAGGCTCAGTCTG 780
721  GATTGCCAGAGCCTCTGTAGGGGGAATGATGAAAGTGGAGCCCGGAAAGGCTCAGTCTG 780
781  GAGCAAAATTGAGAAACATCTTGTGTACTAGCCGGGAAACACGAGCCAGACCCCGTGCCTG 840
781  GAGCAAAATTGAGAAACATCTTGTGTACTAGCCGGGAAACACGAGCCAGACCCCGTGCCTG 840
841  GAGCCAGCCCTGTGCCCCCGGGTAGCCATCGGAGCCTGCCCATCCACGGAGAGCTGCAT 900
841  GAGCCAGCCCTGTGCCCCCGGGTAGCCATCGGAGCCTGCCCATCCACGGAGAGCTGCAT 900
901  CCGACGCTCTAGAGAGCATGGCATCACTGGGCTGCTTCAGGGACCCGAGAGGCTGCAT 960
901  CCGACGCTCTAGAGAGCATGGCATCACTGGGCTGCTTCAGGGACCCGAGAGGCTGCAT 960
961  CGCGAGCTGGCAGTGAAGAGGAGAAACCAAGAAAGATGATATATTCTCTTTTGGAT 1020
961  CGCGAGCTGGCAGTGAAGAGGAGAAACCAAGAAAGATGATATATTCTCTTTTGGAT 1020
1021  CGGAAGAGCGGTATCCAGCTGTGAGGACAGAGCCTGCTCCCGGAAATGATGTTGAC 1080
1021  CGGAAGAGCGGTATCCAGCTGTGAGGACAGAGCCTGCTCCCGGAAATGATGTTGAC 1080
1081  CCCCCCGGAAAGCTGTGGATTCTCCATGCTGAGCGTCAAGGGAGCGGAGCCAGAG 1140
1081  CCCCCCGGAAAGCTGTGGATTCTCCATGCTGAGCGTCAAGGGAGCGGAGCCAGAG 1140
1141  CGGAAGTCCATGGAAGTCTTGAGCATCACGATCCCGGGGTGTGGCTCCCTGTATCCC 1200
1141  CGGAAGTCCATGGAAGTCTTGAGCATCACGATCCCGGGGTGTGGCTCCCTGTATCCC 1200
1201  ACCGACGCGGCTTTGGAGATGGCCACAGCAGCAGAGATCCCGTAGCGTCAGTGGAGCC 1260
1201  ACCGACGCGGCTTTGGAGATGGCCACAGCAGCAGAGATCCCGTAGCGTCAGTGGAGCC 1260
1261  TCACAGGGTCTGTCTCAGCCCTTAAGCAGCCCAAGAGAGTCCGGTCTTTTCTTTTCA 1320
1261  TCACAGGGTCTGTCTCAGCCCTTAAGCAGCCCAAGAGAGTCCGGTCTTTTCTTTTCA 1320
1321  CCGGAGCCGGGGCTGAGATGAGGCTCGAGGCGGGGGCTCCCCGACTTCCAAACGCG 1380
1321  CCGGAGCCGGGGCTGAGATGAGGCTCGAGGCGGGGGCTCCCCGACTTCCAAACGCG 1380
1381  ACGTGTCTTCTCGGGGCTTGGGGGCGCGGGGAGAGAGCCCGCCCGCCCAAGT 1440
1381  ACGTGTCTTCTCGGGGCTTGGGGGCGCGGGGAGAGAGAGCCCGCCCGCCCAAGT 1440
1441  GCGCGCTCCACACCCCTGCGGGCCCCCAGAGTCCCGGGCTCTCTGTGGGGGAGACCC 1500
1441  GCGCGCTCCACACCCCTGCGGGCCCCCAGAGTCCCGGGCTCTCTGTGGGGGAGACCC 1500
1501  TTGCACTCGCTCTGACAGCCCGGGGCGAGTCCCAACGGGACCCCGGGGAGACACCA 1560
1501  TTGCACTCGCTCTGACAGCCCGGGGCGAGTCCCAACGGGACCCCGGGGAGACACCA 1560
1561  CCCCCAGCCCGCGGCTGGGCTCGGGGAGAGCCCTCTGGAGAGTCTCTCAACTCCATC 1620
1561  CCCCCAGCCCGCGGCTGGGCTCGGGGAGAGCCCTCTGGAGAGTCTCTCAACTCCATC 1620
1621  CGCAACAGTCTCTGGGCTCTCTGCTTTTCAACGGGCGAAGATGCAAGTCTCTACCGCT 1680
1621  CGCAACAGTCTCTGGGCTCTCTGCTTTTCAACGGGCGAAGATGCAAGTCTCTACCGCT 1680
1681  GAGGAGATGTCAGTCTGAGCAGAGTCTCTCCCGGAGCTGGGAGAAAGCTCTGGTTC 1740
1681  GAGGAGATGTCAGTCTGAGCAGAGTCTCTCTCCCGGAGCTGGGAGAAAGCTCTGGTTC 1740
```

```
QY 1741 GGGAACTTCATCTCTTGGACAAAGAAACAAATATTCTCTGCTTAAAGGACAAACCT 1800
Db 1741 GGGAACTTCATCTCTTGGACAAAGAAACAAATATTCTCTGCTTAAAGGACAAACCT 1800
QY 1801 CTGAGCAGCATCAAGACAGACATCGTCATCGCTTTCTGTCGATCCCGAGCCTGAGTCAC 1860
Db 1801 CTGAGCAGCATCAAGACAGACATCGTCATCGCTTTCTGTCGATCCCGAGCCTGAGTCAC 1860
QY 1861 AGTGTGTGTCAAGACAGCAGTTCAGGCGCGAGTACAGGCGCAGTGGCGGCCCTCGGTC 1920
Db 1861 AGTGTGTGTCAAGACAGCAGTTCAGGCGCGAGTACAGGCGCAGTGGCGGCCCTCGGTC 1920
QY 1921 TTCCAAAGCCCGTCCGCTTCCAGGTGACATCAGCTCTCTGAGGTCCAGAGCCCTCC 1980
Db 1921 TTCCAAAGCCCGTCCGCTTCCAGGTGACATCAGCTCTCTGAGGTCCAGAGCCCTCC 1980
QY 1981 CCGCAGCGGACGCGAGCGAGTGGTGGCATCTACTCCGTCACCTTCACTCATCTCG 2040
Db 1981 CCGCAGCGGACGCGAGCGAGTGGTGGCATCTACTCCGTCACCTTCACTCATCTCG 2040
QY 2041 GGTCCGACCGTGGTTCAGCGAGTGGTGGAGACCATCCAGGACAGCTCCTGAGCACT 2100
Db 2041 GGTCCGACCGTGGTTCAGCGAGTGGTGGAGACCATCCAGGACAGCTCCTGAGCACT 2100
QY 2101 CATGACAGCCCTCGGTGAGCGCTTCAAGCGAGTGGTGGAGACCATCCAGGACAGCTCCTGAGCACT 2160
Db 2101 CATGACAGCCCTCGGTGAGCGCTTCAAGCGAGTGGTGGAGACCATCCAGGACAGCTCCTGAGCACT 2160
QY 2161 GCTGTGTCGCCACCCGAGGCTTCAGCGCCCTCGAGACGAGAAACGGGGCCAGACCCGGCCT 2220
Db 2161 GCTGTGTCGCCACCCGAGGCTTCAGCGCCCTCGAGACGAGAAACGGGGCCAGACCCGGCCT 2220
QY 2221 AGCTCTCCCGCGAGGCCCCCAGGACAGAGCTCTCTGGGCCACCAACGGGACCCCT 2280
Db 2221 AGCTCTCCCGCGAGGCCCCCAGGACAGAGCTCTCTGGGCCACCAACGGGACCCCT 2280
QY 2281 CTGCGCTGA 2289
Db 2281 CTGCGCTGA 2289
```

```
RESULT 3
US-10-116-326-5
; Sequence 5, Application US/10116326
; Publication No. US2003016889A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US2003016889A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-116-326-5
```

```
Query Match 88.3%; Score 2020.2; DB 16; Length 2112;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 265 TTTAGTACTCGTGTCTGAGCAGCTCTCGGGGGGTGAGCTATTGAGTACTCTGTTAAAG 324
Db 88 TATTGTACTCGTGTCTGAGCAGCTCTCGGGGGGTGAGCTATTGAGTACTCTGTTAAAG 147
QY 325 AAGGGGAGACTGACGCCCAAGAGGCGCCGAAAGTTCTTCCGCCAGATTGTGTCTCGGCTG 384
```

```
Db 148 AAGGGGAGACTGACGCCCAAGAGGCGCCGAAAGTTCTTCCGCAGATTGTGTCTCGGCTG 207
QY 385 GACTTCTGCCACAGCTTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 444
Db 208 GACTTCTGCCACAGCTTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 267
QY 445 GATGAGAAAAACAACATCCGCATTGCGGATGCGGATGCGCTCTGAGGTGGGGAC 504
Db 268 GATGAGAAAAACAACATCCGCATTGCGGATGCGGATGCGCTCTGAGGTGGGGAC 327
QY 505 AGCTCTCTGGAGACAGCTGCGGCTCCGCCATATGCGTGTCCAGAGGTGATTAAAGGG 564
Db 328 AGCTCTCTGGAGACAGCTGCGGCTCCGCCATATGCGTGTCCAGAGGTGATTAAAGGG 387
QY 565 GAAAAATATGATGGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG 624
Db 388 GAAAAATATGATGGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG 447
QY 625 CTCGTGGGGCTCTGCGCTTTGATGACGACAACTCCGCGAGCTGTGAGAGGTGAA 684
Db 448 CTCGTGGGGCTCTGCGCTTTGATGACGACAACTCCGCGAGCTGTGAGAGGTGAA 507
QY 685 CGGGGCTCTTCCACATGCCCACTTCACTTCCAGATTGCCAGAGCTCTCTGAGGGGA 744
Db 508 CGGGGCTCTTCCACATGCCCACTTCACTTCCAGATTGCCAGAGCTCTCTGAGGGGA 567
QY 745 ATGATCGAAGTGGAGCGCGAAAAAGGCTCAGTCTGGAGCAATTCAGAAAAATCTTTGG 804
Db 568 ATGATCGAAGTGGAGCGCGAAAAAGGCTCAGTCTGGAGCAATTCAGAAAAATCTTTGG 627
QY 805 TACTAGGGGGGAAAACAGAGCGAGACCCGCTGCTGGAGCAGCCCTCTGCGCGCGGGTA 864
Db 628 TACTAGGGGGGAAAACAGAGCGAGACCCGCTGCTGGAGCAGCCCTCTGCGCGCGGGTA 687
QY 865 GCGTGGGGGCTGCGCTCCATCCAGCGAGCTGAGACCCGAGCTCTAGAGAGCATGGCA 924
Db 688 GCGTGGGGGCTGCGCTCCATCCAGCGAGCTGAGACCCGAGCTCTAGAGAGCATGGCA 747
QY 925 TCACTGGGCTGCTTTCAGGGACCGCGAGAGCTGCTCATCGGAGCTGCGAGTGAAGGAG 984
Db 748 TCACTGGGCTGCTTTCAGGGACCGCGAGAGCTGCTCATCGGAGCTGCGAGTGAAGGAG 807
QY 985 AACCAAGAAAGATGATATATTATCTGCTTTGGATCGGAGAGCGGTATCCAGCTGT 1044
Db 808 AACCAAGAAAGATGATATATTATCTGCTTTGGATCGGAGAGCGGTATCCAGCTGT 867
QY 1045 GAGGACCGAGCCTGCTCCCGGAAATGATGTTGACCCCGCGAGCGGTATCCAGCTGT 1104
Db 868 GAGGACCGAGCCTGCTCCCGGAAATGATGTTGACCCCGCGAGCGGTATCCAGCTGT 927
QY 1105 CCCATGCTGAGCGCTCAAGCGGAAAGCGGAGCGGAGTCCATGGAAGTCTCTGAGC 1164
Db 928 CCCATGCTGAGCGCTCAAGCGGAAAGCGGAGCGGAGTCCATGGAAGTCTCTGAGC 987
QY 1165 ATCACCGATCGCGGGGTGTGGCTCCCTGTATCCACCCGAGGCGCTTGGAGATGGCC 1224
Db 988 ATCACCGATCGCGGGGTGTGGCTCCCTGTATCCACCCGAGGCGCTTGGAGATGGCC 1047
QY 1225 CAGCACAGCAGAGATCCCGTAGCGTCAGTGGAGCTTCCAGCGGTCTGTCTCCAGGCCCT 1284
Db 1048 CAGCACAGCAGAGATCCCGTAGCGTCAGTGGAGCTTCCAGCGGTCTGTCTCCAGGCCCT 1107
QY 1285 CTAAGCAGCCCAAGGAGTCCGCTTTTCTTTTACCGAGCGCGGGGTGAGAGATGAG 1344
Db 1108 CTAAGCAGCCCAAGGAGTCCGCTTTTCTTTTACCGAGCGCGGGGTGAGAGATGAG 1167
QY 1345 GCTCAGCGCGGGGCTCCCGCATTTCCAAAACGAGAGCGCTGCTTCTCGGGGCCCGAGG 1404
Db 1168 GCTCAGCGCGGGGCTCCCGCATTTCCAAAACGAGAGCGCTGCTTCTCGGGGCCCGAGG 1227
QY 1405 GGTGCGGGCGCGCGGGGAGAGCCCCCGCCCGCTCCAGTCCCGCTCCACACCCCTCCCGGC 1464
```

Db 1228 GGTGGGGGCGCGGGGAGCAGCCCCCGCCCCCAGTGCCTCCACACCCCTGCCCGGC 1287  
Qy 1465 CCCCCAGGCTCCCGCGCTCTCTGGGGGAGACCCCTTTGCACTGCGCTCTGCAACAGCC 1524  
Db 1288 CCCCCAGGCTCCCGCGCTCTCTGGGGGAGACCCCTTTGCACTGCGCTCTGCAACAGCC 1347  
Qy 1525 CGGGCCAGTCCACCGGGAGCCCGGGGACACACACCCCGCCAGCCCGGGGTGGGCTC 1584  
Db 1348 CGGGCCAGTCCACCGGGAGCCCGGGGACACACACCCCGCCAGCCCGGGGTGGGCTC 1407  
Qy 1585 GGGGAGCCCGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1644  
Db 1408 GGGGAGCCCGCTGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1467  
Qy 1645 CGCTTTACCGCGGCAAGATGAGGTCTTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1704  
Db 1468 CGCTTTACCGCGGCAAGATGAGGTCTTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1527  
Qy 1705 GAGTCCTCCCGGAGCTGGCAAAAGCTCTCTGGTTCGGGAACTTCATCTCTGGCAAA 1764  
Db 1528 GAGTCCTCCCGGAGCTGGCAAAAGCTCTCTGGTTCGGGAACTTCATCTCTGGCAAA 1587  
Qy 1765 GAAGAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAAGCAGCATC 1824  
Db 1588 GAAGAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAAGCAGCATC 1647  
Qy 1825 GTCCATGCTTTGTGTCATCCCGAGCTGAGTCAAGTGTGTGTCAAGACAGCTTC 1884  
Db 1648 GTCCATGCTTTGTGTCATCCCGAGCTGAGTCAAGTGTGTGTCAAGACAGCTTC 1707  
Qy 1885 AGGGCCAGTACAAGGCGAGTGGGGGCGCCCTCCGCTTCCAAAGCCCGTCCGCTTCAG 1944  
Db 1708 AGGGCCAGTACAAGGCGAGTGGGGGCGCCCTCCGCTTCCAAAGCCCGTCCGCTTCAG 1767  
Qy 1945 GTGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGAGCGGAGGT 2004  
Db 1768 GTGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGAGCGGAGGT 1827  
Qy 2005 GTGGGATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCCGAGCCGTCGCTTCAAGCGA 2064  
Db 1828 GTGGGATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCCGAGCCGTCGCTTCAAGCGA 1887  
Qy 2065 GTGGTGAGACCATCAGGCGACAGCTCTGAGCACTCATGACAGCCCTCGGTGACGGCC 2124  
Db 1888 GTGGTGAGACCATCAGGCGACAGCTCTGAGCACTCATGACAGCCCTCGGTGACGGCC 1947  
Qy 2125 CTGGCAGACGAGAGAAACGGGGCCAGACCCGCGCTGCTGTGCCCCCAGCCGAGCCTG 2184  
Db 1948 CTGGCAGACGAGAGAAACGGGGCCAGACCCGCGCTGCTGTGCCCCCAGCCGAGCCTG 2007  
Qy 2185 CAGCCCCCAGCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGCCCGCC 2244  
Db 2008 CAGCCCCCAGCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGCCCGCC 2067  
Qy 2245 AAGGACAAAGTCTCTGGGCCACCAAGGGAGCCCTCTGCCCTGA 2289  
Db 2068 AAGGACAAAGTCTCTGGGCCACCAAGGGAGCCCTCTGCCCTGA 2112

## RESULT 4

US-10-803-277-5  
; Sequence 5, Application US/10803277  
; Publication No. US20040180416A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0332-USA  
; CURRENT APPLICATION NUMBER: US/10/803,277  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/10/116,326  
; PRIOR FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,036  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 2112  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; US-10-803-277-5

Query Match 88.3%; Score 2020.2; DB 18; Length 2112;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 265 TTTAGGTACTGTCTCGAGACAGCTCTCGGGGGTGTGAGTATTCGACTACTCGTGAAG 324  
Db 88 TATTGTGTACCTGTCTCGAGACAGCTCTCGGGGGTGTGAGTATTCGACTACTCGTGAAG 147  
Qy 325 AAGGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCCAGATTGTCTCGCGCTG 384  
Db 148 AAGGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCCAGATTGTCTCGCGCTG 207  
Qy 385 GACTTCTGCCACAGCTACTCCATCTGCAACAGACAGCTAAAGCCCGAGAACTCTTTTG 444  
Db 208 GACTTCTGCCACAGCTACTCCATCTGCAACAGACAGCTAAAGCCCGAGAACTCTTTTG 267  
Qy 445 GATGAGAAAAACAATCCGATTTGAGATTGCGCATGCGCTCCCTGCGAGGTGGGGAC 504  
Db 268 GATGAGAAAAACAATCCGATTTGAGATTGCGCATGCGCTCCCTGCGAGGTGGGGAC 327  
Qy 505 AGCTCTCGAGAGACAGCTCGGGTCCCGCCATTTATCGGTGTCAGAGGTGATTAAAGGG 564  
Db 328 AGCTCTCGAGAGACAGCTCGGGTCCCGCCATTTATCGGTGTCAGAGGTGATTAAAGGG 387  
Qy 565 GAAAAATATGATGCGCGCGGAGACATGTGGAGCTGTGGAGTCATCTCTCGCCCTG 624  
Db 388 GAAAAATATGATGCGCGCGGAGACATGTGGAGCTGTGGAGTCATCTCTCGCCCTG 447  
Qy 625 CTGTTGGGGCTCTGCGCTTTGATGACACAACCTCCCGCAGCTGTGGAGAAAGTGA 684  
Db 448 CTGTTGGGGCTCTGCGCTTTGATGACACAACCTCCCGCAGCTGTGGAGAAAGTGA 507  
Qy 685 CGGGGCTCTTCCACATGCGCCCTTCTTCTCCAGATTGCCAGAGCTCTCGAGGGGA 744  
Db 508 CGGGGCTCTTCCACATGCGCCCTTCTTCTCCAGATTGCCAGAGCTCTCGAGGGGA 567  
Qy 745 ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 804  
Db 568 ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG 627  
Qy 805 TACCTAGCGGGGAAACACGAGCCAGACCCGTCCTGGAGCCAGCCCTTGGCCCGGGTA 864  
Db 628 TACCTAGCGGGGAAACACGAGCCAGACCCGTCCTGGAGCCAGCCCTTGGCCCGGGTA 687  
Qy 865 GCAATGCGGAGCTGCGCATCAACGAGAGCTGAGACCCCGACGTCCTAGAGAGCATGGCA 924  
Db 688 GCAATGCGGAGCTGCGCATCAACGAGAGCTGAGACCCCGACGTCCTAGAGAGCATGGCA 747  
Qy 925 TCATGCGGCTGCTTCAGGGACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAGAGGAG 984  
Db 748 TCATGCGGCTGCTTCAGGGACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAGAGGAG 807  
Qy 985 AACCAAGAAAAGATGATATATTTCTCTTTTGGATCGGAGGAGCGGTATCCAGCTGT 1044  
Db 808 AACCAAGAAAAGATGATATATTTCTCTTTTGGATCGGAGGAGCGGTATCCAGCTGT 867  
Qy 1045 GAGCAACAGAGCTGCTCCCGGAAATGATTTGACCCCCCGGAAAGCGGTGTGATTC 1104  
Db 868 GAGCAACAGAGCTGCTCCCGGAAATGATTTGACCCCCCGGAAAGCGGTGTGATTC 927  
Qy 1105 CCCATGCTGAGCCGTCAAGGGAGCGGAGCCAGAGCGGAGTCCATGGAAGTCTTGAGC 1164  
Db 928 CCCATGCTGAGCCGTCAAGGGAGCGGAGCCAGAGCGGAGTCCATGGAAGTCTTGAGC 987

1165 ATACCGATGCCGGGGTGTGCTCCCTGTATCCACCGAGCGGCTTGGAGATGCC 1224  
Db  
988 ATACCGATGCCGGGGTGTGCTCCCTGTATCCACCGAGCGGCTTGGAGATGCC 1047  
1225 CAGCAGCCAGAGATCCCGTAGCGTCAGTGGAGCCTCCACGGGCTGTCTCCAGCCCT 1284  
Db  
1048 CAGCAGCCAGAGATCCCGTAGCGTCAGTGGAGCCTCCACGGGCTGTCTCCAGCCCT 1107  
1285 CTAAGCAGCCCAAGGAGTCGGTCTTTTCTTTTCAACCGAGCGGGGCTGGAGATGAG 1344  
Db  
1108 CTAAGCAGCCCAAGGAGTCGGTCTTTTCTTTTCAACCGAGCGGGGCTGGAGATGAG 1167  
1345 GCTCGAGCGGGGCTCCCGAGCTTCCAAACCGAGCGCTCTTCTTGGGGCCCCAGG 1404  
Db  
1168 GCTCGAGCGGGGCTCCCGAGCTTCCAAACCGAGCGCTCTTCTTGGGGCCCCAGG 1227  
1405 GGTGGGGCGCGGGGAGCAGCCCGCCCGCCCGAGTCCCGCTCCACACCCCTGCCCGGC 1464  
Db  
1228 GGTGGGGCGCGGGGAGCAGCCCGCCCGCCCGAGTCCCGCTCCACACCCCTGCCCGGC 1287  
1465 CCCCCAGGCTCCCGCGCTCTCTGGGGGAGCCCGCCCGCCCGAGTCCCGCTCCACACGCC 1524  
Db  
1288 CCCCCAGGCTCCCGCGCTCTCTGGGGGAGCCCGCCCGCCCGAGTCCCGCTCCACACGCC 1347  
1525 CGGGCAGTCCACCGGGAGCCCGGGGAGCAACACCCCGCCCGAGCCCGCGGTGGCGTC 1584  
Db  
1348 CGGGCAGTCCACCGGGAGCCCGGGGAGCAACACCCCGCCCGAGCCCGCGGTGGCGTC 1407  
1468 CGCTTTACCGGGCGAAGATCAGGTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1527  
1585 GGGGAGCGGCTCGGAGAGTGTCTCAACTTCCATCCGCAACAGCTTCTGGGGTCCCT 1644  
Db  
1408 GGGGAGCGGCTCGGAGAGTGTCTCAACTTCCATCCGCAACAGCTTCTGGGGTCCCT 1467  
1645 CGCTTTACCGGGCGAAGATCAGGTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1704  
Db  
1468 CGCTTTACCGGGCGAAGATCAGGTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1527  
1705 GAGTCTCCCGGAGCTGGCAAAAGCTCTCTGGTTCGGGAACTTCATCTCTTGGAACA 1764  
Db  
1528 GAGTCTCCCGGAGCTGGCAAAAGCTCTCTGGTTCGGGAACTTCATCTCTTGGAACA 1587  
1765 GAAGAACAAATATTCCTCGTAAAGAGCAAACTCTCAGCAGCATCAAGCAGATC 1824  
Db  
1588 GAAGAACAAATATTCCTCGTAAAGAGCAAACTCTCAGCAGCATCAAGCAGATC 1647  
1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTACAGTGTGTGTACAGCAGCTTC 1884  
Db  
1648 GTCCATGCTTTCTGTGATCCCGAGCTGAGTACAGTGTGTGTACAGCAGCTTC 1707  
1885 AGGGCCGAGTACAAGGCCAGTGGCGGCCCTCCCGTCTTCCAAAGCCCGTCCGTTCCAG 1944  
Db  
1708 AGGGCCGAGTACAAGGCCAGTGGCGGCCCTCCCGTCTTCCAAAGCCCGTCCGTTCCAG 1767  
1945 GTGGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCAGCGGAGCGGAGGT 2004  
Db  
1768 GTGGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCAGCGGAGCGGAGGT 1827  
2005 GTGGCATCTACTCCGTCACTTCACTCTCATCTCGGCTCCAGCCGCTCGGTTCAAGCGA 2064  
Db  
1828 GTGGCATCTACTCCGTCACTTCACTCTCATCTCGGCTCCAGCCGCTCGGTTCAAGCGA 1887  
2065 GTGGTGGAGACCATCCAGSCACAGTCTCTGAGCACTCATGACACCGCTTCGTTGAGGCC 2124  
Db  
1888 GTGGTGGAGACCATCCAGSCACAGTCTCTGAGCACTCATGACACCGCTTCGTTGAGGCC 1947  
2125 CTGGCAGACAGAGAAACCGGGGCGAGCCCGGCTGCTGGTGGCCACCCCGAGCGCTG 2184  
Db  
1948 CTGGCAGACAGAGAAACCGGGGCGAGCCCGGCTGCTGGTGGCCACCCCGAGCGCTG 2007  
2185 CAGCCCCACCGGGCGGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGCCCCCC 2244  
Db  
2008 CAGCCCCACCGGGCGGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGCCCCCC 2067

2245 AAGGACAAAGAGCTCTCGGCCACCAACCGGAGCCCTCTGCGCTGA 2289  
Db  
2068 AAGGACAAAGAGCTCTCGGCCACCAACCGGAGCCCTCTGCGCTGA 2112  
RESULT 5  
US-10-116-326-1  
; Sequence 1, Application US/10116326  
; Publication No. US20030166889A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fridlie, Carl Johan  
; TITLE OF INVENTION: No. US20030166889A1 Human Kinases and Polynucleotides Encoding t  
; FILE REFERENCE: LEX-0332-USA  
; CURRENT APPLICATION NUMBER: US/10/116,326  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/282,036  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2337  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; US-10-116-326-1  
Query Match 88.3%; Score 2020.2; DB 16; Length 2337;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
265 TTTAGTACTGTTCTGGAGCAGCTCTCGGGGGTGGAGTATTCGACTACCTGGTAAAG 324  
Db  
313 TATTTGTACTGTTCTGGAGCAGCTCTCGGGGGTGGAGTATTCGACTACCTGGTAAAG 372  
QY  
325 AAGGGAGACTGACGCGCCAAAGAGGCCCGAAAGTCTTCCGCGAGATTGTGTGCGCTG 384  
Db  
373 AAGGGAGACTGACGCGCCAAAGAGGCCCGAAAGTCTTCCGCGAGATTGTGTGCGCTG 432  
QY  
385 GACTTCTGCGACAGTACTCCATCTGCCACAGAGACTTAAGCCCGAGACCTGCTTTTG 444  
Db  
433 GACTTCTGCGACAGTACTCCATCTGCCACAGAGACTTAAGCCCGAGACCTGCTTTTG 492  
QY  
445 GATGAGAAACAACTCCGATTCGAGACTTCGGCATGCGCTCCGAGGTGGGGGAC 504  
Db  
493 GATGAGAAACAACTCCGATTCGAGACTTCGGCATGCGCTCCGAGGTGGGGGAC 552  
QY  
505 AGCTCTCGAGACCAAGCTCGGGTCCCGCCATTATGCGTGTCCAGAGTGAATAGGGG 564  
Db  
553 AGCTCTCGAGACCAAGCTCGGGTCCCGCCATTATGCGTGTCCAGAGTGAATAGGGG 612  
QY  
565 GAAAAATATGATGGCGCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 624  
Db  
613 GAAAAATATGATGGCGCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 672  
QY  
625 CTGCTGGGGCTGCGCTTTTGTATGACACAACTCCGCGAGCTGTGGAAGAGTGA 684  
Db  
673 CTGCTGGGGCTGCGCTTTTGTATGACACAACTCCGCGAGCTGTGGAAGAGTGA 732  
QY  
685 CGGGGCTCTTCCACATGCCCTTCACTTCCTCCAGATTGCCAGAGCTCTGAGGGGA 744  
Db  
733 CGGGGCTCTTCCACATGCCCTTCACTTCCTCCAGATTGCCAGAGCTCTGAGGGGA 792  
QY  
745 ATGATCGAGTGGAGCCCGGAGAGGCTCAGTCTGGAGCAAAATTCAAGAACTCTTGG 804  
Db  
793 ATGATCGAGTGGAGCCCGGAGAGGCTCAGTCTGGAGCAAAATTCAAGAACTCTTGG 852  
QY  
805 TACCTAGCGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGGGTA 864  
Db  
853 TACCTAGCGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGCGCGGGTA 912  
QY  
865 GCCATGCGGAGCTGCGCATCCACGAGAGCTGAGCCCGAGCTCTTAGAGAGCATGCA 924

Db 913 GCCATGCGGAGCGCTGCCATCCAAACGAGAGCTGGACCCCGAGCGTCTTAGAGAGCATGCA 972  
Qy 925 TCACTGGGCTGCTTCAAGGACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAAGAGAG 984  
Db 973 TCACTGGGCTGCTTCAAGGACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAAGAGAG 1032  
Qy 985 AACCAAGAAAGATGATATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044  
Db 1033 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1092  
Qy 1045 GAGGACCAAGGACCTGCCCTCCCGGAATGATTTGACCCCCCCCCCGGAAGCGGTGATTTCT 1104  
Db 1093 GAGGACCAAGGACCTGCCCTCCCGGAATGATTTGACCCCCCCCCCGGAAGCGGTGATTTCT 1152  
Qy 1105 CCAATGTGAGCGCTCAGCGGAACGGGGAACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1164  
Db 1153 CCAATGTGAGCGCTCAGCGGAACGGGGAACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1212  
Qy 1165 ATACCCGATGCGGGGGTGGTCTCCCTCTGACCCAGCGGCGCTTGAGATGGCC 1224  
Db 1213 ATACCCGATGCGGGGGTGGTCTCCCTCTGACCCAGCGGCGCTTGAGATGGCC 1272  
Qy 1225 CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCTCCAGCGTCTGTCTCCAGCGCT 1284  
Db 1273 CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCTCCAGCGTCTGTCTCCAGCGCT 1332  
Qy 1285 CTAAGCAGCCCAAGAGTCCGCTCTTTTCTTTTCAACGAGCGCGGGGCTGAGATGAG 1344  
Db 1333 CTAAGCAGCCCAAGAGTCCGCTCTTTTCTTTTCAACGAGCGCGGGGCTGAGATGAG 1392  
Qy 1345 GCTCAGCGGGGGCTCCCGACTTCCAAACAGAGCGTCTCTCGGGGGCCGAGG 1404  
Db 1393 GCTCAGCGGGGGCTCCCGACTTCCAAACAGAGCGTCTCTCGGGGGCCGAGG 1452  
Qy 1405 GGTGGGGCGCGGGGAGCAGCCCCCGCCCCCAGTGCCTCCACACCCCTGCCCGGC 1464  
Db 1453 GGTGGGGCGCGGGGAGCAGCCCCCGCCCCCAGTGCCTCCACACCCCTGCCCGGC 1512  
Qy 1465 CCCCAGGCTCCCGCGCTCTCTGGGGGAGCCCCCTTGCATCGCTCTGCAACAGCCCC 1524  
Db 1513 CCCCAGGCTCCCGCGCTCTCTGGGGGAGCCCCCTTGCATCGCTCTGCAACAGCCCC 1572  
Qy 1525 CGGGCCAGTCCACCGGGACCCCGGGGACACACACCCCGCGCGGGGGTGGGTC 1584  
Db 1573 CGGGCCAGTCCACCGGGACCCCGGGGACACACACCCCGCGCGGGGGTGGGTC 1632  
Qy 1585 GGGGGAGCGCTGGAGAGTGTCTCAATCCATCCGCAACAGCTTCTGGGGTCCCT 1644  
Db 1633 GGGGGAGCGCTGGAGAGTGTCTCAATCCATCCGCAACAGCTTCTGGGGTCCCT 1692  
Qy 1645 CGCTTTACCGGGCAAGATGAGTCCCTACCGCTGAGGAGTGTCCAGTTGACGCCA 1704  
Db 1693 CGCTTTACCGGGCAAGATGAGTCCCTACCGCTGAGGAGTGTCCAGTTGACGCCA 1752  
Qy 1705 GAGTCTCTCCCGGAGTGGCAAAAGCTCTGGTTCCGGAACTTCATCTCTTGGACAAA 1764  
Db 1753 GAGTCTCTCCCGGAGTGGCAAAAGCTCTGGTTCCGGAACTTCATCTCTTGGACAAA 1812  
Qy 1765 GAAGAACAAATATTTCTGCTGCTAAAGAGCAAAACCTCTCAGCAGCATCAAGCAGCATC 1824  
Db 1813 GAAGAACAAATATTTCTGCTGCTAAAGAGCAAAACCTCTCAGCAGCATCAAGCAGCATC 1872  
Qy 1825 GTCCATGCTTTCTGTGATCCCCAGGCTGAGTCAAGTGTGTGTCACAGACAGCTTC 1884  
Db 1873 GTCCATGCTTTCTGTGATCCCCAGGCTGAGTCAAGTGTGTGTCACAGACAGCTTC 1932  
Qy 1885 AGGCGCAGTACAGGCGAGTGGGCGCCCTCCGTCTTCCAAAAGCCCGTCCGTTCCAG 1944  
Db 1933 AGGCGCAGTACAGGCGAGTGGGCGCCCTCCGTCTTCCAAAAGCCCGTCCGTTCCAG 1992  
Qy 1945 GTGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGGACGGCGAGGT 2004  
Db 1993 GTGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGGACGGCGAGGT 2052

## RESULT 6

US-10-543-12

; Sequence 12, Application US/10423543

; Publication No. US20040058355A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: Libermann, Rosana K.

; APPLICANT: Hunter, John J.

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Rudolph-Owen, Laura A.

; APPLICANT: Curtiss, Rory A.J.

; APPLICANT: Olandt, Peter J.

; APPLICANT: Teai, Fong-Ying

; APPLICANT: Galvin, Katherine M.

; APPLICANT: Chun, Miyoung

; APPLICANT: Williams, Mark J.

; APPLICANT: Silos-Santiago, Immaculada

; APPLICANT: Bandaru, Rajasekhara

; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,

; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,

; TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES

; TITLE OF INVENTION: AND USES THEREFOR

; FILE REFERENCE: MP103-0230NMIM

; CURRENT APPLICATION NUMBER: US/10/423,543

; CURRENT FILING DATE: 2003-04-25

; PRIOR APPLICATION NUMBER: US 10/278,036

; PRIOR FILING DATE: 2002-10-22

; PRIOR APPLICATION NUMBER: US 09/711,216

; PRIOR FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: US 60/205,447

; PRIOR FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: US 10/012,055

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/248,325

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: US 10/003,690

; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/248,893

; PRIOR FILING DATE: 2000-11-15

; PRIOR APPLICATION NUMBER: US 09/797,039

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: US 60/186,061

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: US 10/217,168

; PRIOR FILING DATE: 2002-08-12

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 119

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 2337

; TYPE: DNA



; ORGANISM: Homo Sapiens									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (1)...(2337)									
US-10-423-543-12									
Query Match									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Qy	265	TTTAGGTACCTGGTTCTGGAGACAGCTCTCGGGGGGTGAGCTATTGCACTACCTGGTAAAG	324						
Db	313	TAITTTGTACTGTCTTGGAGACAGCTCTCGGGGGGTGAGCTATTGCACTACCTGGTAAAG	372						
Qy	325	AAGGGGAGATGACGCCCAAGAGAGGCCGAAAGTTCTTCGGCCAGATTGTCTGCGCTG	384						
Db	373	AAGGGGAGATGACGCCCAAGAGAGGCCGAAAGTTCTTCGGCCAGATTGTCTGCGCTG	432						
Qy	385	GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAAGACCTGCTTTTG	444						
Db	433	GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAAGACCTGCTTTTG	492						
Qy	445	GATGAGAAAAACAATCTCGCATTCGACACTTCGGCATGCGCTCCCTGACAGGTGGGGAC	504						
Db	493	GATGAGAAAAACAATCTCGCATTCGACACTTCGGCATGCGCTCCCTGACAGGTGGGGAC	552						
Qy	505	AGCTTCTGGAGACAGCTCGGGTCCCCCAATTATGCGTGTCCAGAGGTGATTAGGGG	564						
Db	553	AGCTTCTGGAGACAGCTCGGGTCCCCCAATTATGCGTGTCCAGAGGTGATTAGGGG	612						
Qy	565	GAAATAATGATGGCCGGGGGACAGATGTGGAGCTGTGGAGTCACTCTTCGCCCTG	624						
Db	613	GAAATAATGATGGCCGGGGGACAGATGTGGAGCTGTGGAGTCACTCTTCGCCCTG	672						
Qy	625	CTCGGGGGTCTGCTCTTTGATGACGAACTCTCGGAGCTGTGGAGTCACTCTTCGCCCTG	684						
Db	673	CTCGGGGGTCTGCTCTTTGATGACGAACTCTCGGAGCTGTGGAGTCACTCTTCGCCCTG	732						
Qy	685	CGGGGGTCTTCCATGCTCCCATCTTCATCTCTCAGATTGCCAGAGCTCTCGAGGGGA	744						
Db	733	CGGGGGTCTTCCATGCTCCCATCTTCATCTCTCAGATTGCCAGAGCTCTCGAGGGGA	792						
Qy	745	ATGATCGAAGTGGAGCCCGGAAAAAGGCTCACTGTGGAGCAAAATTCAGAAACATCTTGG	804						
Db	793	ATGATCGAAGTGGAGCCCGGAAAAAGGCTCACTGTGGAGCAAAATTCAGAAACATCTTGG	852						
Qy	805	ATCCTAGGGGGAAACACAGAGCCAGACCCGTGCTGGAGCCAGCCCTGGCCGCGGGTA	864						
Db	853	TACCTAGGGGGAAACACAGAGCCAGACCCGTGCTGGAGCCAGCCCTGGCCGCGGGTA	912						
Qy	865	GCCATGCGGAGCTGCTCATCCAAACGAGAGCTGGACCCCGGAGCTCTTAGAGAGCATGGCA	924						
Db	913	GCCATGCGGAGCTGCTCATCCAAACGAGAGCTGGACCCCGGAGCTCTTAGAGAGCATGGCA	972						
Qy	925	TCACTGGGTGCTTACGGAACCCGAGAGGCTGCATCGGAGCTCGGAGCTGGAGAGGAG	984						
Db	973	TCACTGGGTGCTTACGGAACCCGAGAGGCTGCATCGGAGCTCGGAGCTGGAGAGGAG	1032						
Qy	985	AACCAAGAAAGATGATATATCTGCTTTTGGATCGGAAGAGCGGTATCCCAAGCTGT	1044						
Db	1033	AACCAAGAAAGATGATATATCTGCTTTTGGATCGGAAGAGCGGTATCCCAAGCTGT	1092						
Qy	1045	GAGGACACAGGACTGCTGCTCCCGGAAATGATGTGACCCCGGAGAGCGGTGTGATTTCT	1104						
Db	1093	GAGGACACAGGACTGCTGCTCCCGGAAATGATGTGACCCCGGAGAGCGGTGTGATTTCT	1152						
Qy	1105	CCATGCTGAGCGCTACCGGAAGCGGACACAGAGGAGATTCATGGAAGTCTCTGAGC	1164						
Db	1153	CCATGCTGAGCGCTACCGGAAGCGGACACAGAGGAGATTCATGGAAGTCTCTGAGC	1212						
Qy	1165	ATCACCGATCCCGGGGTGTGGCTCCCTGTGTACCCACCGGACCGGCTTGGAGATGGCC	1224						
Db	1213	ATCACCGATCCCGGGGTGTGGCTCCCTGTGTACCCACCGGACCGGCTTGGAGATGGCC	1272						

Qy	1225	CAGCACAGCCAGAGATCCCGTAGCGTCACTGGAGCCCTCCACGGGTCTGTCTCCAGCCCT	1284						
Db	1273	CAGCACAGCCAGAGATCCCGTAGCGTCACTGGAGCCCTCCACGGGTCTGTCTCCAGCCCT	1332						
Qy	1285	CTAAGAGCCCAAGAGTCCGGTCTTTTCTTTTTCACGGAGCCGGGGCTGGAGATGAG	1344						
Db	1333	CTAAGAGCCCAAGAGTCCGGTCTTTTCTTTTTCACGGAGCCGGGGCTGGAGATGAG	1392						
Qy	1345	GCTGAGCGGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCTCGGGGGCCCGAGG	1404						
Db	1393	GCTGAGCGGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCTCGGGGGCCCGAGG	1452						
Qy	1405	GCTGAGCGGGGGAGAGCGCCCGCCCGCCCGAGTCCCGCTCCACACCCCTGCGCGGC	1464						
Db	1453	GCTGAGCGGGGGAGAGCGCCCGCCCGCCCGAGTCCCGCTCCACACCCCTGCGCGGC	1512						
Qy	1465	CCCCAGAGCTCCCGCGCTCTCTGGGGGAGCCCTTGGCACTGGCTTCTCCACACGCC	1524						
Db	1513	CCCCAGAGCTCCCGCGCTCTCTGGGGGAGCCCTTGGCACTGGCTTCTCCACACGCC	1572						
Qy	1525	CGGGCAGTCCCAACCGGGACCCCGGGGACAAACACACCCCGAGCCCGCGGTGGCTC	1584						
Db	1573	CGGGCAGTCCCAACCGGGACCCCGGGGACAAACACACCCCGAGCCCGCGGTGGCTC	1632						
Qy	1585	GGGGAGCGCGCTGGAGAGTCTCACTCCATCCGCTGAGGAGATGTCCAGCTTACGCA	1644						
Db	1633	GGGGAGCGCGCTGGAGAGTCTCACTCCATCCGCTGAGGAGATGTCCAGCTTACGCA	1692						
Qy	1645	CGCTTTCACCGCGCAAGATGAGGTCCCTACCGCTGAGGAGATGTCCAGCTTACGCA	1704						
Db	1693	CGCTTTCACCGCGCAAGATGAGGTCCCTACCGCTGAGGAGATGTCCAGCTTACGCA	1752						
Qy	1705	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCGTTCGGGAACTTCACTCTCTTGGACAA	1764						
Db	1753	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCGTTCGGGAACTTCACTCTCTTGGACAA	1812						
Qy	1765	GAAGAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGATCAAAAGCAGCATC	1824						
Db	1813	GAAGAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGATCAAAAGCAGCATC	1872						
Qy	1825	GTCCATGCTCTTCTGTGATCCCGACCTGAGTCAAGTGTGTGTCAAGACAGCTTC	1884						
Db	1873	GTCCATGCTCTTCTGTGATCCCGACCTGAGTCAAGTGTGTGTCAAGACAGCTTC	1932						
Qy	1885	AGGGCCGAGTCAAGGCGAGTGGCGCCCTCGCTTCCAAAGCCCTCGCTTCCAG	1944						
Db	1933	AGGGCCGAGTCAAGGCGAGTGGCGCCCTCGCTTCCAAAGCCCTCGCTTCCAG	1992						
Qy	1945	GTGACATCAGCTCCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGACCGGAGGT	2004						
Db	1993	GTGACATCAGCTCCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGACCGGAGGT	2052						
Qy	2005	GCTGGCATCTACTCCGTCACTTCACTCTCATCTCGGGTCCAGCCGTGGTTCAGGCGA	2064						
Db	2053	GCTGGCATCTACTCCGTCACTTCACTCTCATCTCGGGTCCAGCCGTGGTTCAGGCGA	2112						
Qy	2065	GTGCTGAGACCATCCAGGACAGCTCTCAGCACTCATGACAGCCCTCCGTGCAAGGCC	2124						
Db	2113	GTGCTGAGACCATCCAGGACAGCTCTCAGCACTCATGACAGCCCTCCGTGCAAGGCC	2172						
Qy	2125	CTGGCAGACGAGAGAACGGGGCCCGACCCCGGCTGTGTGCTGCTCCACCCGAGCGCTG	2184						
Db	2173	CTGGCAGACGAGAGAACGGGGCCCGACCCCGGCTGTGTGCTGCTCCACCCGAGCGCTG	2232						
Qy	2185	CAGCCCCCAACCGGCGCCAGACCCAGAGTGGAGCTCTCCCGCGGAGGCGCCCGCC	2244						
Db	2233	CAGCCCCCAACCGGCGCCAGACCCAGAGTGGAGCTCTCCCGCGGAGGCGCCCGCC	2292						
Qy	2245	AAGGACAAAGAGCTCTTGGGCCACCAACGGGACCCCTCTGCGCTGA	2289						
Db	2293	AAGGACAAAGAGCTCTTGGGCCACCAACGGGACCCCTCTGCGCTGA	2337						

RESULT 7  
US-10-803-277-1  
; Sequence 1, Application US/10803277  
; Publication No. US20040180416A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friidie, Carl Johan  
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0332-USA  
; CURRENT APPLICATION NUMBER: US/10/803,277  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/10/116,326  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/282,036  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2337  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-803-277-1

Query Match 88.3%; Score 2020.2; DB 18; Length 2337;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	265	TTTAGGTACCTGGTCTGGAGCAGTCTCGGGGGGTGAGCTATTTCGACTACCTCGTAAAG	324
Db	313	TATTTGTACCTGGTCTGGAGCAGTCTCGGGGGGTGAGCTATTTCGACTACCTCGTAAAG	372
Qy	325	AAGGGAGACTGACGCCCAAGAGGCGCGAAGTTCTTCGCCACAGATTGTCTCGCGCTG	384
Db	373	AAGGGAGACTGACGCCCAAGAGGCGCGAAGTTCTTCGCCACAGATTGTCTCGCGCTG	432
Qy	385	GACTTCTGCCACAGCTACTCCTATCTGCCACACAGACCTAAAGCCCGAGAACCTCTTTTG	444
Db	433	GACTTCTGCCACAGCTACTCCTATCTGCCACACAGACCTAAAGCCCGAGAACCTCTTTTG	492
Qy	445	GATCAGAAAACACATCCGATTCGACATTCGGCATGGCTGGCTCCGAGTGGGGGAC	504
Db	493	GATCAGAAAACACATCCGATTCGACATTCGGCATGGCTGGCTCCGAGTGGGGGAC	552
Qy	505	AGCTCTCTGGAGACAGCTGCGGTCCCGCATTTATGCTCCAGAGGTGATTAAAGGG	564
Db	553	AGCTCTCTGGAGACAGCTGCGGTCCCGCATTTATGCTCCAGAGGTGATTAAAGGG	612
Qy	565	GAATAATATGATGCGCGCGGCAGACATGTGGAGCTGTGGAGTCATCTCTTCGCCCTG	624
Db	613	GAATAATATGATGCGCGCGGCAGACATGTGGAGCTGTGGAGTCATCTCTTCGCCCTG	672
Qy	625	CTCTGGGGGTCTGCCCTTTGATGACGACAACTCCGCGAGCTGCTGGAGAGGTGAAA	684
Db	673	CTCTGGGGGTCTGCCCTTTGATGACGACAACTCCGCGAGCTGCTGGAGAGGTGAAA	732
Qy	685	CGGGCGCTTCTCCACATGCCCGCATTTANTCTCCAGATTCCAGAGCTCTCAGAGGGA	744
Db	733	CGGGCGCTTCTCCACATGCCCGCATTTANTCTCCAGATTCCAGAGCTCTCAGAGGGA	792
Qy	745	ATGATCGAAGTGGAGCGCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTTG	804
Db	793	ATGATCGAAGTGGAGCGCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTTG	852
Qy	805	TACTAGCGGGAACACAGCCAGACCCGCTGCTGGAGCCAGCCCTGGCGCGGGTA	864
Db	853	TACTAGCGGGAACACAGCCAGACCCGCTGCTGGAGCCAGCCCTGGCGCGGGTA	912
Qy	865	GCCATGCGGAGCTGCCATCCAAACGAGAGCTGGACCCCGAGCTCCTAGAGAGCATGCA	924
Db	913	GCCATGCGGAGCTGCCATCCAAACGAGAGCTGGACCCCGAGCTCCTAGAGAGCATGCA	972

Qy	925	TCATGGGCTGCTTCAGGGACCGGAGAGGCTGCATCGGAGCTGCCAGTGGAGGAG	984
Db	973	TCATGGGCTGCTTCAGGGACCGGAGAGGCTGCATCGGAGCTGCCAGTGGAGGAG	1032
Qy	985	AACCAAGAAAAGATGATATATTATCTCTTTTGGATCGGAAGAGCGGTATCCAGCTGT	1044
Db	1033	AACCAAGAAAAGATGATATATTATCTCTTTTGGATCGGAAGAGCGGTATCCAGCTGT	1092
Qy	1045	GAGGACGAGACCTGCTCCCGGGAATGATTTGACCCCCCGGAAAGCGGTGATTC	1104
Db	1093	GAGGACGAGACCTGCTCCCGGGAATGATTTGACCCCCCGGAAAGCGGTGATTC	1152
Qy	1105	CCCATGCTGAGCGCTCAGGGGAGCGGAGCGGAGTCCATGGAAGTCTCTGAGC	1164
Db	1153	CCCATGCTGAGCGCTCAGGGGAGCGGAGCGGAGTCCATGGAAGTCTCTGAGC	1212
Qy	1165	ATACCCATGCGGGGGTGGTCCCTGTATCCACCGAGCGGCTTGGAGATGGCC	1224
Db	1213	ATACCCATGCGGGGGTGGTCCCTGTATCCACCGAGCGGCTTGGAGATGGCC	1272
Qy	1225	CAGCACGACGAGATCCCGTAGCGTCAGTGGAGCTTCCAGGGTCTGTCTCAGGCC	1284
Db	1273	CAGCACGACGAGATCCCGTAGCGTCAGTGGAGCTTCCAGGGTCTGTCTCAGGCC	1332
Qy	1285	CTAAGCAGCCNAGAGTCCGGTCTTTCTTTTTCACCGGAGCGGGGCTGGAGATGAG	1344
Db	1333	CTAAGCAGCCNAGAGTCCGGTCTTTTCTTTTTCACCGGAGCGGGGCTGGAGATGAG	1392
Qy	1345	GCTCGAGCGGGGCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGCCCCAGG	1404
Db	1393	GCTCGAGCGGGGCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGCCCCAGG	1452
Qy	1405	GGTGGGGCGCGGGGAGCAGCCCCCGCCAGTCCCGCTCCACACCCCTGCCCGC	1464
Db	1453	GGTGGGGCGCGGGGAGCAGCCCCCGCCAGTCCCGCTCCACACCCCTGCCCGC	1512
Qy	1465	CCCCCAGGCTCCCGCGCTCTCTGGCGGAGCCCCCTTGACCTGCTGTGACACGCC	1524
Db	1513	CCCCCAGGCTCCCGCGCTCTCTGGCGGAGCCCCCTTGACCTGCTGTGACACGCC	1572
Qy	1525	CGGSCAGTCCACCGGGACCCCGGGGACAAACACACCCCGAGCGGGGCTGGGCTC	1584
Db	1573	CGGSCAGTCCACCGGGACCCCGGGGACAAACACACCCCGAGCGGGGCTGGGCTC	1632
Qy	1585	GGGGGAGCGCTCGGAGAGTCTCACTCAATCCGCAACAGCTTCTGGGCTCCCT	1644
Db	1633	GGGGGAGCGCTCGGAGAGTCTCACTCAATCCGCAACAGCTTCTGGGCTCCCT	1692
Qy	1645	CGCTTTCACGGCGCAAGATGCGGTCCCTACCGCTGAGGAGATGTCCAGCTTGA	1704
Db	1693	CGCTTTCACGGCGCAAGATGCGGTCCCTACCGCTGAGGAGATGTCCAGCTTGA	1752
Qy	1705	GAGTCTCCCGGAGCTGGCAAAACGCTCTGTTTCGGGAACCTTCATCTCTCGACA	1764
Db	1753	GAGTCTCCCGGAGCTGGCAAAACGCTCTGTTTCGGGAACCTTCATCTCTCGACA	1812
Qy	1765	GAAGAAACAAATATTCCTCGTCTGCTAAAGGACAAACCTCTCAGCAGCATCA	1824
Db	1813	GAAGAAACAAATATTCCTCGTCTGCTAAAGGACAAACCTCTCAGCAGCATCA	1872
Qy	1825	GTCCATGCTTCTGTGATCCCGCAGCTGAGTCAAGTGTGTGTGACACAGCTTC	1884
Db	1873	GTCCATGCTTCTGTGATCCCGCAGCTGAGTCAAGTGTGTGTGACACAGCTTC	1932
Qy	1885	AGGGCCAGTACAGGCGGAGTGGCGGCTCCGCTTCCAAAGACCGCTCCGCTCCAG	1944
Db	1933	AGGGCCAGTACAGGCGGAGTGGCGGCTCCGCTTCCAAAGACCGCTCCGCTCCAG	1992
Qy	1945	GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGGACGGGAGCGGAGGT	2004
Db	1993	GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGGACGGGAGCGGAGGT	2052
Qy	2005	GGTGGCATCTACTCCGTCACCTTCACTCATCTCTCGGGTCCAGCGCTTCAGGCGA	2064



Db 2053 GGTGGCATCTACTCGTCACTTCACTCATCTCGGGTCCAGCGCTCGGTTCAGGGA 2112  
Qy 2065 GTGGTGAGACCATCCAGGCACAGCTCCCTGAGCACTCATGACAGCCCTCCGTGCGAGGCC 2124  
Db 2113 GTGGTGAGACCATCCAGGCACAGCTCCCTGAGCACTCATGACAGCCCTCCGTGCGAGGCC 2172  
Qy 2125 CTGSCAGACGAGAAGAACGGGGCCAGACCCGGCTCTGCTGGTGCCCAACCCGAGGCTTG 2184  
Db 2173 CTGSCAGACGAGAAGAACGGGGCCAGACCCGGCTCTGCTGGTGCCCAACCCGAGGCTTG 2232  
Qy 2185 CAGCCCCACCCGGCCCGCCAGACCCGAGCTGAGCACTCTCCCGCGAGGSCCCCCC 2244  
Db 2233 CAGCCCCACCCGGCCCGCCAGACCCGAGCTGAGCACTCTCCCGCGAGGSCCCCCC 2292  
Qy 2245 AAGGACAGAGCTCTCTGGCCACCAAGGAGCCCTCTGCGCCCTGA 2289  
Db 2293 AAGGACAGAGCTCTCTGGCCACCAAGGAGCCCTCTGCGCCCTGA 2337

RESULT 8  
US-10-311-034-43  
; Sequence 43, Application US/10311034  
; Publication No. US20040023242A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YUE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BOROWSKY, Mark L.  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: LU, Yan  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: LU, Dying Aina M.  
; APPLICANT: GREENWALD, Sara R.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: KEARNEY, Liam  
; APPLICANT: BURFORD, Neil  
; APPLICANT: NGUYEN, Danniell B.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: HE, Ann  
; APPLICANT: THORNTON, Michael  
; APPLICANT: HAFALIA, April  
; APPLICANT: ARVIZU, Chandra S.  
; APPLICANT: GURURAJAN, Rajagopal  
; APPLICANT: LO, Terence P.  
; APPLICANT: KHAH, Farrah A.  
; APPLICANT: RECIPON, Shirley A.  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: POLICKY, Jennifer L.  
; APPLICANT: DING, Li  
; APPLICANT: GREYER, Megan  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: BATRA, Sajeev  
; APPLICANT: ISON, Craig H.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0125 PCT  
; CURRENT APPLICATION NUMBER: US/10/311,034  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
60/228,056  
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-15  
25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PERL Program  
; SEQ ID NO 43  
; LENGTH: 2897

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20040023242A1 7477486CB1  
US-10-311-034-43

Query Match 88.3%; Score 2020.2; DB 17; Length 2897;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 265 TTTAGGTACCTGGTTCGAGACAGCTCTCGGGGGTGGCTATTTCGACTACCTGGTAAAG 324  
Db 361 TATTGTACTCTGGTTCGAGACAGCTCTCGGGGGTGGCTATTTCGACTACCTGGTAAAG 420  
Qy 325 AAGGGAGACTGAGCCCAAGAGGCGCGAAAGTCTTCGCGCCAGATTGTCTGCGCTG 384  
Db 421 AAGGGAGACTGAGCCCAAGAGGCGCGAAAGTCTTCGCGCCAGATTGTCTGCGCTG 480  
Qy 385 GACTTCTGCCACAGCTACTCATCTGCGACAGACCTAAAGCCCGAGAACCTCTTTTG 444  
Db 481 GACTTCTGCCACAGCTACTCATCTGCGACAGACCTAAAGCCCGAGAACCTCTTTTG 540  
Qy 445 GATGAGAAAAACAATCCGCAATTCAGACTTCGCGCATGGCGTCCCTGAGGTGGGAC 504  
Db 541 GATGAGAAAAACAATCCGCAATTCAGACTTCGCGCATGGCGTCCCTGAGGTGGGAC 600  
Qy 505 AGCTCTCTGGAGACAGCTGCGGGTCCCGCCATATGCTGTCAGAGTGAATTAAGGG 564  
Db 601 AGCTCTCTGGAGACAGCTGCGGGTCCCGCCATATGCTGTCAGAGTGAATTAAGGG 660  
Qy 565 GAAAAATATGATGGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTCTCCCGCTG 624  
Db 661 GAAAAATATGATGGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTCTCCCGCTG 720  
Qy 625 CTCGTGGGGGCTCTGCGCTTTTGATGACGACAACTCCCGCAGCTCTGAGAGAGTGA 684  
Db 721 CTCGTGGGGGCTCTGCGCTTTTGATGACGACAACTCCCGCAGCTCTGAGAGAGTGA 780  
Qy 685 CGGGGGCTCTTCACATGCCCCCACTTCCTCCAGATTGCGAGAGCTCTCTGAGGGGA 744  
Db 781 CGGGGGCTCTTCACATGCCCCCACTTCCTCCAGATTGCGAGAGCTCTCTGAGGGGA 840  
Qy 745 ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGAGCAAAATTCAGAAAAATCCTTGG 804  
Db 841 ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGAGCAAAATTCAGAAAAATCCTTGG 900  
Qy 805 TACCTAGCGGGGAAACACAGAGCCAGACCCGCTGCTGGAGCCAGCCCTCGCGCCGGGTA 864  
Db 901 TACCTAGCGGGGAAACACAGAGCCAGACCCGCTGCTGGAGCCAGCCCTCGCGCCGGGTA 960  
Qy 865 GCATGCGAGCCCTGCCATCCAAAGGAGAGCTGAGCCCGAGCTCTAGAGAGCATGGCA 924  
Db 961 GCATGCGAGCCCTGCCATCCAAAGGAGAGCTGAGCCCGAGCTCTAGAGAGCATGGCA 1020  
Qy 925 TCCTGCGGCTCTTCAGGAGCCCGAGAGGCTGCATCGGAGCTGCGCAGTGAAGAGGAG 984  
Db 1021 TCCTGCGGCTCTTCAGGAGCCCGAGAGGCTGCATCGGAGCTGCGCAGTGAAGAGGAG 1080  
Qy 985 AACCAAGAAAAAGATGATATATTCGCTTTTGGATCGGAGAGCGGATTCACAGCTGT 1044  
Db 1081 AACCAAGAAAAAGATGATATATTCGCTTTTGGATCGGAGAGCGGATTCACAGCTGT 1140  
Qy 1045 GAGGACGAGGACCTGCGCTCCCGGAATGATGTTGACCCCCCCCCCGGAAGCGTGTGATCT 1104  
Db 1141 GAGGACGAGGACCTGCGCTCCCGGAATGATGTTGACCCCCCCCCCGGAAGCGTGTGATCT 1200  
Qy 1105 CCCATGCTGAGCCGTTCACGGGAACCGGAGCCAGAGCGGAAGTCCATGGAAGCTCTGAGC 1164  
Db 1201 CCCATGCTGAGCCGTTCACGGGAACCGGAGCCAGAGCGGAAGTCCATGGAAGCTCTGAGC 1260  
Qy 1165 ATCACCAGTCCGGGGTGTGGCTCCCTGTATCCCAACCCGAGCGCTTGGAGATGGCC 1224





```

; TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MPI03-0230MNM
; CURRENT APPLICATION NUMBER: US/10/423,543
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 10/278,036
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 09/711,216
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/205,447
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 10/012,055
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248,325
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 10/003,690
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/248,893
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 10/217,168
; PRIOR FILING DATE: 2002-08-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2980
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86) ... (2419)
US-10-423-543-10

```

Query Match	88.3%	Score 2020.2;	DB 17;	Length 2980;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 2022;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	265	TTTATGGTACTCTGGTCTCTGGAGCAGCTCTCGGGGGTGAGCTATTTCGACTACCTCGTTAAAG	324	
Db	398	TATTGTGTACTGTGTCTGGAGCAGCTCTCGGGGGTGAGCTATTTCGACTACCTCGTTAAAG	457	
Qy	325	AAGGGGAGACTGACGCCCAAGGAGGCCCGAAAGTTCTTCGCCCAGATTGTCTGTGCGCTG	384	
Db	458	AAGGGGAGACTGACGCCCNAGGAGGCCCGAAAGTTCTTCGCCCAGATTGTCTGTGCGCTG	517	
Qy	385	GACTTCTGCCACAGCTACTCCATCTGCCACAGACACTTAAAGCCCGAGAACCTCTCTTTTG	444	
Db	518	GACTTCTGCCACAGCTACTCCATCTGCCACAGACACTTAAAGCCCGAGAACCTCTCTTTTG	577	
Qy	445	GATGAGAAAAACAATCCGCAATTGCGACATTCGGGCATGCGGCTCCCTGCAGGTGGGGGAC	504	
Db	578	GATGAGAAAAACAACATCCGCAATTGCGACATTCGGGCATGCGGCTCCCTGCAGGTGGGGGAC	637	
Qy	505	AGCCTCTCGGAGACAGCTCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTTAAGGGG	564	
Db	638	AGCCTCTCGGAGACAGCTCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTTAAGGGG	697	
Qy	565	GMAAAATATGATGCGCGCGGGCAGACATGTGGAGCTGTGGAGTCACTCTCTCGCCCTTG	624	
Db	698	GMAAAATATGATGCGCGCGGGCAGACATGTGGAGCTGTGGAGTCACTCTCTCGCCCTTG	757	
Qy	625	CTCGTGGGGGCTCTGTGCCCTTTTGATGACGACAACCTCCGCCAGCTGCTGGAGAAAGGTGAAA	684	
Db	758	CTCGTGGGGGCTCTGTGCCCTTTTGATGACGACAACCTCCGCCAGCTGCTGGAGAAAGGTGAAA	817	
Qy	685	CGGGGGGTCTTTCACATGCGCCCACTTCAATTCCTCAAGATTGCCAGAGCTTCTCAGGGGA	744	
Db	818	CGGGGGGTCTTTCACATGCGCCCACTTCAATTCCTCAAGATTGCCAGAGCTTCTCAGGGGA	877	

Qy	745	ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTGAAAAACATCTCTTGG	804
Db	878	ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTGAAAAACATCTCTTGG	937
Qy	805	TACCTAGCGGGAAAAACAGAGCCAGACCCGCTGCTGGAGCAGCCCTGCGCCGGGGA	864
Db	938	TACCTAGCGGGAAAAACAGAGCCAGACCCGCTGCTGGAGCAGCCCTGCGCCGGGGA	997
Qy	865	GCCATGCGGAGCCTGCCATCAACGGAGAGCTGGACCCCGACGTCCTTAGAGAGCATGGCA	924
Db	998	GCCATGCGGAGCCTGCCATCAACGGAGAGCTGGACCCCGACGTCCTTAGAGAGCATGGCA	1057
Qy	925	TCACTGGGCTGCTTCAGGGACCGGAGAGGCTGGATGCGAGCTGCGCAGTAGGAGGAG	984
Db	1058	TCACTGGGCTGCTTCAGGGACCGGAGAGGCTGGATGCGAGCTGCGCAGTAGGAGGAG	1117
Qy	985	AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGAGCGGTATCCACGCTGT	1044
Db	1118	AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGAGCGGTATCCACGCTGT	1177
Qy	1045	GAGGACCAGGACCTGCCCTCCCGGAATGATGTTGACCCCCCGGAAGCGGTATGGATTCT	1104
Db	1178	GAGGACCAGGACCTGCCCTCCCGGAATGATGTTGACCCCCCGGAAGCGGTATGGATTCT	1237
Qy	1105	CCCATGCTGAGCCGTACAGGGAACGGCGACACAGAGCGGAAGTCCATGGAAGTCTCTGAGC	1164
Db	1238	CCCATGCTGAGCCGTACAGGGAACGGCGACACAGAGCGGAAGTCCATGGAAGTCTCTGAGC	1297
Qy	1165	ATCACCGATCCCGGGGTGTGTCTCCCTGTACCCACCGAGCGGGCTTTGGAGATGGCC	1224
Db	1298	ATCACCGATCCCGGGGTGTGTCTCCCTGTACCCACCGAGCGGGCTTTGGAGATGGCC	1357
Qy	1225	CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCCCTCACGGGTCTGTCTCCAGCCCT	1284
Db	1358	CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCCCTCACGGGTCTGTCTCCAGCCCT	1417
Qy	1285	CTAAGCAGCCAAAGAGTCCGGTCTTTTCTTTTACCGAGCCGGGGCTGGAGATGAG	1344
Db	1418	CTAAGCAGCCAAAGAGTCCGGTCTTTTCTTTTACCGAGCCGGGGCTGGAGATGAG	1477
Qy	1345	GCTCGAGCGGGGGCTCCCGACTTCCAAACCGAGAGCTGCTTCTCGGGGCCCCAGG	1404
Db	1478	GCTCGAGCGGGGGCTCCCGACTTCCAAACCGAGAGCTGCTTCTCGGGGCCCCAGG	1537
Qy	1405	GGTGGGGGCGCGGGAGCAGCCCGCCCGCCAGTGCCTCCCAACCGCTGCCCCGCGC	1464
Db	1538	GGTGGGGGCGCGGGAGCAGCCCGCCCGCCAGTGCCTCCCAACCGCTGCCCCGCGC	1597
Qy	1465	CCCCCAGGCTCCCGCGCTCCTCTGCGGGAGACCCCTTGTGACCTCTGCAACGCGCC	1524
Db	1598	CCCCCAGGCTCCCGCGCTCCTCTGCGGGAGACCCCTTGTGACCTCTGCAACGCGCC	1657
Qy	1525	CGGGCAGTCCACCGGAGCCCGGGACAAACCAACCCCGAGCCCGCGGGTGGGTC	1584
Db	1658	CGGGCAGTCCACCGGAGCCCGGGAGAAACCAACCCCGAGCCCGCGGGTGGGTC	1717
Qy	1585	GGGGGAGCCGCTGGAGAGTCTCTCAAATCCATCGCAACAGTCTCTTGGGCTCCCTCT	1644
Db	1718	GGGGGAGCCGCTGGAGAGTCTCTCAAATCCATCGCAACAGTCTCTTGGGCTCCCTCT	1777
Qy	1645	CGCTTTCCCGGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCAGCTTGAAGCCA	1704
Db	1778	CGCTTTCCCGGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCAGCTTGAAGCCA	1837
Qy	1705	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGGTTGGGAACTTTCATCTCTTGGACAAA	1764
Db	1838	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGGTTGGGAACTTTCATCTCTTGGACAAA	1897
Qy	1765	GAGAACAAATATTCTCTGCTGTAAAGGACAAACCTCTCTAGCAGCATCAAGCAGACATC	1824
Db	1898	GAGAACAAATATTCTCTGCTGTAAAGGACAAACCTCTCTAGCAGCATCAAGCAGACATC	1957
Qy	1825	GTCCATGCCTTTCTGTGTCATCCCGAGCCTGAGTCACAGTGTGCTGTCACAGACCGAGTTC	1884

Db 1958 GTCCATGCTTTCTGTGATCCCAAGCTGAGTCAAGTGTCTGTCAAGACCAAGCTTC 2017  
Qy 1885 AGGGCCGAGTACAAAGCCAGTGGCGCCCTCGCTTCCAAAGCCCGCTCCGCTTCCAG 1944  
Db 2018 AGGGCCGAGTACAAAGCCAGTGGCGCCCTCGCTTCCAAAGCCCGCTCCGCTTCCAG 2077  
Qy 1945 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2004  
Db 2078 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2137  
Qy 2005 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2064  
Db 2138 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2197  
Qy 2065 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2124  
Db 2198 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2257  
Qy 2125 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2184  
Db 2258 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2317  
Qy 2185 CAGCCCCCAGCGGCGCCAGAGCCAGAGCTGAGCAGCTCTCCCGCGAGCGGAGCGGAGGCT 2244  
Db 2318 CAGCCCCCAGCGGCGCCAGAGCCAGAGCTGAGCAGCTCTCCCGCGAGCGGAGCGGAGGCT 2377  
Qy 2245 AAGGACAAAGAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2289  
Db 2378 AAGGACAAAGAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGCT 2422

RESULT 11

US-10-757-262-135  
; Sequence 135, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karicheti, Venkateswarlu  
; APPLICANT: Eliabof, Scott D.  
; APPLICANT: Eliabof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5587, 984,  
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,  
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 51164,  
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 68112, 14990,  
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,  
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,  
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,  
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32878 OR  
; FILE REFERENCE: MPI03-007P1RNMNIN  
; CURRENT APPLICATION NUMBER: US/10/757,262  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/444,783  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/478,742  
; PRIOR FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/488,529  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/491,156  
; PRIOR FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 60/499,594  
; PRIOR FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US 60/506,332  
; PRIOR FILING DATE: 2003-09-26

; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 135  
; LENGTH: 2980  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (86)...(2422)  
US-10-757-262-135  
  
Query Match 88.3%; Score 2020.2; DB 18; Length 2980;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 265 TTTAGGTACCTTGTCTGTGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGTTAAAG 324  
Db 398 TATTTGTACCTTGTCTGTGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGTTAAAG 457  
Qy 325 AAGGGGAGACTGACGCCCAAGAGGGCCGAAAGTTCTTCGCCAGATTGTCTCGCGCTG 384  
Db 458 AAGGGGAGACTGACGCCCAAGAGGGCCGAAAGTTCTTCGCCAGATTGTCTCGCGCTG 517  
Qy 385 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTTAAAGCCCGAGAACCTCTTTT 444  
Db 518 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTTAAAGCCCGAGAACCTCTTTT 577  
Qy 445 GATGAGAAAAAACAATCCGCAATTGACAGCTTCGGCATGGCGTCCCTGACAGTGGGGAC 504  
Db 578 GATGAGAAAAAACAATCCGCAATTGACAGCTTCGGCATGGCGTCCCTGACAGTGGGGAC 637  
Qy 505 AGCTCTCTGGAGACAGCTGGGGTCCCGCCATTATGCTGTCCAGAGAGTGAATTAAGGG 564  
Db 638 AGCTCTCTGGAGACAGCTGGGGTCCCGCCATTATGCTGTCCAGAGAGTGAATTAAGGG 697  
Qy 565 GAAAAATATGATGGCGCCCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCGCCCTG 624  
Db 698 GAAAAATATGATGGCGCCCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCGCCCTG 757  
Qy 625 CTCGTGGGGCTCTGCGCTTTGATGACGACACCTCCGCGAGCTCTCGGAGAGTGAAA 684  
Db 758 CTCGTGGGGCTCTGCGCTTTGATGACGACACCTCCGCGAGCTCTCGGAGAGTGAAA 817  
Qy 685 CGGGGGCTCTTCCACATGCGCCCACTTCACTTCCAGATTGCGAGAGCTCTCGAGGGGA 744  
Db 818 CGGGGGCTCTTCCACATGCGCCCACTTCACTTCCAGATTGCGAGAGCTCTCGAGGGGA 877  
Qy 745 ATGATCGAAGTGGAGCCCGGAGAGAGCTCAGTCTGGGCAAAATTCAGAAAAATCTCTGG 804  
Db 878 ATGATCGAAGTGGAGCCCGGAGAGAGCTCAGTCTGGGCAAAATTCAGAAAAATCTCTGG 937  
Qy 805 TACCTAGGCGGAGAAACACGAGCGCAGACCCGCTGCTTGGAGCGACCCCTCGCGCGGGTA 864  
Db 938 TACCTAGGCGGAGAAACACGAGCGCAGACCCGCTGCTTGGAGCGACCCCTCGCGCGGGTA 997  
Qy 865 GCCATGCGGAGCTTCCATCCAAACGAGAGCTGGAACCCGAGCTCTTAGAGAGCATGGCA 924  
Db 998 GCCATGCGGAGCTTCCATCCAAACGAGAGCTGGAACCCGAGCTCTTAGAGAGCATGGCA 1057  
Qy 925 TCACCTGGGCTCTTACGAGGACCCGAGAGCTGCTCATCGCGAGCTGCGCAGTGGAGGAG 984  
Db 1058 TCACCTGGGCTCTTACGAGGACCCGAGAGCTGCTCATCGCGAGCTGCGCAGTGGAGGAG 1117  
Qy 985 AACCAAGAAAAAGATGATATATTTATCTCTTTTGGATCGGAAGGCGGTATCCAGCTGT 1044  
Db 1118 AACCAAGAAAAAGATGATATATTTATCTCTTTTGGATCGGAAGGCGGTATCCAGCTGT 1177  
Qy 1045 GAGGACACGAGACCTGCTCTCCCGGAGTGTTCGACCCCGGAGAGCGTGTGGATTCT 1104  
Db 1178 GAGGACACGAGACCTGCTCTCCCGGAGTGTTCGACCCCGGAGAGCGTGTGGATTCT 1237  
Qy 1105 CCCATGCTGAGCGCTCAGCGGAAGCGGAGCCAGAGCGGAGTCCATGGAAGTCTCAGC 1164

Db 1238 CCCATGCTGAGCCGTACCGGAAGCGGCGACGAGCGGAAGTCCATCGAAGTCTTGAGC 1297  
Qy 1165 ATCAACCATGTCGGGGGTGGTGGCTCCCTCTTATCCACCGACCGGGCTTGGAGATGGCC 1224  
Db 1298 ATCAACCATGTCGGGGGTGGTGGCTCCCTCTTATCCACCGACCGGGCTTGGAGATGGCC 1357  
Qy 1225 CAGCACAGCAGAGATCCCGTAGCGTCACTGAGGAGCTCCACGGGTCTGTCTCCAGCCCT 1284  
Db 1358 CAGCACAGCAGAGATCCCGTAGCGTCACTGAGGAGCTCCACGGGTCTGTCTCCAGCCCT 1417  
Qy 1285 CTAAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTACCGGAGCGGGGGCTGGAGATGAG 1344  
Db 1418 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTACCGGAGCGGGGGCTGGAGATGAG 1477  
Qy 1345 GCTCAGCGGGGGCTCCCGACTTCCAAACGAGAGCGTCTTCTCGGGGGCCCGAGG 1404  
Db 1478 GCTCAGCGGGGGCTCCCGACTTCCAAACGAGAGCGTCTTCTCGGGGGCCCGAGG 1537  
Qy 1405 GGTGGGGGGCGGGGAGCAGCCCGCCCGCCAGTGCCTCCACACCCCTGCCCGGC 1464  
Db 1538 GGTGGGGGGCGGGGAGCAGCCCGCCCGCCAGTGCCTCCACACCCCTGCCCGGC 1597  
Qy 1465 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTTGCACTCGCTCTGCAACGCCC 1524  
Db 1598 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTTGCACTCGCTCTGCAACGCCC 1657  
Qy 1525 CGGGCAGTCCACCGGGACCCCGGGGACAAACACACCCCGCAGCCCGGGGTGGGTC 1584  
Db 1658 CGGGCAGTCCACCGGGACCCCGGGGACAAACACACCCCGCAGCCCGGGGTGGGTC 1717  
Qy 1585 GGGGGAGCGGCTGAGAGTGTCTCACTCCATCCGACAGCTTCCTGGGCTCCCT 1644  
Db 1718 GGGGGAGCGGCTGAGAGTGTCTCACTCCATCCGACAGCTTCCTGGGCTCCCT 1777  
Qy 1645 CGCTTTTCAACCGGCGCAAGATCAGGTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1704  
Db 1778 CGCTTTTCAACCGGCGCAAGATCAGGTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1837  
Qy 1705 GAGTCTCTCCCGAGCTGGGAAAAAGCTCTCGTGGTTGGGAACTTCATCTCTCTGGACAAA 1764  
Db 1838 GAGTCTCTCCCGAGCTGGGAAAAAGCTCTCGTGGTTGGGAACTTCATCTCTCTGGACAAA 1897  
Qy 1765 GAGAAACAATATTCCTGCTTAAGGACAAACCTCTCAGCAGCATCAAGCAGATC 1824  
Db 1898 GAGAAACAATATTCCTGCTTAAGGACAAACCTCTCAGCAGCATCAAGCAGATC 1957  
Qy 1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCACTGAGTGTCTCAGACACAGCTTC 1884  
Db 1958 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCACTGAGTGTCTCAGACACAGCTTC 2017  
Qy 1885 AGGCCGAGTACAAAGGCGAGTGGCGGCCCTCCCTCTTCCAAAAGCCCGTCCAG 1944  
Db 2018 AGGCCGAGTACAAAGGCGAGTGGCGGCCCTCCCTCTTCCAAAAGCCCGTCCAG 2077  
Qy 1945 GTGACATCAGTCTCTGAGGTTCCAGAGCCCTCCCGGACGGGACGGGAGGT 2004  
Db 2078 GTGACATCAGTCTCTGAGGTTCCAGAGCCCTCCCGGACGGGACGGGAGGT 2137  
Qy 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGTTCCAGCCGCTCGGTTCAAGCGA 2064  
Db 2138 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGTTCCAGCCGCTCGGTTCAAGCGA 2197  
Qy 2065 GTGTGGAGACCATCCAGGCAAGCTCTGAGCACTCATGACAGCCCTCCGTGAGGCC 2124  
Db 2198 GTGTGGAGACCATCCAGGCAAGCTCTGAGCACTCATGACAGCCCTCCGTGAGGCC 2257  
Qy 2125 CTGACAGAGAGAAAGGGGGCCAGACCCGGCTGTGTGTGTCGCCACCCGAGGCTG 2184  
Db 2258 CTGACAGAGAGAAAGGGGGCCAGACCCGGCTGTGTGTGTCGCCACCCGAGGCTG 2317  
Qy 2185 CAGCCCCACCGGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGGAGGCCCCCC 2244  
Db 2318 CAGCCCCACCGGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGGAGGCCCCCC 2377

Qy 2245 AAGCACAAGAGCTCTGGCCACCAACGGGACCCCTCTGCCCTGA 2289  
Db 2378 AAGCACAAGAGCTCTGGCCACCAACGGGACCCCTCTGCCCTGA 2422

## RESULT 12

US-10-479-532-2

; Sequence 2, Application US/10479532

; Publication No. US20040151713A1

; GENERAL INFORMATION:

; APPLICANT: TAIHO PHARMACEUTICAL CO., LTD

; TITLE OF INVENTION: CELL CYCLE REGULATORY FACTOR

; FILE REFERENCE: 44B00JP

; CURRENT APPLICATION NUMBER: US/10/479,532

; CURRENT FILING DATE: 2003-12-03

; PRIOR APPLICATION NUMBER: JP 2001-168792

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 2

; LENGTH: 2799

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (50)..(2311)

US-10-479-532-2

Query Match 80.3%; Score 1839; DB 18; Length 2799;

Best Local Similarity 95.5%; Pred. No. 0;

Matches 1933; Conservative 0; Mismatches 20; Indels 72; Gaps 1;

Qy 265 TTTAGTACCTGGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTTCGACTACCTGGTAAAG 324  
Db 362 TATTGTACCTGGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTTCGACTACCTGGTAAAG 421  
Qy 325 AAGGGAGACTGACGCCCAAGAGAGGCCGAAAGTTCTTCGCCAGAGATTGTGTGCGCTG 384  
Db 422 AAGGGAGACTGACGCCCAAGAGAGGCCGAAAGTTCTTCGCCAGAGATTGTGTGCGCTG 481  
Qy 385 GACTCTTGCCACAGCTACTCCATCTGCCACAGAGACTTAAGCCCGAGAGACCTGCTTTTG 444  
Db 482 GACTCTTGCCACAGCTACTCCATCTGCCACAGAGACTTAAGCCCGAGAGACCTGCTTTTG 541  
Qy 445 GATCAGAAAAACAACATCCCATTTGAGACTTCGGCATGGCTCCCTGCGAGTGGGGGAC 504  
Db 542 GATCAGAAAAACAACATCCCATTTGAGACTTCGGCATGGCTCCCTGCGAGTGGGGGAC 601  
Qy 505 AGCTCTCTGAGACCAAGTCCGGTCCCGCATTTATGCGTGTCCAGAGGTGATTAAAGGG 564  
Db 602 AGCTCTCTGAGACCAAGTCCGGTCCCGCATTTATGCGTGTCCAGAGGTGATTAAAGGG 661  
Qy 565 GAAAAATATGATGGCGCGGCGAGACATGCGAGCTGTGGAGTCTCATCTTCGCGCTG 624  
Db 662 GAAAAATATGATGGCGCGGCGAGACATGCGAGCTGTGGAGTCTCATCTTCGCGCTG 721  
Qy 625 CTGCTGGGGGCTCTGCGCTTTTGATGACACAACTCCCGCAGGTGCTGGAGAGGTGAAA 684  
Db 722 CTGCTGGGGGCTCTGCGCTTTTGATGACACAACTCCCGCAGGTGCTGGAGAGGTGAAA 781  
Qy 685 CGGGGGTCTTTCACATGCCCCACTTCATTTCTCCAGATTGCCAGAGCCTCTTGAGGGGA 744  
Db 782 CGGGGGTCTTTCACATGCCCCACTTCATTTCTCCAGATTGCCAGAGCCTCTTGAGGGGA 841  
Qy 745 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGGAGCAATTCAGAAACATCTTGG 804  
Db 842 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGGAGCAATTCAGAAACATCTTGG 901  
Qy 805 TACTAGCGGGGAAAAACAGAGCCAGAGCCCGTGTGGAGCAGCCCTGCGCGCGCGGTA 864  
Db 902 TACTAGCGGGGAAAAACAGAGCCAGAGCCCGTGTGGAGCAGCCCTGCGCGCGCGGTA 961



QY 865 GCATGCGGAGCCTGCCATCCAAACGAGAGCTGGACCCCGACGTCTCTAGAGCATGSCA 924  
DB 962 GCCATGCGGAGCCTGCCATCCAAACGAGAGCTGGACCCCGACGTCTCTAGAGCATGSCA 1021  
QY 925 TCACTGGGCTGCTTACAGGAGCCGCGAGAGCTGCATCGGAGCTGGCAGTGCAGAGGAG 984  
DB 1022 TCACTGGGCTGCTTACAGGAGCCGCGAGAGCTGCATCGGAGCTGGCAGTGCAGAGGAG 1081  
QY 985 AACCAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044  
DB 1082 AACCAAGAAAGATGATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1141  
QY 1045 GAGGACAGAGCTGCTTCCCGGAGATGATTTGAACCCCGGAGAGCGGTGGAATCT 1104  
DB 1142 GAGGACAGAGCTGCTTCCCGGAGATGATTTGAACCCCGGAGAGCGGTGGAATCT 1201  
QY 1105 CCAATGCTGAGCGCTACGCGGAGCGGACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1164  
DB 1202 CCAATGCTGAGCGCTACGCGGAGCGGACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1261  
QY 1165 ATCAACGATGCGGGGGTGGTGTCTCCCTGTACCCACCGAGCGGCTTTGGAGATGGCC 1224  
DB 1262 ATCAACGATGCGGGGGTGGTGTCTCCCTGTACCCACCGAGCGGCTTTGGAGATGGCC 1321  
QY 1225 CAGCACAGCAGATCCCGTAGCTGCTGAGGAGCTCCAGGCTGTCTCCAGCCCT 1284  
DB 1322 CAGCACAGCAGATCCCGTAGCTGCTGAGGAGCTCCAGGCTGTCTCCAGCCCT 1381  
QY 1285 TTAAGCAGCCAAAGAGTCCGCTCTTTTCCCTTTTACCGGAGCGGGGCTTGAGATGAG 1344  
DB 1382 CTNAGCAGCCAAAGAGTCCGCTCTTTTCCCTTTTACCGGAGCGGGGCTTGAGATGAG 1441  
QY 1345 GCTGAGGCGGGGGTCCCGCATTCCTCAAAACGAGAGCTGCTTCTCGGGGCCCCAGG 1404  
DB 1442 GCTGAGGCGGGGGTCCCGCATTCCTCAAAACGAGAGCTGCTTCTCGGGGCCCCAGG 1480  
QY 1405 GTTGGGGGCGCGGGGAGCAGCCCCCGCCCCCGCTCCAGTGCCTCCACACCCCTCGCGGC 1464  
DB 1481 -----CTGCCCGGC 1489  
QY 1465 CCCCAGGCTCCCGCGCTCTCTGCGGGGACCCCTTGCTGACTGCTGCTCCACAGCCC 1524  
DB 1490 CCCCAGGCTCCCGCGCTCTCTGCGGGGACCCCTTGCTGACTGCTGCTCCACAGCCC 1549  
QY 1525 CCGGCGAGTCCACCGGAGCCCGGGGACAAACACACCCCGCGCGGCTGGGGTTC 1584  
DB 1550 CCGGCGAGTCCACCGGAGCCCGGGGACAAACACACCCCGCGCGGCTGGGGTTC 1609  
QY 1585 GGGGAGCGCGCTGAGGAGTCTCTCAACTCCATCCGCAACAGCTTCTGCGGCTCCCT 1644  
DB 1610 GGGGAGCGCGCTGAGGAGTCTCTCAACTCCATCCGCAACAGCTTCTGCGGCTCCCT 1669  
QY 1645 CGCTTTACCGGCGCAAGATCGAGTCCCTACCGCTGAGGAGTCTCCAGCTTGACGCCA 1704  
DB 1670 CGCTTTACCGGCGCAAGATCGAGTCCCTACCGCTGAGGAGTCTCCAGCTTGACGCCA 1729  
QY 1705 GAGTCTCTCCCGGAGTGGCAAAACGCTCTGCTGCTGGGAACTTCTCTTTGACAAA 1764  
DB 1730 GAGTCTCTCCCGGAGTGGCAAAACGCTCTGCTGCTGGGAACTTCTCTTTGACAAA 1789  
QY 1765 GAAGAAACAAATATCTCTGCTGCTAAAGAGCAAACTCTCAGCAGATCAAGCAGCATC 1824  
DB 1790 GAAGAGCAAAATATCTCTGCTGCTAAAGAGCAAACTCTCAGCAGATCAAGCAGCATC 1849  
QY 1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTGCTGTCACAGACCAAGCTTC 1884  
DB 1850 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTGCTGTCACAGACCAAGCTTC 1909  
QY 1885 AGGCGCGAGTACAGGCGCAGTGGCGCCCTCGCTGTTTCAAAAGCCGCTCGCTTCAG 1944  
DB 1910 AGGCGCGAGTACAGGCGCAGTGGCGCCCTCGCTGTTTCAAAAGCCGCTCGCTTCAG 1969  
QY 1945 GTGACATACGCTCTCTGAGGGTCCAGAGCCCTCCCGCGACCGGACGCGAGGAGT 2004

DB 1970 GTGACATACGCTCTCTGAGGGTCCAGAGCCCTCCCGCGACGCGACGCGAGGT 2029  
QY 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGCTCCAGAGCCGCTCGGTTCAAGCGA 2064  
DB 2030 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGCTCCAGAGCCGCTCGGTTCAAGCGA 2089  
QY 2065 GTGTGGAGACCATCCAGGCGACAGCTCTCTGAGCATCTCATGACAGCCCTCGGTGAGGCC 2124  
DB 2090 GTGTGGAGACCATCCAGGCGACAGCTCTCTGAGCATCTCATGACAGCCCTCGGTGAGGCC 2149  
QY 2125 CTGGCAGACGAGAAACGCGGCCCCAGACCCGCGCTGTGTGCTCCCGCCACCCCGAAGCTG 2184  
DB 2150 CTGGCAGACGAGAAACGCGGCCCCAGACCCGCGCTGTGTGCTCCCGCCACCCCGAAGCTG 2209  
QY 2185 CAGCCCCCAGCCCGCGGCCAGAGCCAGAGCTGAGCAGCTCTCCCGCGAGGCCCCCC 2244  
DB 2210 CAGCCCCCAGCCCGCGGCCAGAGCCAGAGCTGAGCAGCTCTCCCGCGAGGCCCCCC 2269  
QY 2245 AAGGACAAAGAGCTCTCTGCGCCACCAACGCGGACCCCTCTGCCCCCTGA 2289  
DB 2270 AAGGACAAAGAGCTCTCTGCGCCACCAACGCGGACCCCTCTGCCCCCTGA 2314

RESULT 13

US-10-425-114-26847  
; Sequence 26847, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 26847  
; LENGTH: 1949  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB4653-002-EI\_FLI  
US-10-425-114-26847

Query Match 66.4%; Score 1518.8; DB 17; Length 1949;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1520; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 768 AAGGCTCAGTCTGAGCAAAATTCAGAAAATCTCTGTTGTTACCTAGGCGGGAACACCGAGCC 827  
DB 1 AAGGCTCAGTCTGAGCAAAATTCAGAAAATCTCTGTTGTTACCTAGGCGGGAACACCGAGCC 60  
QY 828 AGACCTCTGCTGAGCCAGCCCTGCGCCCGGGTAGCCATCGCGAGCTGCGCATCCAA 887  
DB 61 AGACCTCTGCTGAGCCAGCCCTGCGCCCGGGTAGCCATCGCGAGCTGCGCATCCAA 120  
QY 888 CCGAGAGCTGACCCCGACCGCTCTCTAGAGAGCATGGCATCTCTGGGCTGCTTCAGGAGCCG 947  
DB 121 CCGAGAGCTGACCCCGACCGCTCTCTAGAGAGCATGGCATCTCTGGGCTGCTTCAGGAGCCG 180  
QY 948 CGAGAGCTGATCGCAGCTGCGCAGTGGAGGAGCAACCAAGAAAGATGATATATTA 1007  
DB 181 CGAGAGCTGATCGCAGCTGCGCAGTGGAGGAGCAACCAAGAAAGATGATATATTA 240  
QY 1008 TCTGCTTTTGTATCGGAGGAGCGGTATCCAGCTGTGAGGACAGGACTGCTCCCTCCCG 1067  
DB 241 TCTGCTTTTGTATCGGAGGAGCGGTATCCAGCTGTGAGGACAGGACTGCTCCCTCCCG 300



1068 GAAATGATGTTGACCCCGCCGGAAGCGTGTGATTTCTCCCATGCTGAGCCGCTACGGGAA 1127  
Db  
301 GAATGATGTTGACCCCGCCGGAAGCGTGTGATTTCTCCCATGCTGAGCCGCTACGGGAA 360  
1128 GCGGACACGAGAGCGGAAGTCCATGGAAGTCTCTGAGCATCACCGATGCGGGGGTGTGG 1187  
Db  
361 GCGGACACGAGAGCGGAAGTCCATGGAAGTCTCTGAGCATCACCGATGCGGGGGTGTGG 420  
1188 CTCCCTGTATCCACCCGACCGGCTTGGAGATGGCCCGACAGCACCGAGATCCCGTAG 1247  
Db  
421 CTCCCTGTATCCACCCGACCGGCTTGGAGATGGCCCGACAGCACCGAGATCCCGTAG 480  
1248 CGTCAGTGGAGCTTCCAGCGTCTGTCTCTCAGCCCTCTAAGCAGCCCAAGAGTCCGGT 1307  
Db  
481 CGTCAGTGGAGCTTCCAGCGTCTGTCTCTCAGCCCTCTAAGCAGCCCAAGAGTCCGGT 540  
1308 CTTTTCTTTTACCGGACCGCGGGCTGTGAGATGAGGCTCGAGCGGGGCTCCCCGAC 1367  
Db  
541 CTTTTCTTTTACCGGACCGCGGGCTGTGAGATGAGGCTCGAGCGGGGCTCCCCGAC 600  
1368 TTCAAAACGAGAGCGTGTCTTCTCGGGGCCCCAGAGGCTGGGGCGCGGGAGCGAGCC 1427  
Db  
601 TTCCAAAACGAGAGCGTGTCTTCTCGGGGCCCCAGAGGCTGGGGCGCGGGAGCGAGCC 660  
1428 CCGGCCCCAGTGCCTCCACACCTCTCGCGGCCCGCCAGGCTCCCGCGCTCCTC 1487  
Db  
661 CCGGCCCCAGTGCCTCCACACCTCTCGCGGCCCGCCAGGCTCCCGCGCTCCTC 720  
1488 TGGGGGACCCCTTGCATCGCTCTGTGCACACCGCCCGGCGGCTCCACCGGGAGCCCC 1547  
Db  
721 TGGGGGACCCCTTGCATCGCTCTGTGCACACCGCCCGGCGGCTCCACCGGGAGCCCC 780  
1548 GGGGACAAACACCCCGCGCGGCTGTGGGCTGGGGGAGCGGCTGTGAGAGTGG 1607  
Db  
781 GGGGACAAACACCCCGCGCGGCTGTGGGCTGGGGGAGCGGCTGTGAGAGTGG 840  
1608 TCTCAATCCATCCGACAGCTTCTCGGGCTCCCTCGCTTTCACCGGCGAGAGTGA 1667  
Db  
841 TCTCAATCCATCCGACAGCTTCTCGGGCTCCCTCGCTTTCACCGGCGAGAGTGA 900  
1668 GGTCCCTACCGCTGAGAGATGTCTCAGCTTGACGCGCAGAGTCTCCCGGAGCTGGCAA 1727  
Db  
901 GGTCCCTACCGCTGAGAGATGTCTCAGCTTGACGCGCAGAGTCTCCCGGAGCTGGCAA 960  
1728 AGCTCTCTGTGGGAACTTCATCTCTTGGACAAAGAGAAACAATATTTCTCTGTGCT 1787  
Db  
961 AGCTCTCTGTGGGAACTTCATCTCTTGGACAAAGAGAAACAATATTTCTCTGTGCT 1020  
1788 AAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTCCATCGCTTCTGTGATCCC 1847  
Db  
1021 AAGGACAAACCTCTCAGCAGCATCAAGCAGACATCGTCCATCGCTTCTGTGATCCC 1080  
1848 CAGCTGAGTCAAGTGTGCTGTCAAGCAGCTTCAAGGCGGAGTACAGGCGCAGTGG 1907  
Db  
1081 CAGCTGAGTCAAGTGTGCTGTCAAGCAGCTTCAAGGCGGAGTACAGGCGCAGTGG 1140  
1908 GGGCCCTCTCGTTTCCAAAAGCCCGTCCGCTTCCAGTGGACATCAGCTCCTCTGAGGG 1967  
Db  
1141 GGGCCCTCTCGTTTCCAAAAGCCCGTCCGCTTCCAGTGGACATCAGCTCCTCTGAGGG 1200  
1968 TCCAGAGCCCTCCCGGACCGGACCGGAGGAGTGGGATCTACTCCGTCACCTT 2027  
Db  
1201 TCCAGAGCCCTCCCGGACCGGACCGGAGGAGTGGGATCTACTCCGTCACCTT 1260  
2028 CACTCTCATCTCGGTCCTCAGCGTCTCAAGCGAGTGTGGAGACCATCCAGGACACA 2087  
Db  
1261 CACTCTCATCTCGGTCCTCAGCGTCTCAAGCGAGTGTGGAGACCATCCAGGACACA 1320  
2088 GCTCTGAGCACTCATGACCGCCCTCTCGTACGCGCTTGGCAGACGAGAGAAACGGGGC 2147  
Db  
1321 GCTCTGAGCACTCATGACCGCCCTCTCGTACGCGCTTGGCAGACGAGAGAAACGGGGC 1380  
2148 CCAGACCGGCGCTGTGTGTGCCCCACCCCGGAGCGCTGACGAGCCCCCAACCGGCGCCCGCAGA 2207

Db 1381 CCAGACCGGCGCTGTGTGTGCCCCCAGCCCGAGGCTTGAGGCCCCACCCAGCCGCCGAGA 1440  
Qy 2208 CCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCGCCCAAGGACAAGAGCTCTCTGGCCAC 2267  
Db 1441 CCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCCGCCCAAGGACAAGAGCTCTCTGGCCAC 1500  
Qy 2268 CAACGGGACCCCTCTGCGCTGA 2289  
Db 1501 CAACGGGACCCCTCTGCGCTGA 1522

RESULT 14  
US-10-120-988-221  
; Sequence 221, Application US/10120988  
; Publication No. US20030219745A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and  
; FILE OF INVENTION: Polypeptides  
; FILE REFERENCE: 802CON  
; CURRENT APPLICATION NUMBER: US/10/120,988  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: 09/774,528  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 441  
; SOFTWARE: pt\_fl\_genes Version 2.0  
; SEQ ID NO 221  
; LENGTH: 1797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (15)..(1787)  
US-10-120-988-221

Query Match 42.8%; Score 980; DB 17; Length 1797;  
Best Local Similarity 75.4%; Pred. No. 1.7e-273;  
Matches 1470; Conservative 0; Mismatches 0; Indels 480; Gaps 1;

Qy 268 AGGTACCTGTGTTCTGGAGCAGCTCTCGGGGGTGTGAGTATTCGACTACCTGGTAAAGAG 327  
Db 87 AGGTACCTGTGTTCTGGAGCAGCTCTCGGGGGTGTGAGTATTCGACTACCTGGTAAAGAG 146  
Qy 328 GGGAGACTGACGCCCAAGGAGGCCCGAAAGTTCTTCGCGCAGATGTGTCTGCGCTGGAC 387  
Db 147 GGGAGACTGACGCCCAAGGAGGCCCGAAAGTTCTTCGCGCAGATGTGTCTGCGCTGGAC 206  
Qy 388 TTCTGCCACAGCTACTCCATCTGCCACAGACAGCTTAAGCCCGAGAACCTGCTTTTGAT 447  
Db 207 TTCTGCCACAGCTACTCCATCTGCCACAGACAGCTTAAGCCCGAGAACCTGCTTTTGAT 266  
Qy 448 GAGAAAAACAATCCCGCATTCGAGACTTCGGCATGGCGTCCCTGCGAGTGGGGGACAGC 507  
Db 267 GAGAAAAACAATCCCGCATTCGAGACTTCGGCATGGCGTCCCTGCGAGTGGGGGACAGC 326  
Qy 508 CTCTGTGAGACCAAGCTCGGGTCCCCCAATATGCGTGTCCAGAGGTGATTAAGGGGAA 567  
Db 327 CTCTGTGAGACCAAGCTCGGGTCCCCCAATATGCGTGTCCAGAGGTGATTAAGGGGAA 386  
Qy 568 AAATATGATGCGCGCGGAGACATGTGGAGCTGTGAGTCACTCTTCGCGCTGCTC 627  
Db 387 AAATATGATGCGCGCGGAGACATGTGGAGCTGTGAGTCACTCTTCGCGCTGCTC 446  
Qy 628 GTGGGGGCTCTGCGCTTTGATGACGACAACTCCGCGCAGCTGTGGAGAGGTGAACGG 687  
Db 447 GTGGGGGCTCTGCGCTTTGATGACGACAACTCCGCGCAGCTGTGGAGAGGTGAACGG 506

QY	688	GGGCTCTTCCACATGCCCACTTCATTCCTCCAGATTCGACAGCCTCTCAGAGGGAATG	747	Db	1107	GAAACAATATTCCTCGTGTAAAGGACAAACCTCTCAGACGATCAAGACAGACATCGTC	1166
Db	507	GGCGCTTCCACATGCCCACTTCATTCCTCCAGATTCGACAGCCTCTCAGAGGGAATG	566	QY	1828	CATGCTTTCTGTGATCCCGAGCCTGAGTCACAGTGTGTGTACACAGACCACTTCAGG	1887
QY	748	ATCGAAGTGAGCCGGAAGAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTCTGGTAC	807	Db	1167	CATGCTTTCTGTGATCCCGAGCCTGAGTCACAGTGTGTGTACACAGACCACTTCAGG	1226
Db	567	ATCGAAGTGAGCCGGAAGAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTCTGGTAC	626	QY	1888	GCCAGGTACAAAGGCAAGTGGCGGCCCTCTCGTCTTCCAAAAGGCCGCTCCGCTTCAGGTG	1947
QY	808	CTAGCGGGGAAAACACGAGCCAGACCCGTCGCTGGAGCCAGCCCTCTGGCCGCGGGTAGCC	867	Db	1227	GCCGAGTACAAAGGCAAGTGGCGGCCCTCTCGTCTTCCAAAAGGCCGCTCCGCTTCAGGTG	1286
Db	627	CTAGCGGGGAAAACACGAGCCAGACCCGTCGCTGGAGCCAGCCCTCTGGCCGCGGGTAGCC	686	QY	1948	GACATCAGCTCCTCTGAGGCTCCAGAGCCTCCCGGAGCGGACGCGAGGAGTGGT	2007
QY	868	ATGCGGAGCCTGCATCAACAGGAGCTGGACCCCGAGCTCTAGAGAGCATGGCATCA	927	Db	1287	GACATCAGCTCCTCTGAGGCTCCAGAGCCTCCCGGAGCGGACGCGAGGAGTGGT	1346
Db	687	ATGCGGAGCCTGCATCAACAGGAGCTGGACCCCGAGCTCTAGAGAGCATGGCATCA	746	QY	2008	GGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCCTCGGTTCACAGGAGT	2067
QY	928	CTGGGCTGCTCAGGAGCCGAGAGCTGCATCGCGAGCTGCGCAGTGGAGGAGGAGAAC	987	Db	1347	GGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCCTCGGTTCACAGGAGT	1406
Db	747	CTGGGCTGCTCAGGAGCCGAGAGCTGCATCGCGAGCTGCGCAGTGGAGGAGGAGAAC	806	QY	2068	GTGGAGACCATCCAGGCAAGCTCCTGAGCACTCATGACAGCCCTCCGTGAGGCCCTG	2127
QY	988	CAAGAAAAGATGATATATTTATCTCTTTTGGATCGGAAGAGCGGTATCCAGCTGTGAG	1047	Db	1407	GTGGAGACCATCCAGGCAAGCTCCTGAGCACTCATGACAGCCCTCCGTGAGGCCCTG	1466
Db	807	CAAGAAAAGATGATATATTTATCTCTTTTGGATCGGAAGAGCGGTATCCAGCTGTGAG	866	QY	2128	GCAGACGAGAAACGCGGCCCGAGACCCGCGCTGCTGTGCGCCACCCCGAGAGCTGCAG	2187
QY	1048	GACAGGACCTGCTCCCGGAATGATTTGACCCCGGAGCGCTGTGGATTCTCC	1107	Db	1467	GCAGACGAGAAACGCGGCCCGAGACCCGCGCTGCTGTGCGCCACCCCGAGAGCTGCAG	1526
Db	867	GACAGGACCTGCTCCCGGAATGATTTGACCCCGGAGCGCTGTGGATTCTCC	926	QY	2188	CCCCACCCGCGGCCCGAGACCCAGAGCTG	2217
QY	1108	ATGCTGAGCCGTACGCGGAAGCGCGACACGAGCGGAAGTCCATGGAAGTCTTGAGCATC	1167	Db	1527	CCCCACCCGCGGCCCGAGACCCAGAGCTG	1556
Db	927	ATGCTGAGCCGTACGCGGAAGCGCGACACGAGCGGAAGTCCATGGAAGTCTTGAGCATC	986	RESULT 15			
QY	1168	ACCGATGCGGGGTFGTGGCTCCCTGTACCCACCGCGCGCTTGGAGTGGCCAG	1227	US-10-283-247-4			
Db	987	ACCGATGCGGGGTFGTGGCTCCCTGTACCCACCGCGCGCTTGGAGTGGCCAG	1046	; Sequence 4, Application US/10283247			
QY	1228	CACAGCAGAGATCCCGTAGCTCAGTGGAGCCTCCAGGGTCTGTCTCCAGCCCTCTA	1287	; Publication No. US20030119037A1			
Db	1047	CACAGCAGAGATCCCGTAGCTCAGTGGAGCCTCCAGGGTCTGTCTCCAGCCCTCTA	1057	; GENERAL INFORMATION:			
QY	1288	AGCAGCCCAAGAGTCCGCTCTTTTCTTTTACCGGAGCCGCGGGCTGGAGATGAGGCT	1347	; APPLICANT: NEELAW, Beena et al.			
Db	1058	-----	1057	; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC			
QY	1348	CGAGGCGGGGCTCCCGGACTTCCAAAGCAGAGCTGCTTCTCAGGGGCCCGAGGGT	1407	; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES			
Db	1058	-----	1057	; FILE OF INVENTION: THEREOF			
QY	1408	GGGGGCGCGGGGAGCAGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCGGCC	1467	; FILE REFERENCE: CL001304			
Db	1058	-----	1057	; CURRENT APPLICATION NUMBER: US/10/283,247			
QY	1468	CCAGGCTCCCGGCTCTCTGCGGGAGCCCTTTCGCTCTGACATCGCCTCTGCACAGCCCGG	1527	; CURRENT FILING DATE: 2002-10-30			
Db	1058	-----	1057	; NUMBER OF SEQ ID NOS: 10			
QY	1528	GCCAGTCCCAACCGGAGCCCGGGGCAACACACCCCGCGCGGGTGGGCTCGG	1587	; SOFTWARE: FastSeq for Windows Version 4.0			
Db	1058	-----	1057	; SEQ ID NO 4			
QY	1588	GGAGCCGCTTGGAGGAGTGTCTCAACTCCATCCGCAACAGCTTCTGCGGCTCCCTCGC	1647	; LENGTH: 1911			
Db	1058	-----	1057	; TYPE: DNA			
QY	1648	TTTCAACCGGCGAAGATGAGTCCCTACCGCTGAGGAGATGTCAGCTTTCAGCCAGAG	1707	; ORGANISM: Homo sapiens			
Db	1058	-----	1057	; US-10-283-247-4			
QY	1708	TCCTCCCGGAGCTGGCAAAACGCTCTGTTTGGGAACTTCACTCTCTTGGAGCAAGAA	1767	Query Match			
Db	1058	-----	1057	Best Local Similarity 68.4%; Pred. No. 1.7e-221; Indels 129; Gaps 7;			
QY	1768	GAAACAATATTCCTCGTGTAAAGGACAAACCTCTCAGAGCATCAAGACAGACATCGTC	1827	Matches 1277; Conservative 0; Mismatches 462;			
Db	1058	-----	1057	QY 265 TTTAGTACCTGCTTCTGGAGCAGCTCTCGGGGGTGGAGCTATTTCGACTACCTGGTAAAG 324			
QY	1768	GAAACAATATTCCTCGTGTAAAGGACAAACCTCTCAGAGCATCAAGACAGACATCGTC	1827	Db 88 TATTGTACCTTGGTGTGTAGAACAGCTGTGAGTGTGAGCTTTCGACTACCTGGTGAAG 147			
Db	1058	-----	1057	QY 325 AAGGGAGAGCTGACCGCCCAAGAGGCGCCGAAAGTTCTTCGCGCAGATTGTCTGCGCTG 384			
QY	1768	GAAACAATATTCCTCGTGTAAAGGACAAACCTCTCAGAGCATCAAGACAGACATCGTC	1827	Db 148 AAGGGAGGCTGACCGCTAAGGAGGCTCGGAAGTTCTTCGCGCAGATCATCTCTGCGCTG 207			
Db	1058	-----	1057	QY 395 GACTTCTGCGCAGCTACTCTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG 444			
QY	1768	GAAACAATATTCCTCGTGTAAAGGACAAACCTCTCAGAGCATCAAGACAGACATCGTC	1827	Db 208 GACTTCTGCCACAGCCACTCCATATGCCACAGGATCTGAAACCTGAAACCTCTGCTG 267			
Db	1058	-----	1057	QY 445 GATGAGAAAAACACATCCGCAATTGACAGCTTCGCGATGGCGTCCCTGAGGTGGGGAC 504			
QY	1768	GAAACAATATTCCTCGTGTAAAGGACAAACCTCTCAGAGCATCAAGACAGACATCGTC	1827	Db 268 GACGAGAGAACACATCCGCAATCGCAGATTTTGGCATGGGCTCCCTGCGAGGTTGGCGAC 327			
Db	1058	-----	1057	QY 505 AGCTCTCTGGAGACAGCTGCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG 564			

328	Db		AGCCTGTTGGAGACAGCTGTGGGTGCCCCCACTACGCTGCCCGAGGTGATCCGGGGG	387
565	Qy	GAATAATATGATGTCGCGGCGAGACATGTGGAGCTGTGAGTCATCTCTCTCGCCCTG	624	
388	Db	GAGAGTATGACGCGCGGAGCGGAGCGTGTGGAGCTGCGGCGTATCTCTGTTGCGCTTG	447	
625	Qy	CTCGTGGGGCTCTGCCCTTTTGATGACGACAACTCCGCCAGCTGCTGGAGAAAGGTGAAA	684	
448	Db	CTGTGGGGGCTCTGCCCTTCGACGATGACAACTTGCGACAGCTGCTGGAGAGGTGAAG	507	
685	Qy	CGGGGCTCTTCACATGCCCCACTTCATTCCTCCAGATTGCCAGAGCTCTCTGAGGGGA	744	
508	Db	CGGGGCTGTTCACATGCCGCACTTTATCCGCGCACTTCATCCGCGCACTGCTACGCGGGC	567	
745	Qy	ATGATCGAAGTGGAGCCGGAAGAGCTCAGTCTGGAGCAAAATTCAGAAACATCTCTTGG	804	
568	Db	ATGATCGAGGTGAGCGCGCACGCGGCTCAGCGTAGAGACATTCAGAAACATATATGG	627	
805	Qy	TACCTAGCGGGAAACAGAGCCAGACCCGTGCTGGAGCCAGCCCTGCGCGCGGGTA	864	
628	Db	TATATAGGGGCAAGATGAGCCGAACC-----AGAGCAGCCCATTCCTCGCAAGGTG	681	
865	Qy	GCCATGCGGAGCTGCCATCCACGGAGAGCTGACCCCGACGCTCTAGAGAGCATGCGCA	924	
682	Db	CAGATCGCTCGTCTGCCGAGCTGTGGAGGACATCGACCCGACGCTGTGGACATCAC	741	
925	Qy	TCATCGGCTGCTTCAGGGACCGGAGAGGTGTCATCGAGCTGCGCAGTGGAGGAGGAG	984	
742	Db	TCATCGGCTGCTTCGAGAGCCGACACAGCTGCTGCAGGACCTGCTGTCGAGGAGGAG	801	
985	Qy	AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGTGTG	1044	
802	Db	AACCAGAGAGATGATTACTTCTCTCTCTGACCGGAAGAAAGTACCCGAGCAG	861	
1045	Qy	GAGGACAGGACTGCTCTCCCGGAATGATGTTGACCCCGGGAAGCGTGTGGAATCT	1104	
862	Db	GAGGATGAGGACCTGCCCCCGGAACGAGATAGACCTCTCCCGGAAGCGTGTGGAATCT	921	
1105	Qy	CCCATGCTGAGCGCTACGGAAGCGGACACGAGCGGAAGTCCATGGAAGTCTCTGAC	1164	
922	Db	CCGATGCTGAACCGGACAGCGACGCGGCGGCAGAACGCAATCCATGGAAGTCTCAGC	981	
1165	Qy	ATCACCGATGCGGGGGTGGTGGCTCCCTGTATCCCAACCGGAGCGGGCTTTGGAGATGCC	1224	
982	Db	GTGAC-----GGAGCGGGCTCCCGGTGCTCGCGGGGGGCCATTGAGATGCC	1032	
1225	Qy	CAGCACGACGAGATCCGTAGGCTCAGTGGAGCTTCACGGGTCTGTCTCTCAGCGCTT	1284	
1033	Db	CAGCACGCGCAGAGTAAAGCAATGTTCAAGTAAAGCCTGGATATCGCTGAGGCCATCCC	1092	
1285	Qy	CTAAGCAGCCCCAAGGAGTCCGGTCTTTTCTTTTTCACGGGAGCGGGGCTGGAGATGAG	1344	
1093	Db	CAATTTCAGCA-AAGAACAGGTCTC-----qGTC	1121	
1345	Qy	GCTCGAGCGGGGGCTCCCGACTTCAAAAACGACAGCGTGTCTCTCGGGGGCCCGAGG	1404	
1122	Db	CATCAGCGGTGCTCTCTCAGGCTTTTCCACGAGCCCACTCAGCAGCCCCGGGTGACCC	1181	
1405	Qy	GGTGGGGGCGCGGGGAGCAGCCCCCGCCCGCCAGTCCCGCTCCACACCCCTGCCCCGGC	1464	
1182	Db	TCACCCCTCAAGGGGCGAGTCCCTCCCG-----	1212	
1465	Qy	CCCCAGGCTCCCGCGCTCTCTGCGGGGAGCCCCCTTGCACTCGCCTCTGCAACGCCCC	1524	
1213	Db	-----ACCCCCAAGGGGAGCACTGTGTCACACGCCA	1242	
1525	Qy	CGGGCCAGTCCCAACCGGGAACCCGGGAGCAACACACACCCCGCCCGCGGTGGCGTC	1584	
1243	Db	AAGGAGAGCCGGTGGGACGCCCCAACCCCGCCCGCTCCAGCCCC-----AGGTC	1296	
1585	Qy	GGGGAGCGCGCTGGAGAGTGTCTCAATTCATTCGCAACAGTTCCTTGGGTCCCTCT	1644	

Db	1297	GGAGGGGTGCCCTGGAGGGCGGGCTCAA	CTCCATCAAGAACAGAGCTTTCTGGGGCTCACCC	1356
Qy	1645	CGCTTTTCACCGCGCAAGATGCAGGTCCTTACCGCTGAGAGATGTCACAGTCTTGACGCCA	1704	
Db	1357	CGCTTTCACCGCGCGGAAACTGCAAGTTCGACGCCCGGAGGAGATGTCACAACTGCACCA	1416	
Qy	1705	GAGTCTCTCCCGGAGCTGGCAAAACGCTCCTGGTTCGGGAACTTCATCTCTTGGACAAA	1764	
Db	1417	GAGTCGCTCCCGAGCTGGCGAAGAAAGTCTGGTTTGGGAACTTTCATCAGCCTGGGAGAAG	1476	
Qy	1765	GAAGAACAAATATNTCTCGTGTCTAAAGGACAAACCTCTCAGCAGCATCAAGAGACATC	1824	
Db	1477	GAGGAGCAGATCTTCGTGGTGCATCAAGACAAACCTCTGAGCTCCATCAAGGCTGCATCT	1536	
Qy	1825	GTCCATGCCCTTCTGTGTCATCCCGAGCTGAGTGCAGTGTGCTGTGCACAGACCAAGCTTC	1884	
Db	1537	GTGCACGCCCTTCTGTGATTTCCAGTCTCAGCCACAGCGTATCTTCCAAACGAGCTTC	1596	
Qy	1885	AGGCCCGAGTACAAGGCCAGTGGCGGCCCTCCGTCTTCCAAAAGCCGCTCCGCTTCCAG	1944	
Db	1597	CGGGCCGAGTACAAGGCCACCGGGGGGCCAGCGGTGTCCAGAAAGCCGCTCAAGTTCCAG	1656	
Qy	1945	GTGACATCAGCTCCTCTGAGGGTCCAGAGCCCTCCCGCGACGGGACGGCAGCGAGGT	2004	
Db	1657	GTTGATATCACCTACACGGAGGT-----GGGGAGGCGCAGAGGAG	1698	
Qy	2005	GGTGGCATCTACTCCGCTCACCTTCATCTCGGGTCCAGCGCGTCCGGTTCAGCGA	2064	
Db	1699	AACGGCATCTACTCCGCTCACCTTCACCGTCTCTCAGGCCCCAGCGCTCGCTTCAAGAGG	1758	
Qy	2065	GTGGTGAGACCATTCAGGCACAGCTCCTGAGCATCTCATGACAGGCCCTCCGTGCGAGGCC	2124	
Db	1759	GTGGTGAGACCATTCAGGCCCCAGCTGCTGAGGCACACAGACCCGCTCTGGGCCACAGCAC	1818	
Qy	2125	CTGGCAGA	2132	
Db	1819	TTGTGCA	1826	

Search completed: February 19, 2005, 17:04:03  
Job time : 1219 secs

— This Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 08:09:53 ; Search time 9587 Seconds  
(without alignments)  
11569.207 Million cell updates/sec

Title: US-10-803-277-3  
Perfect score: 2289  
Sequence: 1 atgggaacttgagtttggttt.....acgggaacccctctgcctga 2289

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hgc.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pi.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match %	Length DB ID		
1	2020.2	88.3	2385	6	AX166526 Sequence
2	2020.2	88.3	2576	6	BD185210 Novel Gen
3	2020.2	88.3	2576	9	AB058714 Homo sapi
4	2020.2	88.3	2870	9	AY458602 Homo sapi
5	2020.2	88.3	2897	6	AX642966 Sequence
6	2020.2	88.3	3007	9	AF479826 Homo sapi
7	2020.2	88.3	3109	9	AF479827 Homo sapi
8	1839	80.3	2799	6	BD186023 Cell cycl
9	1727.8	75.5	2331	10	AY533671 Mus muscu
10	1510.4	66.0	1902	6	CQ841950 Sequence
11	1510.4	66.0	1902	9	AK124999 Homo sapi
12	1473.6	64.4	2128	9	BC016681 Homo sapi
13	1033.2	45.1	1623	6	CQ727250 Sequence
14	980	42.8	1797	6	AR541973 Sequence
15	780.4	34.1	3364	6	AR232171 Sequence
16	778.8	34.0	2908	6	AR232170 Sequence
17	777.2	34.0	1827	6	AX661193 Sequence
18	777.2	34.0	2007	6	AX661191 Sequence
19	777.2	34.0	2647	6	AX766346 Sequence

20	777.2	34.0	3576	9	AK131534	Homo sapi
21	776	33.9	4133	10	AK173268	Mus muscu
22	775.6	33.9	3117	9	AF533876	Homo sapi
23	775.6	33.9	3516	9	AY166857	Homo sapi
24	775.6	33.9	3586	9	AF533879	Homo sapi
25	773.2	33.8	1956	9	HSAG701	Homo sapi
26	773.2	33.8	2025	6	AX327995	Sequence
27	773.2	33.8	2025	6	AX750714	Sequence
28	773.2	33.8	2219	6	AX327993	Sequence
29	773.2	33.8	3164	9	AF533877	Homo sapi
30	773.2	33.8	3212	9	AF533880	Homo sapi
31	773.2	33.8	3532	9	AK122851	Homo sapi
32	773.2	33.8	4888	9	AF533878	Homo sapi
33	772.8	33.8	2160	10	AY533674	Mus muscu
34	772.6	33.8	4055	10	AY660739	Mus muscu
35	770.4	33.7	2028	10	AY533673	Mus muscu
36	769.4	33.6	1962	10	AY533672	Mus muscu
37	690	30.1	3342	10	BC056498	Mus muscu
38	541	23.6	1014	9	HSB803233	Homo sapi
39	491.8	21.5	3156	9	AK074411	Homo sapi
40	463.8	20.3	1115	6	CQ731316	Sequence
41	408.4	17.8	38000	9	AC008974	Homo sapi
42	371	16.2	134793	9	AC020922	Homo sapi
43	337.2	14.7	2720	6	CQ585216	Sequence
44	337.2	14.7	5609	3	AY080288	Drosophil
45	315.2	13.8	226060	2	AC079583	Mus muscu

ALIGNMENTS

RESULT 1  
AX166526  
LOCUS AX166526 2385 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 17 from Patent WO0138503.  
ACCESSION AX166526  
VERSION AX166526.1 GI:14546871  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,  
Flanagan,P. and Clary,D.S.  
TITLE Novel human protein kinases and protein kinase-like enzymes  
JOURNAL Patent: WO 0138503-A 17 31-MAY-2001,  
Sugen, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..2385  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 88.3%; Score 2020.2; DB 6; Length 2385;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 202; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 265 TTTAGGTACTGTTCTGGAGCAGCTTCGGGGGTGAGCTATTCGACTACCTGTTAAAG 324  
Db 361 TATTGTGACCTGTTCTGGAGCAGCTTCGGGGGTGAGCTATTCGACTACCTGTTAAAG 420  
Qy 325 AAGGGGAGACTGACGCCCAAGGAGGCCCGCAAGTTCTTCGCGAGATTGTCTGCGCTG 384  
Db 421 AAGGGGAGACTGACGCCCAAGGAGGCCCGCAAGTTCTTCGCGAGATTGTCTGCGCTG 480  
Qy 385 GACTTCTGCCACAGCTACTCCATCTGCGACAGACCTAAAGCCCGAGAACCTGCTTTTG 444  
Db 481 GACTTCTGCCACAGCTACTCCATCTGCGACAGACCTAAAGCCCGAGAACCTGCTTTTG 540  
Qy 445 GATGAGAAAAACATCCGCATTGCGAGCTTGGCATGGGCTCCCTCGAGTGGGGAC 504



FEATURES		Location/Qualifiers		Query Match	
source	FT	CDS	Location/Qualifiers	Best Local Similarity	Matches 2022; Conservative
1. .2576			/organism="Homo sapiens"	88.3%; Score 2020.2; DB 6; Length 2576;	0; Mismatches 3; Indels 0; Gaps 0;
/mol_type="genomic DNA"					
ORIGIN					
Qy	265	TTTAGTACCTGGTCTCGAGCAGCTCTCGGGGGTGAGCTATTGCACTACTCGTAAAG	324	1165	ATCACCGATGCCGGGGTGGTGGCTCCCTGTATCCACCCGACGGGGCTTGGAGATGGCC
Db	125	TATTTGTACTGGTCTCGAGCAGCTCTCGGGGGTGAGCTATTGCACTACTCGTAAAG	184	1025	ATCACCGATGCCGGGGTGGTGGCTCCCTGTATCCACCCGACGGGGCTTGGAGATGGCC
Qy	325	AAGGGAGACTGACGCCCAAGAGGCCGGAAGTTCTTCCGCCAGATTGTCTGCGCTG	384	1225	CAGCACAGCAGAGATCCCGTAGCGTCACTAGTGGAGCTTCCAGCGTCTGTCTCCAGCCCT
Db	185	AAGGGAGACTGACGCCCAAGAGGCCGGAAGTTCTTCCGCCAGATTGTCTGCGCTG	244	1085	CAGCACAGCAGAGATCCCGTAGCGTCACTAGTGGAGCTTCCAGCGTCTGTCTCCAGCCCT
Qy	385	GACTTCTGCCACAGTACTCTCATCTGCGACAGACCTTAAAGCCCGAAGCTCTTTTG	444	1285	CTAAGCAGCCAAAGAGTCCGGTCTTTTCTTTTTCACCGAGCCGGGGCTTGGAGATGAG
Db	245	GACTTCTGCCACAGTACTCTCATCTGCGACAGACCTTAAAGCCCGAAGCTCTTTTG	304	1145	CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACCGAGCCGGGGCTTGGAGATGAG
Qy	445	GATGAGAAAAACAATCCGCAATTGACAGACTTTCGCGATGGCGTCCCTGCAAGTGGGGAC	504	1345	GCTCGAGCGGGGCTCCCGACTTTCAAAACGAGACGCTGCTTCTCGGGGGCCCGAGG
Db	305	GATGAGAAAAACAATCCGCAATTGACAGACTTTCGCGATGGCGTCCCTGCAAGTGGGGAC	364	1205	GCTCGAGCGGGGCTCCCGACTTTCAAAACGAGACGCTGCTTCTCGGGGGCCCGAGG
Qy	505	AGCTCTCTGGAGACAGCTGCGGGTCCCGCCATTTATGCTGTCAGAGGTGATTAAAGGG	564	1405	GGTGGGGCGCGGGGAGACGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCCGCG
Db	365	AGCTCTCTGGAGACAGCTGCGGGTCCCGCCATTTATGCTGTCAGAGGTGATTAAAGGG	424	1265	GGTGGGGCGCGGGGAGACGCCCGCCCGCCAGTGCCTCCACACCCCTGCGCCGCG
Qy	565	GAATAATATGATGGCGCGCGGACAGACATGTGGAGTCACTCTCTCGCCCTG	624	1465	CCCCAGGCTCTCCCGCGCTCTCTGCGGGGACCCCTTTGCACTCGCTCTGCAACAGCCC
Db	425	GAATAATATGATGGCGCGCGGACAGACATGTGGAGTCACTCTCTCGCCCTG	484	1325	CCCCAGGCTCTCCCGCGCTCTCTGCGGGGACCCCTTTGCACTCGCTCTGCAACAGCCC
Qy	625	CTCGTGGGGCTCTGCGCTTTTGATGACGACCAACTCCGCCAGCTGCTGGAGAGGTGAAA	684	1525	CGGGCAATGCCACCGGACCCCGGGGACAAACACACCCCGCCAGCCCGGGTGGCGTC
Db	485	CTCGTGGGGCTCTGCGCTTTTGATGACGACCAACTCCGCCAGCTGCTGGAGAGGTGAAA	544	1385	CGGGCAATGCCACCGGACCCCGGGGACAAACACACCCCGCCAGCCCGGGTGGCGTC
Qy	685	CGGGGCTCTTCCATGCGCCCATTTTCATTTCTCCAGATTGCGAGAGCTCTCGAGGGGA	744	1585	GGGGAGCGCGCTGGAGAGTCTCAACTCCATCCGCAACAGCTTCTTGGGGTCCCT
Db	545	CGGGGCTCTTCCATGCGCCCATTTTCATTTCTCCAGATTGCGAGAGCTCTCGAGGGGA	604	1445	GGGGAGCGCGCTGGAGAGTCTCTCAACTCCATCCGCAACAGCTTCTTGGGGTCCCT
Qy	745	ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG	804	1645	CGCTTTTCAACGGGCAAGATGCAGTCCCTTACCCCTGAGGAGATGTCCAGTTTGAAGCA
Db	605	ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTGG	664	1505	CGCTTTTCAACGGGCAAGATGCAGTCCCTTACCCCTGAGGAGATGTCCAGTTTGAAGCA
Qy	805	TACCTAGGGGGGAAAAACAGAGCCGACAGCCCGTCCCTGGAGCCAGCCCTTGGCCGGGATA	864	1705	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGGTTCGGGAATTCATCTCTTGGACAAA
Db	665	TACCTAGGGGGGAAAAACAGAGCCGACAGCCCGTCCCTGGAGCCAGCCCTTGGCCGGGATA	724	1565	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGGTTCGGGAATTCATCTCTTGGACAAA
Qy	865	GCCATGCGGAGCTGCCATCCAAACGAGAGCTGGACCCCGAGCTCTTAGAGAGCATGGCA	924	1765	GAAGAACAAATATTCCTCGTGTAAAGACAAACCTCTCAGCAGCATCAAAAGCAGATC
Db	725	GCCATGCGGAGCTGCCATCCAAACGAGAGCTGGACCCCGAGCTCTTAGAGAGCATGGCA	784	1625	GAAGAACAAATATTCCTCGTGTAAAGACAAACCTCTCAGCAGCATCAAAAGCAGATC
Qy	925	TCACTGGGCTGCTTCAAGGACCGGAGAGCTGCATCCGAGCTGCGCAGTGAGAGGAG	984	1825	GTCCATGCTTCTGTGTCGATCCCGAGCTGAGTCACTAGTGTGTGTCAAGACAGCTTC
Db	785	TCACTGGGCTGCTTCAAGGACCGGAGAGCTGCATCCGAGCTGCGCAGTGAGAGGAG	844	1685	GTCCATGCTTCTGTGTCGATCCCGAGCTGAGTCACTAGTGTGTGTCAAGACAGCTTC
Qy	985	AACCAAGAAAAAGATGATATATTCTGCTTTTGGATTCGGAAGAGCGGTATCCAGAGCTGT	1044	1885	AGGGCCGAGTACAAGGCGCAGTGGCGGCCCTCCGCTTCTTCCAAAAGCCGCTCCGATC
Db	845	AACCAAGAAAAAGATGATATATTCTGCTTTTGGATTCGGAAGAGCGGTATCCAGAGCTGT	904	1745	AGGGCCGAGTACAAGGCGCAGTGGCGGCCCTCCGCTTCTTCCAAAAGCCGCTCCGATC
Qy	1045	GAGGACAGGACCTGCTCCCGGAATGATGTTGACCCCGCCCGGAGAGCGTGTGGAATCT	1104	1945	GTGGAATCAGTCTCTGAGGGTCCAGAGCCCTCCCGGAGCGGAGCGGAGGT
Db	905	GAGGACAGGACCTGCTCCCGGAATGATGTTGACCCCGCCCGGAGAGCGTGTGGAATCT	964	1805	GTGGAATCAGTCTCTGAGGGTCCAGAGCCCTCCCGGAGCGGAGCGGAGGT
Qy	1105	CCCATGCTGAGCGTCAACGGGAAGCGGCGACCAAGAGCGGAGTCCATGGAAGTCTTGAGC	1164	2005	GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGCTCGGTTCAGCGA
Db	965	CCCATGCTGAGCGTCAACGGGAAGCGGCGACCAAGAGCGGAGTCCATGGAAGTCTTGAGC	1024	1865	GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGCTCGGTTCAGCGA



Db	2105	AAGGACAAAGAGTCTCGCCACCAACGAGCCCTCTCGCCCTGA	2149		185	AAGGGGAGACTGACGCCCAAGAGGCGCGAAAGTTCTTCGCCAGATTGTGTCTGCGCTG	244
RESULT 3	AB058714	2576 bp mRNA linear	PRI 05-JUN-2001				
LOCUS	Homo sapiens mRNA for KIAA1811 protein, partial cds.						
ACCESSION	AB058714				QY	385	GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG
VERSION	AB058714.1	GI:14017838			Db	245	GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG
KEYWORDS					QY	445	GATGAGAAAAACAACATCCGATGTCAGATTTCGGCATGGGCTCCCTGCAAGTGGGGGAC
SOURCE	Homo sapiens (human)				Db	305	GATGAGAAAAACAACATCCGATGTCAGACTTCGGCATGGGCTCCCTGCAAGTGGGGGAC
ORGANISM	Homo sapiens				QY	505	AGCCTCTCTGGAGACAGCTGCGGGTCCGCCCATTTATGCTGTCTCAGAGGTGATTAAAGGGG
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Db	365	AGCCTCTCTGGAGACAGCTGCGGGTCCGCCCATTTATGCTGTCTCAGAGGTGATTAAAGGGG
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				QY	565	GAATAATATGATGGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCATCTCTGCGCCCTG
REFERENCE	1 (sites)				Db	425	GAATAATATGATGGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCATCTCTGCGCCCTG
AUTHORS	Nagase, T., Nakayama, M., Nakajima, D., Kikuno, R. and Ohara, O.				QY	625	CTCGTGGGGGCTCTGCGCTTTGATGACGACAACTCTCGCAGCTGTCTGGAGAGGTGAAA
TITLE	Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro				Db	485	CTCGTGGGGGCTCTGCGCTTTGATGACGACAACTCTCGCAGCTGTCTGGAGAGGTGAAA
JOURNAL	DNA Res. 8 (2), 85-95 (2001)				QY	685	CGGGGGCTCTTCCACATGCCCATCTTCAATCTCCATGTCAGATTGCGCAGAGCTCTCTGAGGGA
MEDLINE	21245130				Db	545	CGGGGGCTCTTCCACATGCCCATCTTCAATCTCCATGTCAGATTGCGCAGAGCTCTCTGAGGGA
PUBMED	11347906				QY	745	ATGATCGAAGTGGAGCCCGGAAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTCTGG
REFERENCE	2 (bases 1 to 2576)				Db	605	ATGATCGAAGTGGAGCCCGGAAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTCTGG
AUTHORS	Ohara, O., Nagase, T. and Kikuno, R.				QY	805	TACCTAGGCGGGAACACAGAGCAGACCCGCTGCTGGAGCCAGCCCTTGGCCCGCGGGTA
TITLE	Direct Submission				Db	665	TACCTAGGCGGGAACACAGAGCAGACCCGCTGCTGGAGCCAGCCCTTGGCCCGCGGGTA
JOURNAL	Submitted (27-MAR-2001) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba				QY	865	GCCATGCGGAGCTGCCATCCAAACGAGAGCTGGACCCGACCTCTTAGAGAGCATGCGCA
	292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913, Fax:81-438-52-3914)				Db	725	GCCATGCGGAGCTGCCATCCAAACGAGAGCTGGACCCGACCTCTTAGAGAGCATGCGCA
FEATURES	Location/Qualifiers				QY	925	TCACTGGGCTGCTTTCAGGAGCCGCGAGAGCTGCAATCGCAGCTGCGCAGTGGAGAGAG
source	1..2576				Db	785	TCACTGGGCTGCTTTCAGGAGCCGCGAGAGCTGCAATCGCAGTGGAGAGAGAGAG
	/organism="Homo sapiens"				QY	985	AACCAAGAAAAAGATATATATATATCTGCTTTTGGATTCGGAAGAGCGGTATCCAGCTGT
	/mol_type="mRNA"				Db	845	AACCAAGAAAAAGATATATATATATCTGCTTTTGGATTCGGAAGAGCGGTATCCAGCTGT
	/db_xref="taxon:9606"				QY	1045	GAGGACACGAGCTGCTCCCGGGAATGATGTTGATGACCCCGGAGCGGTATCCAGCTGT
	/clone="ha06731"				Db	905	GAGGACACGAGCTGCTCCCGGGAATGATGTTGATGACCCCGGAGCGGTATCCAGCTGT
	/tissue_type="brain"				QY	1105	CCCATGCTGAGCCGTCAACGGAAGCGGCGACACAGAGCGGAGTCCATGGAAGTCTGAGC
gene	1..2576				Db	965	CCCATGCTGAGCCGTCAACGGAAGCGGCGACACAGAGCGGAGTCCATGGAAGTCTGAGC
CDS	<1..2149				QY	1165	ATCACCGATGCGGGGGTGGTGGCTCCCTGTACCCACCGCAGCGGCTTGGAGATGCCC
	/gene="KIAA1811"				Db	1025	ATCACCGATGCGGGGGTGGTGGCTCCCTGTACCCACCGCAGCGGCTTGGAGATGCCC
	/notes="Start codon is not identified."				QY	1225	CAGCAGCCAGAGATCCCGTAGCTCAGTGAGAGCTCCAGGGTCTGCTCTCCAGCCCT
	/codon_start=2				Db	1085	CAGCAGCCAGAGATCCCGTAGCTCAGTGAGAGCTCCAGGGTCTGCTCTCCAGCCCT
	/product="KIAA1811 protein"				QY	1285	CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACCGGAGCGGGGGTGGAGATGAG
	/protein_id="BAB47440.1"				Db	1145	CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACCGGAGCGGGGGTGGAGATGAG
	/db_xref="GI:14017839"				QY	1345	GCTCGAGGGGGGGTCTCCCGCATTCACAAAAACGACAGACGCTGCTTCTCGGGGGCCCCAGG
	/translations="IVNRKLGESVLMKVERIAILKLTIEHPVLKLDHYENKKLYL LVLEHVGSLFDYLVKGLRTPKEARFROIIVSALDFCHSYISCHRDLPENLLLD EKXNRIADFMASLQVDSILLETSCGSPHYACPEVIKGEYDGRADMWCSGLTFA LLVGLPDDNNLRQLKRGVFMFHFIPDQSLLRGMIEVEPEKRLSLQIQK HPWYLGCKHDPDLCDFAPGRVAMKSLPSNGELDPDLVESNASLGCPRDRERLHREL RSEENQEKMIYYLLDRKERYPSDDQDLPDRNDVDPKRKVDSPMLSRHGRPER KSMVELSI1DAGGGSPVTKTQTLPSRPGGGAGQPPPPPSARSTPLPGPSPRSSG SPREGDEARGGSPSTKTQTLPSRPGGGAGQPPPPPSARSTPLPGPSPRSSG GTPHLSPLHTPRASPTGTPTPPSPSGGVGGAARSLNIRNSLFSRPREHRKM QVPAEEMSLTPESSPELAKSNFNLSDKEQIQFLVLKDFLSSIKADIVHAFI SIPLSHSLVLSQTSFRAEYKASGSPVFOKPVRFQVDSSEGGPEPSPRRDSGGGI YSVTFPLDISGSRFRVETIQALLSTHDPFSQALADEKNGAOTRPAAPPRLSQ PPGCRPDPELSSPRRPPPKDKLLATNGTLP"				Db	1265	GCTCGAGGGGGGGTCTCCCGCATTCACAAAAACGACAGACGCTGCTTCTCGGGGGCCCCAGG
					QY	1405	GGTGGGGGGCGCGGGGAGCAGCCCGCCCCCGCCAGTCCCGCTCCACACCCCTGCGCCGCG
					Db	1265	GGTGGGGGGCGCGGGGAGCAGCCCGCCCCCGCCAGTCCCGCTCCACACCCCTGCGCCGCG
					QY	1325	AAGGGGAGACTGACGCCCAAGAGGCGCGGAAAGTTCTTCGCCAGATTGTGTCTGCGCTG
					Db	1345	GGT



QY 805 TACTAGGCGGGAACACAGAGCCAGACCCGCTGCTGAGCCAGCCCTTGGCGCGCGGTA 864  
DB |||||  
QY 902 TACTAGGCGGGAACACAGAGCCAGACCCGCTGCTGAGCCAGCCCTTGGCGCGGTA 961  
DB |||||  
QY 865 GGCATGCGGAGCCTGCGCATCAACGAGAGCTGGAACCCGAGCTCTTGAAGAGCATGGCA 924  
DB |||||  
QY 925 TCACTGGGCTGCTTACGGAGCCGAGAGGCTGCATCGGAGCTGCGCAGTGAAGAGGAG 984  
DB |||||  
QY 1022 TCACTGGGCTGCTTACGGAGCCGAGAGGCTGCATCGGAGCTGCGCAGTGAAGAGGAG 1081  
DB |||||  
QY 985 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044  
DB |||||  
QY 1082 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1141  
DB |||||  
QY 1045 GAGGACAGAGCCTGCTCCCGGAATGATGTTGAACCCCGGAGAGCGTGTGATTTCT 1104  
DB |||||  
QY 1142 GAGGACAGAGCCTGCTCCCGGAATGATGTTGAACCCCGGAGAGCGTGTGATTTCT 1201  
DB |||||  
QY 1105 CCNATGCTGAGCCGTCACGGGAGCGGACGAGCGGAAGTCCATGGAAGTCTCTGAGC 1164  
DB |||||  
QY 1202 CCCATGCTGAGCCGTCACGGGAGCGGACGAGCGGAAGTCCATGGAAGTCTCTGAGC 1261  
DB |||||  
QY 1165 ATCAACGATGCGGGGGTGTGGCTCCCTGTATCCACCGAGCGGCTTTGGAGATGGCC 1224  
DB |||||  
QY 1262 ATCAACGATGCGGGGGTGTGGCTCCCTGTATCCACCGAGCGGCTTTGGAGATGGCC 1321  
DB |||||  
QY 1225 CAGCACAGCAGAGATCCCGTAGGCTCAGTGGAGCCTTCAAGGCTCTGCTCTCAGCCCT 1284  
DB |||||  
QY 1322 CAGCACAGCAGAGATCCCGTAGGCTCAGTGGAGCCTTCAAGGCTCTGCTCTCAGCCCT 1381  
DB |||||  
QY 1285 CTAGACGACCAAGAGTCCGCTCTTTTTCACCGAGCGGGGCTGGAGATGAG 1344  
DB |||||  
QY 1382 CTAGACGACCAAGAGTCCGCTCTTTTTCACCGAGCGGGGCTGGAGATGAG 1441  
DB |||||  
QY 1345 GCTCAGGCGGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCTCGGGGCCCCCAGG 1404  
DB |||||  
QY 1442 GCTCAGGCGGGGGCTCCCGACTTCCAAACGAGAGCTGCTTCTCGGGGCCCCCAGG 1501  
DB |||||  
QY 1405 GGTGGGGCGCGGGGAGCAGCCCGCCCGAGTGGCGCTCCACACCCCTGCCCGGC 1464  
DB |||||  
QY 1502 GGTGGGGCGCGGGGAGCAGCCCGCCCGAGTGGCGCTCCACACCCCTGCCCGGC 1561  
DB |||||  
QY 1465 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGACTCGCTCTGCAACGCC 1524  
DB |||||  
QY 1562 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGACTCGCTCTGCAACGCC 1621  
DB |||||  
QY 1525 CGGGCCAGTCCACCGGACCCCGGGGACACACACCCCGAGCCCGGGGTGGGCTC 1584  
DB |||||  
QY 1622 CGGGCCAGTCCACCGGACCCCGGGGACACACACCCCGAGCCCGGGGTGGGCTC 1681  
DB |||||  
QY 1585 GGGGAGCGGCTGAGAGTCTGCTCACTCCATCCGACAGCTTCTGGGCTCCCT 1644  
DB |||||  
QY 1682 GGGGAGCGGCTGAGAGTCTGCTCACTCCATCCGACAGCTTCTGGGCTCCCT 1741  
DB |||||  
QY 1645 GCCTTTACCGGCGCAGATGAGTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCCA 1704  
DB |||||  
QY 1742 GCCTTTACCGGCGCAGATGAGTCCCTACCGCTGAGGAGATGTCCAGCTTGAGGCCA 1801  
DB |||||  
QY 1705 GAGTCTCCCGGAGCTGGCAAAACGCTCTGTTGGGAACTTCTCTCTTGGACAAA 1764  
DB |||||  
QY 1802 GAGTCTCCCGGAGCTGGCAAAACGCTCTGTTGGGAACTTCTCTCTTGGACAAA 1861  
DB |||||  
QY 1765 GAAGAACAAATATCTCGTCTGAAGGACAAACCTCTCAGCAGATCAAAAGCAGACATC 1824  
DB |||||  
QY 1862 GAAGAACAAATATCTCGTCTGAAGGACAAACCTCTCAGCAGATCAAAAGCAGACATC 1921  
DB |||||  
QY 1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTCTGTCAAGACAGGCTTC 1884  
DB |||||  
QY 1922 GTCCATGCTTTCTGTGATCCCGAGCTGAGTCAAGTGTCTGTCAAGACAGGCTTC 1981  
DB |||||  
QY 1885 AGGGCGGAGTACAAGCCAGTGGGGCCCTCGTCTTCCAAAAGCCCGTCCGCTTCCAG 1944  
DB |||||

DB 1982 AGGGCGGAGTACAAGCCAGTGGGGCCCTTCCGCTTTTCCAAAAGCCCGTCCGCTTCCAG 2041  
QY |||||  
DB 1945 GTGGACATCAGCTCTCTGAGGCTCCAGAGCCCTCCCGCGACGCGGAGCGGAGGAGT 2004  
QY |||||  
DB 2042 GTGGACATCAGCTCTCTGAGGCTCCAGAGCCCTCCCGCGACGCGGAGCGGAGGAGT 2101  
QY |||||  
DB 2005 GTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGCTCCAGCCGCTCGGTTCAAGGA 2064  
QY |||||  
DB 2102 GTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGCTCCAGCCGCTCGGTTCAAGGA 2161  
QY |||||  
DB 2065 GTGGTGAGACCATCCAGGACAGCTCTGAGCAGCTCATGACGAGCCCTCGTGAGGAG 2124  
QY |||||  
DB 2162 GTGGTGAGACCATCCAGGACAGCTCTGAGCAGCTCATGACGAGCCCTCGTGAGGAG 2221  
QY |||||  
DB 2125 CTGGCAGACGAGAAAGCGGGCCAGACCCGGGCTCTGCTGGTGGCCCAACCCCGAGGCTG 2184  
QY |||||  
DB 2222 CTGGCAGACGAGAAAGCGGGCCAGACCCGGGCTCTGCTGGTGGCCCAACCCCGAGGCTG 2281  
QY |||||  
DB 2185 CAGCCCGGACCCCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGAGCCCGCC 2244  
QY |||||  
DB 2282 CAGCCCGGACCCCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGGAGGAGCCCGCC 2341  
QY |||||  
DB 2245 AAGGACAGAGCTCTCTGGCCACCAAGGAGCCCTCTGCGCTGA 2289  
QY |||||  
DB 2342 AAGGACAGAGCTCTCTGGCCACCAAGGAGCCCTCTGCGCTGA 2386  
QY |||||

RESULT 5  
AX642966 2897 bp DNA linear PAT 24-FEB-2003  
LOCUS Sequence 43 from Patent WO01096547.  
DEFINITION AX642966  
ACCESSION AX642966  
VERSION AX642966.1 GI:28550113  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Yue H., Lai P., Bandman O., Borowsky M., Au-Young J., Lu Y.,  
Greenwald S.R., Ramkumar J., Griffin J.A., Kearney L., Burford N.,  
Nguyen D.B., Tang Y.T., Baughn M.R., He A., Thornton M.,  
Hafalia A., Patterson C., Gururajan R., Lo T.P., Khan F.,  
Recipon S.A., Azimzai Y., Policky J.L., Ding L., Grether M.,  
Elliot V.S., Thangavelu K., Batra S. and Ison C.H.  
HUMAN KINASES  
TITLE Patent: WO 01096547-A 43 20-DEC-2001;  
JOURNAL Incyte Genomics, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..2897  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Incyte ID No: 7477486CB1"

ORIGIN  
Query Match 88.3%; Score 2020.2; DB 6; Length 2897;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 265 TTTAGGTACCTGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTTCAGCTACCTGGTAAAG 324  
DB 361 TATTGTACCTGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTTCAGCTACCTGGTAAAG 420  
QY 325 AAGGGAGAGCTGACCGCCAAAGGAGGCCGAAAGTTCTTCGCCAGATTTGTCTGCGCTG 384  
DB 421 AAGGGAGAGCTGACCGCCAAAGGAGGCCGAAAGTTCTTCGCCAGATTTGTCTGCGCTG 480  
QY 385 GACTTCTGCCACAGCTACTCCATCTGCCCACAGAGACCTTAAGCCCGAGACCTGCTTTTG 444  
DB 481 GACTTCTGCCACAGCTACTCCATCTGCCCACAGAGACCTTAAGCCCGAGACCTGCTTTTG 540

QY 445 GATGAGAAAACAAATCCGATTCGACATTCCTGGCATGGCTCCCTCCGACGAGTGGGGAC 504  
DB 541 GATGAGAAAACAAATCCGATTCGACATTCCTGGCATGGCTCCCTCCGACGAGTGGGGAC 600  
QY 505 AGCTCTCTGGAGACAGTGGGGTCCCGCCCATTCATTCGCTGTCAGAGGTGATTAAGGGG 564  
DB 601 AGCTCTCTGGAGACAGTGGGGTCCCGCCCATTCATTCGCTGTCAGAGGTGATTAAGGGG 660  
QY 565 GAAAAATATGATGCGCGCGGACAGATGTTGGAGCTGTGAGTATCCTCTTCGCGCTG 624  
DB 661 GAAAAATATGATGCGCGCGGACAGATGTTGGAGCTGTGAGTATCCTCTTCGCGCTG 720  
QY 625 CTCTGCGGGCTCTGCGCTTGTGAGACAACTCCGACGCTGCTGGAGAGGTGAAA 684  
DB 721 CTCTGCGGGCTCTGCGCTTGTGAGACAACTCCGACGCTGCTGGAGAGGTGAAA 780  
QY 685 CGGGCGCTTTCACATGCCCCCATTCATTCCTCCAGATTGCCAGAGCTCCTGAGGGGA 744  
DB 781 CGGGCGCTTTCACATGCCCCCATTCATTCCTCCAGATTGCCAGAGCTCCTGAGGGGA 840  
QY 745 ATGATCGAATGAGCGCGGAAAAAGGCTAGTCTGAGCAAAATTCAGAAACATCTCTGG 804  
DB 841 ATGATCGAATGAGCGCGGAAAAAGGCTAGTCTGAGCAAAATTCAGAAACATCTCTGG 900  
QY 805 TACCTAGCGGGAACAGAGCCAGACCGCTGCTGAGCCAGCCCTGCGCGCGGGTA 864  
DB 901 TACCTAGCGGGAACAGAGCCAGACCGCTGCTGAGCCAGCCCTGCGCGCGGGTA 960  
QY 865 GCCATGCGGAGCTGCCATCCAGCGAGAGCTGACCCCGACGCTCTAGAGAGCATGGCA 924  
DB 961 GCCATGCGGAGCTGCCATCCAGCGAGAGCTGACCCCGACGCTCTAGAGAGCATGGCA 1020  
QY 925 TCACTGGGCTCTTTCAGGGAACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAAGGAG 984  
DB 1021 TCACTGGGCTCTTTCAGGGAACCGGAGAGGCTGATCGCGAGCTGCGCAGTGAAGGAG 1080  
QY 985 AACCAAGAAAGATGATATATATCTGCTTTGATCGGAAGAGCGGTATCCAGCTGT 1044  
DB 1081 AACCAAGAAAGATGATATATATCTGCTTTGATCGGAAGAGCGGTATCCAGCTGT 1140  
QY 1045 GAGGACGAGACCTGCTCCCGGAATGATGTTGACCCCGGAGCGGTGATGTTCT 1104  
DB 1141 GAGGACGAGACCTGCTCCCGGAATGATGTTGACCCCGGAGCGGTGATGTTCT 1200  
QY 1105 CCAATGCTGAGCCGTCAAGGGAAGCGGACGAGCGGAGTCCATGGAAGTCTTGAGC 1164  
DB 1201 CCAATGCTGAGCCGTCAAGGGAAGCGGACGAGCGGAGTCCATGGAAGTCTTGAGC 1260  
QY 1165 ATCAACGATGCGGGGTGTTGGCTCCCTGTATCCCAACCGAGCGGCTTGGAGATGGCC 1224  
DB 1261 ATCAACGATGCGGGGTGTTGGCTCCCTGTATCCCAACCGAGCGGCTTGGAGATGGCC 1320  
QY 1225 CAGCAGACGAGAGATCCGTTAGGTCAGTGGAGCTCCACGGGTCTGCTCCAGCCCT 1284  
DB 1321 CAGCAGACGAGAGATCCGTTAGGTCAGTGGAGCTCCACGGGTCTGCTCCAGCCCT 1380  
QY 1285 CTAAGACGCGCAAGAGTCCGGTCTTTTCTTTTTCACCGAGCGGGGCTGAGATGAG 1344  
DB 1381 CTAAGACGCGCAAGAGTCCGGTCTTTTCTTTTTCACCGAGCGGGGCTGAGATGAG 1440  
QY 1345 GCTGAGCGGGGCTCCCGACTTCGAAACGAGAGCTGCTTCTCGGGGCGCCGAG 1404  
DB 1441 GCTGAGCGGGGCTCCCGACTTCGAAACGAGAGCTGCTTCTCGGGGCGCCGAG 1500  
QY 1405 GGTGGGGCGCGGGAGAGCGCCCGCCCGCTCCGCTCCACACCCCTGCGCGC 1464  
DB 1501 GGTGGGGCGCGGGAGAGCGCCCGCCCGCTCCGCTCCACACCCCTGCGCGC 1560  
QY 1465 CCCCCAGGCTCCCGCGCTCTCTGGCGGAGACCCCTTGCATCTGCTGCAACGCCC 1524  
DB 1561 CCCCCAGGCTCCCGCGCTCTCTGGCGGAGACCCCTTGCATCTGCTGCAACGCCC 1620

QY 1525 CGGGCCAGTCCACCGGGACCCCGGGGACAAACACCCCGGCGGCTGGCGTC 1584  
DB 1621 CGGGCCAGTCCACCGGGACCCCGGGGACAAACACCCCGGCGGCTGGCGTC 1680  
QY 1585 GGGGGAGCCCGCTCGGAGAGTCTCAATCCATCCGCAACAGCTTCCTGGGCTCCCT 1644  
DB 1681 GGGGGAGCCCGCTCGGAGAGTCTCAATCCATCCGCAACAGCTTCCTGGGCTCCCT 1740  
QY 1645 CGCTTTACCGGGCGCAAGATGAGGTCCCTACCGCTGAGGAGTGTCAAGCTTGAAGCA 1704  
DB 1741 CGCTTTACCGGGCGCAAGATGAGGTCCCTACCGCTGAGGAGTGTCAAGCTTGAAGCA 1800  
QY 1705 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTCGGGAACCTCATCTCTCTGGACAA 1764  
DB 1801 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTCGGGAACCTCATCTCTCTGGACAA 1860  
QY 1765 GAAGAAACAAATATTCCTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824  
DB 1861 GAAGAAACAAATATTCCTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1920  
QY 1825 GTCCATGCTCTTCTGTCGATCCCGAGCTGAGTCAAGTGTGTGTCAAGACAGCTTC 1884  
DB 1921 GTCCATGCTCTTCTGTCGATCCCGAGCTGAGTCAAGTGTGTGTCAAGACAGCTTC 1980  
QY 1885 AGGGCCGAGTACAAAGCCAGTGGGGCCCTCTCTCCAAAGCCCTCGCTTCAG 1944  
DB 1981 AGGGCCGAGTACAAAGCCAGTGGGGCCCTCTCTCCAAAGCCCTCGCTTCAG 2040  
QY 1945 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGT 2004  
DB 2041 GTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGT 2100  
QY 2005 GTGGACATCAGCTCTCTGAGGGTCCAGTCTCATCTCGGGTCCCGCTCGGTTCAAGCGA 2064  
DB 2101 GTGGACATCAGCTCTCTGAGGGTCCAGTCTCATCTCGGGTCCCGCTCGGTTCAAGCGA 2160  
QY 2065 GTGGTGGAGACATCCAGGACAGCTCTCTGAGCACTCATGACAGCCCTCGTGCAGGCC 2124  
DB 2161 GTGGTGGAGACATCCAGGACAGCTCTCTGAGCACTCATGACAGCCCTCGTGCAGGCC 2220  
QY 2125 CTGGCAGACGAGAAAGCGGGGCCAGACCCGGCTGCTGGTGGCCCGACCCGAGGCTG 2184  
DB 2221 CTGGCAGACGAGAAAGCGGGGCCAGACCCGGCTGCTGGTGGCCCGACCCGAGGCTG 2280  
QY 2185 CAGCCCCACCGCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGCGCCGCC 2244  
DB 2281 CAGCCCCACCGCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGCGCCGCC 2340  
QY 2245 AAGGACAGAGAGTCTCTGGCCACCAAGCGGACCCCTCTGCGCTGA 2289  
DB 2341 AAGGACAGAGAGTCTCTGGCCACCAAGCGGACCCCTCTGCGCTGA 2385

RESULT 6  
AP479826  
LOCUS  
DEFINITION Homo sapiens putative serine/threonine protein kinase mRNA,  
complete cds.  
ACCESSION AP479826  
VERSION AP479826.1 GI:19401870  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 3007)  
AUTHORS She,X.Y., Guo,J.H. and Yu,L.  
TITLE Direct Submission  
JOURNAL Submitted (02-FEB-2002) School of Life Sciences, Laboratory of Human Genes Research, Institute of Genetics, Fudan University, 220 Handan Road, Shanghai 200433, P. R. China  
FEATURES  
Location/Qualifiers  
source 1..3007





QY 2005 GGTGGCATCTACTCCGTCACCTTCTCACTCTCATCTCGGGTCCAGCGCTCGGTTCAAGCGA 2064  
DB 2228 GGTGGCATCTACTCCGTCACCTTCTCACTCTCATCTCGGGTCCAGCGCTCGGTTCAAGCGA 2287  
QY 2065 GTGGTGGAGACCATCTCAGGACAGCTCTCTGAGCACTCATGACACAGCCCTCGTGACGGCC 2124  
DB 2288 GTGGTGGAGACCATCTCAGGACAGCTCTCTGAGCACTCATGACACAGCCCTCGTGACGGCC 2347  
QY 2125 CTGGCAGACGAGAAAGACGGGGCCAGACACCGGCTCTGCTGTCGCCACCCAGAGCCTG 2184  
DB 2348 CTGGCAGACGAGAAAGACGGGGCCAGACACCGGCTCTGCTGTCGCCACCCAGAGCCTG 2407  
QY 2185 CAGCCCCCAGCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGCCCCCCCC 2244  
DB 2408 CAGCCCCCAGCCGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGCCCCCCCC 2467  
QY 2245 AAGGACAAGAGCTCTTGGGCCACCAACGGGACCCCTCTGCCCTGA 2289  
DB 2468 AAGGACAAGAGCTCTTGGGCCACCAACGGGACCCCTCTGCCCTGA 2512

## RESULT 7

AF479827  
LOCUS AF479827 3109 bp mRNA linear PRI 12-MAR-2002  
DEFINITION Homo sapiens protein kinase-like protein mRNA, complete cds.

## ACCESSION

AF479827

## VERSION

AF479827.1 GI:19401873

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

She,X.Y., Yu,L. and Guo,J.H.

Direct Submission

Submitted (02-FEB-2002) School of Life Sciences, Laboratory of

Human Genes Research, Institute of Genetics, Fudan University, 220

Handan Road, Shanghai 200433, P. R. China

Location/Qualifiers

1. 3109

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/chromosome="19"

278..2614

/codon\_start=1

/product="protein kinase-like protein"

/protein\_id="AAU87698.1"

/db\_xref="GI:19401874"

/translation="MSSGAKEGGGSPAYHLPHPPHQAQVGPYRLKTLGRGQ

TGLVKGVCITGKVAIKIWNREKLSVLMKVERBIAILKLIHPHLKLDVYEN

KYLLVLEHVGSGELFDYLVKGRLLPKEARPFROIIVSALDPCHSYSLCHRLDPE

NILLDEKNIRIADPFCMASIQVDSLLSTSGSPHYACPVIKGEKVDHRAWMSCG

FIPLALLVGLPFDNNQLLEKVKGVFMHPHFIPTDCQSLIRGMIEVEPKRLSL

EQIQHPWYLGSGHEPDCLEPAPGRVAMRSLPSNGELDPDLVLSNASLIGCFDRER

LHRELSEENQERMIYLLIDRKERYPSCDDQLPRNDVDPKRVDSPLMSRHK

RRPRKSMELSLIDAGCGSPVTRRALEMAHORSRSVSGASTGLSSPLSPRS

PVPSFSPGCPGDEARGGSPSTKOTLLPSRPGGAGAGQPPPSARSTPLPGPGS

PRSSGPTPLSPHTPRASPTGTPPTPPSPGGVGGAARSLRSLRNSPLGSPRP

HRKMQVPTAESMSLTPSSPELAKRSWFGNFIISLDKEQOIFLVLDKPLSLIKADI

VHAPLSLPSLHSLVSTPSFAEYKASGPSVFQKPVRFQVDSISSESGPSPRRDGS

GGGIYSVFTLLSGRRPRKRVVETITQAQLLSHDQPSVQALADEKNAGQTRPAGAP

PRSLQPPPGRPDPPELSSSPRRGPPKPKLLATNGTLP"

PRSLQPPPGRPDPPELSSSPRRGPPKPKLLATNGTLP"

PRSLQPPPGRPDPPELSSSPRRGPPKPKLLATNGTLP"

PRSLQPPPGRPDPPELSSSPRRGPPKPKLLATNGTLP"

PRSLQPPPGRPDPPELSSSPRRGPPKPKLLATNGTLP"

PRSLQPPPGRPDPPELSSSPRRGPPKPKLLATNGTLP"

QY 325 AAGGGAGACTGACGCGCCAAAGGAGGCCCGAAAGTTCTTCCGCCAGATTGTGTCTGCCTG 384  
DB 650 AAGGGAGACTGACGCGCCAAAGGAGGCCCGAAAGTTCTTCCGCCAGATTGTGTCTGCCTG 709  
QY 385 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAAACCTGCTTTTG 444  
DB 710 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACCTAAAGCCCGAGAAACCTGCTTTTG 769  
QY 445 GATGAGAAAAACAATCCGCAATTCGAGACTTCGGCATGCGCTCCCTTCGAGGTGGGGAC 504  
DB 770 GATGAGAAAAACAATCCGCAATTCGAGACTTCGGCATGCGCTCCCTTCGAGGTGGGGAC 829  
QY 505 AGCCTCTTGAGACAGCTCGGGTCCGCCATTTATGCGTTCGAGAGGTGATTAAGGGG 564  
DB 830 AGCCTCTTGAGACAGCTCGGGTCCGCCATTTATGCGTTCGAGAGGTGATTAAGGGG 889  
QY 565 GAAAAATATGATCGCGCGCGGAGACATGTGAGCTGTGGAGTTCATCTCTTCGCCCTG 624  
DB 890 GAAAAATATGATCGCGCGCGGAGACATGTGAGCTGTGGAGTTCATCTCTTCGCCCTG 949  
QY 625 CTCGTGGGGCTCTGCCCTTTGATGACACAACCTCCGCCAGCTGCTGGAGAAAGGTGAAA 684  
DB 950 CTCGTGGGGCTCTGCCCTTTGATGACACAACCTCCGCCAGCTGCTGGAGAAAGGTGAAA 1009  
QY 685 CGGGGCGTCTTCCACATGCCCACTTCAATTCCTCCAGATTGCGAGAGCTCTCTGAGGGGA 744  
DB 1010 CGGGGCGTCTTCCACATGCCCACTTCAATTCCTCCAGATTGCGAGAGCTCTCTGAGGGGA 1069  
QY 745 ATCATCGAGTGGAGCGCCGAAAGAGCTCAGTCTGGAGCAATTCAGAACATCTCTTGG 804  
DB 1070 ATCATCGAGTGGAGCGCCGAAAGAGCTCAGTCTGGAGCAATTCAGAACATCTCTTGG 1129  
QY 805 TACTAGCGGGGAAAACACGAGCGAGACCCGCTGCTGGAGCACCCCTGCGCGCGGGTA 864  
DB 1130 TACTAGCGGGGAAAACACGAGCGAGACCCGCTGCTGGAGCACCCCTGCGCGCGGGTA 1189  
QY 865 GCATGCGGAGCTGCGCATCAACGAGAGCTGGAACCCGACGCTCTTAGAGAGCATGGCA 924  
DB 1190 GCATGCGGAGCTGCGCATCAACGAGAGCTGGAACCCGACGCTCTTAGAGAGCATGGCA 1249  
QY 925 TCACTGGCTGCTTCAAGGACCGGAGAGCTGCGAGCTGCGAGCTGCGAGCTGAGGAG 984  
DB 1250 TCACTGGCTGCTTCAAGGACCGGAGAGCTGCGAGCTGCGAGCTGCGAGCTGAGGAG 1309  
QY 985 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044  
DB 1310 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1369  
QY 1045 GAGGACAGGACCTGCTCTCCCGAATGATGTTGAACCCCGGAAAGCGTGTGATCT 1104  
DB 1370 GAGGACAGGACCTGCTCTCCCGAATGATGTTGAACCCCGGAAAGCGTGTGATCT 1429  
QY 1105 CCATGCTGAGCGCTCAAGGAGCGGAGCGGAGCGGAGTCCATGGAAGTCTTGAGC 1164  
DB 1430 CCATGCTGAGCGCTCAAGGAGCGGAGCGGAGCGGAGTCCATGGAAGTCTTGAGC 1489  
QY 1165 ATCAACGATCCCGGGGTGTGCTCCCTGTATCCACACCGAGCGGGCTTTGGAGATGGCC 1224  
DB 1490 ATCAACGATCCCGGGGTGTGCTCCCTGTATCCACACCGAGCGGGCTTTGGAGATGGCC 1549  
QY 1225 CAGCAGACGAGATCCCGTAGCGTCAAGTGGAGCTTCCACGGGTCTGTCTCCAGCCCT 1284  
DB 1550 CAGCAGACGAGATCCCGTAGCGTCAAGTGGAGCTTCCACGGGTCTGTCTCCAGCCCT 1609  
QY 1285 CTAAGCGACCAAGAGTCCGCTCTTTTCTTTTCCCGAGCGCGGGGCTGGAGATGAG 1344  
DB 1610 CTAAGCGACCAAGAGTCCGCTCTTTTCTTTTCCCGAGCGCGGGGCTGGAGATGAG 1669  
QY 1345 GCTCGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTTCGCGGGCCCCCAGG 1404  
DB 1670 GCTCGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTTCGCGGGCCCCCAGG 1729

## ORIGIN

Query Match 88.3%; Score 2020.2; DB 9; Length 3109;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 265 TTTAGGTACCTGGTCTGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACTGCTAAAG 324  
DB 590 TATTGTACCTGGTCTGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACTGCTAAAG 649

QY	1405	GGTGGGGGCGCCGGGAGAGAGCCCCCGCCCGCCAGTGGCCGCTCCACACCCCTGCCCGC	1464
Db	1730	GGTGGGGGCGCCGGGAGAGAGCCCCCGCCCGCCAGTGGCCGCTCCACACCCCTGCCCGC	1789
QY	1465	CCCCCAGGCTCCCGCGGCTCTCTGGCGGAGCCCTTGGCACTCGCTCTGCACAGCC	1524
Db	1790	CCCCCAGGCTCCCGCGGCTCTCTGGCGGAGCCCTTGGCACTCGCTCTGCACAGCC	1849
QY	1525	CGGGCCAGTCCACCGGGAGCCCGGGGACAAACACACCCCGCCAGCCCGCGGCTGGCGTC	1584
Db	1850	CGGGCCAGTCCACCGGGAGCCCGGGGACAAACACACCCCGCCAGCCCGCGGCTGGCGTC	1909
QY	1585	GGGGGAGCGCTGGAGAGTGTCTCAATCCATCGGCAACAGCTTCTGGGCTCCCT	1644
Db	1910	GGGGGAGCGCTGGAGAGTGTCTCAATCCATCGGCAACAGCTTCTGGGCTCCCT	1969
QY	1645	CGCTTTACCGCGGCAAGATGACGCTTACCGCTGAGGAGATGTCAGCTTGACGCCA	1704
Db	1970	CGCTTTACCGCGGCAAGATGACGCTTACCGCTGAGGAGATGTCAGCTTGACGCCA	2029
QY	1705	GAGTCCTCCCGGAGCTGGGAAAAGCTCTGCTGGTTGGGAACTTCATCTCTTGGACAA	1764
Db	2030	GAGTCCTCCCGGAGCTGGGAAAAGCTCTGCTGGTTGGGAACTTCATCTCTTGGACAA	2089
QY	1765	GAAGACAAATATTCCTCGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC	1824
Db	2090	GAAGACAAATATTCCTCGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC	2149
QY	1825	GTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTGTGTCAAGCAGGCTTC	1884
Db	2150	GTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTGTGTCAAGCAGGCTTC	2209
QY	1885	AGGGCCGAGTACAGGCCAGTGGGGCCCTCTCTTCCAAAGCCGCTCCGCTCCAG	1944
Db	2210	AGGGCCGAGTACAGGCCAGTGGGGCCCTCTCTTCCAAAGCCGCTCCGCTCCAG	2269
QY	1945	GTGGACATCAGCTCTCTGAGGCTCCAGAGCCCTCCCGCGACGGGACGGGAGGT	2004
Db	2270	GTGGACATCAGCTCTCTGAGGCTCCAGAGCCCTCCCGCGACGGGACGGGAGGT	2329
QY	2005	GGTGGCATCTACTCGCTCACTTCACTCTCATCTCGGCTCCAGCCGCTTCAAGCGA	2064
Db	2330	GGTGGCATCTACTCGCTCACTTCACTCTCATCTCGGCTCCAGCCGCTTCAAGCGA	2389
QY	2065	GTGGTGAGACCATCCAGCAGCTCTGAGCAGCTCATGACAGCCCTCGTGCAGGCC	2124
Db	2390	GTGGTGAGACCATCCAGCAGCTCTGAGCAGCTCATGACAGCCCTCGTGCAGGCC	2449
QY	2125	CTGGCAGACGAGAAGAAAGGGGCCCCAGACCCCGGCTGTGTGTGCCACCCGAGCCTG	2184
Db	2450	CTGGCAGACGAGAAGAAAGGGGCCCCAGACCCCGGCTGTGTGTGCCACCCGAGCCTG	2509
QY	2185	CAGCCCCACCCGGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGAGGCCCC	2244
Db	2510	CAGCCCCACCCGGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGAGGCCCC	2569
QY	2245	AAGGACAGAGAGCTCTGGCCACCAACGGGACCCCTCTGCCCTGA	2289
Db	2570	AAGGACAGAGAGCTCTGGCCACCAACGGGACCCCTCTGCCCTGA	2614
RESULT 8			
LOCUS	BD186023	2799 bp	DNA linear PAT 17-JUN-2003
DEFINITION	Cell cycle regulatory factor.		
ACCESSION	BD186023		
VERSION	BD186023.1	GI:31878223	
KEYWORDS	WO 0209110-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	(bases 1 to 2799)	
Nakanishi, M.			
Cell cycle regulatory factor			
TITLE			
Patent: WO 0209110-A 1 12-DEC-2002;			
JOURNAL			
MAKOTO NAKANISHI, TAIHO PHARMACEUTICAL CO LTD			
COMMENT			
OS Homo sapiens (human)			
PN WO 0209110-A/1			
PD 12-DEC-2002			
PF 03-JUN-2002 WO 2002JP005411			
PR 04-JUN-2001 JP 01P 168792			
PI MAKOTO NAKANISHI			
PC C12N15/54, C12N5/10, C12P21/02, C12Q1/48, C07K14/47, C07K16/40, PC			
GOIN33/68,			
PC A61K45/00, A61K38/00, A61P35/00, A61P17/02, A61P43/00 CC			
Cell cycle regulatory factor			
FH Key Location/Qualifiers			
FT CDS (50)..(2311).			
FEATURES			
source			
1..2799			
/organism="Homo sapiens"			
/mol_type="genomic DNA"			
/db_xref="taxon:9606"			
ORIGIN			
Query Match 80.3%; Score 1839; DB 6; Length 2799;			
Best Local Similarity 95.5%; Pred No. 0;			
Matches 1913; Conservative 0; Mismatches 20; Indels 72; Gaps 1;			
QY	265	TTTAGTACTCTGTTCTCGAGCAGCTCTCGGGGGTGAAGTATTCGACTACTCTGTTAAAG	324
Db	362	TATTTGTACTCTGTTCTCGAGCAGCTCTCGGGGGTGAAGTATTCGACTACTCTGTTAAAG	421
QY	325	AAGGGAGACTGACGCCCAAGGAGCCGAAAGTTCTTCGCGAGATTGTCTCTGCGCTG	384
Db	422	AAGGGAGACTGACGCCCAAGGAGCCGAAAGTTCTTCGCGAGATTGTCTCTGCGCTG	481
QY	385	GACTTCTGCGCAGACTACTCTCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG	444
Db	482	GACTTCTGCGCAGACTACTCTCATCTGCCACAGAGACCTAAAGCCCGAGAACCTGCTTTTG	541
QY	445	GATGAGAAAAAACAATCCGCAATTCGAGACTTTCCGCGATGGCTCCCTGAGTGGGGGAC	504
Db	542	GATGAGAAAAAACAATCCGCAATTCGAGACTTTCCGCGATGGCTCCCTGAGTGGGGGAC	601
QY	505	AGCTCTCTGAGACAGCTGCGGTCCTCCCATTTATGCGTGTCCAGAGGTGATTAGGGG	564
Db	602	AGCTCTCTGAGACAGCTGCGGTCCTCCCATTTATGCGTGTCCAGAGGTGATTAGGGG	661
QY	565	GAAAAATATGATGGCGCCCGGCGAGACATGTGAGCTGTGAGTCAATCTCTTCCCTG	624
Db	662	GAAAAATATGATGGCGCCCGGCGAGACATGTGAGCTGTGAGTCAATCTCTTCCCTG	721
QY	625	CTCGTGGGGCTCTGCGCTTTGATGACGACACCTCCGCGAGCTGTGAGAGGTGAAA	684
Db	722	CTCGTGGGGCTCTGCGCTTTGATGACGACACCTCCGCGAGCTGTGAGAGGTGAAA	781
QY	685	CGGGGCTCTTCCACATGCCCCCTTCTTCTCCAGATTGCGAGGCTCTCTGAGGGGA	744
Db	782	CGGGGCTCTTCCACATGCCCCCTTCTTCTCCAGATTGCGAGGCTCTCTGAGGGGA	841
QY	745	ATGATCGAAGTGGAGCCGAAAAAAGGCTCAGTCTGGAGCAATTCAGAAACATCTTTGG	804
Db	842	ATGATCGAAGTGGAGCCGAAAAAAGGCTCAGTCTGGAGCAATTCAGAAACATCTTTGG	901
QY	805	TACCTAGCGGGGAAACAGAGCCAGACCCCTGCTGAGCCAGCCCTGCGCCCGGGTA	864
Db	902	TACCTAGCGGGGAAACAGAGCCAGACCCCTGCTGAGCCAGCCCTGCGCCCGGGTA	961
QY	865	GCCATGCGGGAGCTTCCCATCCAAAGAGCTGGAACCCGACGCTCTTAGAGAGCATGGCA	924
Db	962	GCCATGCGGGAGCTTCCCATCCAAAGAGCTGGAACCCGACGCTCTTAGAGAGCATGGCA	1021
QY	925	TCACTGGGCTCTTCCAGGACCGGAGAGCTGATCGAGCTGCGCAGTGGAGAGGAG	984



Db 1022 TCACTGGGCTGCTTCAGGACCGCGAGAGGCTGCATCGGAGCTGCGCAGTGAGGAGGAG 1081  
Qy 985 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044  
Db 1082 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1141  
Qy 1045 GAGCAGCAGGACCTGCTCCCGGAATGATGTCACACCCCGGAGCGGTGATGATCT 1104  
Db 1142 GAGCAGCAGGACCTGCTCCCGGAATGATGTCACACCCCGGAGCGGTGATGATCT 1201  
Qy 1105 CCCATGCTGAGCCCTCAGCGGAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1164  
Db 1202 CCCATGCTGAGCCCTCAGCGGAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1261  
Qy 1165 ATCAACGATGCGGGGTGTTGCTCCCTGTATCCACCGACCGGGCTTGAGATGGCC 1224  
Db 1262 ATCAACGATGCGGGGTGTTGCTCCCTGTATCCACCGACCGGGCTTGAGATGGCC 1321  
Qy 1225 CAGCAGCAGAGATCCCGTAGCTCAGTGGAGCTCCAGGGCTGCTCTCCAGCCCT 1284  
Db 1322 CAGCAGCAGAGATCCCGTAGCTCAGTGGAGCTCCAGGGCTGCTCTCCAGCCCT 1381  
Qy 1285 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTCAACCGAGCGGGCTTGAGATGAG 1344  
Db 1382 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTCAACCGAGCGGGCTTGAGATGAG 1441  
Qy 1345 GCTCAGCGCGGGCTCCCGACTTCCAAACGAGAGCTGCTCTTCGGGGGCCCCAGG 1404  
Db 1442 GCTCAGCGCGGGCTCCCGACTTCCAAACGAGAGCTGCTCTTCGGGGGCCCCAGG 1480  
Qy 1405 GGTGGGGGCGGGGAGCAGCCCCCGCCCCAGTGGCCGCTCCACACCCCTGCCCGG 1464  
Db 1481 -----CTGCCCGG 1489  
Qy 1465 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGCACTCGCTCTGCAACAGCC 1524  
Db 1490 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGCACTCGCTCTGCAACAGCC 1549  
Qy 1525 CGGCGCAGTCCACCGGACCCCGGGGACAAACACCCCGGCGGGCTGGCGTC 1584  
Db 1550 CGGCGCAGTCCACCGGACCCCGGGGACAAACACCCCGGCGGGCTGGCGTC 1609  
Qy 1585 GGGGGAGCGCTGAGGAGTGTCTCACTCCATCCGCAACAGCTTCTGGGCTCCCT 1644  
Db 1610 GGGGGAGCGCTGAGGAGTGTCTCACTCCATCCGCAACAGCTTCTGGGCTCCCT 1669  
Qy 1645 CGCTTTTCAACCGGCGCAAGATCAGGTCCCTACCGCTGAGGAGATGTCAGCTTCACGCCA 1704  
Db 1670 CGCTTTTCAACCGGCGCAAGATCAGGTCCCTACCGCTGAGGAGATGTCAGCTTCACGCCA 1729  
Qy 1705 GAGTCTTCCCGGAGCTGGCAAAAACGCTCTCTGGTTGCGGAACTTCATCTCTTGGACAAA 1764  
Db 1730 GAGTCTTCCCGGAGCTGGCAAAAACGCTCTCTGGTTGCGGAACTTCATCTCTTGGACAAA 1789  
Qy 1765 GAAGAACAAATATCTCTGCTTAAAGACAAACCTCTCAGCAGCATCAAAGCAGATC 1824  
Db 1790 GAAGAACAAATATCTCTGCTTAAAGACAAACCTCTCAGCAGCATCAAAGCAGATC 1849  
Qy 1825 GTCCATGCTTCTGTCGATCCCGAGCTGAGTCAAGTGTGCTGTCAGACAGCTTC 1884  
Db 1850 GTCCATGCTTCTGTCGATCCCGAGCTGAGTCAAGTGTGCTGTCAGACAGCTTC 1909  
Qy 1885 AGGCGCAGTACAAGGCGAGTGGCGGCGCTCCGCTTTCAAAACCGCGCTCCGCTTCAG 1944  
Db 1910 AGGCGCAGTACAAGGCGAGTGGCGGCGCTCCGCTTTCAAAACCGCGCTTCAG 1969  
Qy 1945 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACCGGAGCGGAGGT 2004  
Db 1970 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACCGGAGCGGAGGT 2029  
Qy 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGCTCGGTTCAAGCA 2064  
Db 2030 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCAGCCGCTCGGTTCAAGCA 2089

Qy 2065 GTGCTGAGAGCCATCCAGGACAGCTCTCTGAGCACTCATGACCAAGCCCTCGTGCAGGCC 2124  
Db 2090 GTGCTGAGAGCCATCCAGGACAGCTCTCTGAGCACTCATGACCAAGCCCTCGTGCAGGCC 2149  
Qy 2125 CTGTCAGACGAGAAAGAACCGGGCCAGACCCGGCTCTGCTGCTGCCACCCCGGAAGCTG 2184  
Db 2150 CTGTCAGACGAGAAAGAACCGGGCCAGACCCGGCTCTGCTGCTGCCACCCCGGAAGCTG 2209  
Qy 2185 CAGCCCCACCGCGCCGACCCAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGCCCCCC 2244  
Db 2210 CAGCCCCACCGCGCCGACCCAGACCCAGAGCTGAGCAGCTCTCCCGCGAGGCCCCCC 2269  
Qy 2245 AAGCAGAGAGCTCTCTGGCCACCAACCGGACCCCTCTGCTGCTGA 2289  
Db 2270 AAGCAGAGAGCTCTCTGGCCACCAACCGGACCCCTCTGCTGCTGA 2314

RESULT 9  
AY533671  
LOCUS  
DEFINITION Mus musculus putative serine/threonine kinase SADB mRNA, complete cds.  
ACCESSION AY533671  
VERSION AY533671.1 GI:47013800  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 2331)  
AUTHORS Kishi, M. and Sanes, J. R.  
TITLE Direct Submission  
JOURNAL Submitted (27-JAN-2004) Department of Anatomy and Neurobiology, Washington University School of Medicine, 660 South Euclid, St. Louis, MO 63110, USA

FEATURES  
source  
1..2331  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
1..2331  
/notes="neuronal polarity, specification of axon and dendrite, presynaptic differentiation, synaptic vesicle clustering"  
/codon\_start=1  
/product="putative serine/threonine kinase SADB"  
/protein\_id="AA08446.1"  
/db\_xref="GI:47013801"  
/translation="MSSGSGKEGGSPAYHLPHPPHQAQYVGPYPLEKTLGKQTG  
LVKLGVHCITGQKVAVKIVNREKLSVLMKVEREIALKLIHHPVILKLDHYENKK  
YLYLVLEHVSGBELFDYLVKGRITPKARKFFQIVSALDFHSYICHRDLKPNL  
LLDBKNIRIADFGMASLOVGDLSLSTSCGSPHVACPEVTKGKYDGRADMMSCGVI  
LFALLVGLPDDDLNRLQLLKVKGVEHMPHTPPDCQSILGMIEVEKRLSLAQ  
IQHPVYLGKHEPFDCLPAPGRVAVMSLPSNGELDPDVLSEMSIGCFRDRRLH  
RELRSSENNQKPIYLLDRKPEPCEDDLPFRNDVDFPRKRVDSPLMSRHKRR  
PERKMEVLSITDAGSGSPVTRALMAHQSRSVSGASTGLSSPLSSPSPV  
FSPSPGAGDEARGGSPSTQTPLPSRPGCGGAGEQPPPSARSTPLPGPPSPR  
SSGTPHSPHTPRASPTGTPPTPPSPGGVGAARSLNLSIRNSFLGSPRPHR  
RMQVPTAEMSSSLTPSSPELAKRSWFGNFIQLDKEQIPLVLKDKPLASIKADIHV  
AFUSITPSLSVLSUTSPFRAKYKASGVVFQKPRFQVDISSESGEPFRRRSGSG  
GGYVSTFTLIISGSRFRFRVETIQALLSTHDQPSVALADEKNAQTRPAGTPPR  
SLQPPRGRSDPLSSSPRRGPPKDKLLATNGTLP"

Query Match 75.5%; Score 1727.8; DB 10; Length 2331;  
Best Local Similarity 91.0%; Pred. No. 0;  
Matches 1837; Conservative 0; Mismatches 182; Indels 0; Gaps 0;  
Qy 271 TACTGCTTCTGAGCAGCTCTCGGGGGTGTGAGCTATTTCGACTACCTGGTAAAGAAGGG 330  
Db 313 TACTTGGTTCTTGTGAGCAGCTTCTGTGGTGTGAGCTGTTCGACTACCTGGTAAAGAAGGG 372

331 AGACTGACGCCCAAGGAGGCCGAGAGTTCTTCCGCCAGATTGTGTCCTGCTGACATTC 390  
373 AGACTGACACCAAGGAGGCCGGAAGTTCTTCCGCCAGATGTGACAGATGACATTC 432  
391 TGCCACAGCTACTCCATCTCTGCCACAGAGACTTAAGCCCGAGAACCTGCTTTGGATGAG 450  
433 TGCCATAGCTACTCCATCTGTCTACAGAGACTTGAAGCCAGAGAACCTGTGTGGATGAG 492  
451 AAAAAACAATCCGATTCAGACTCTTCGGGATGCGTCCCTGAGGTGGGGAGACGCTTC 510  
493 AAAAAACAATCCGATTCGAGACTTTTGTGTATGGCGTCCCTGCAAGTGGGGAGACGCTTC 552  
511 CTGGAGACAGCTGCGGGTCCCGCCATTATGCGTGTCCAGAGTGAATTAAGGGGGAAAAA 570  
553 CTGGAGACAGCTGCGGGTCCCGCCATTATGCGTGTCCAGAGTGAATTAAGGGGGAAAAA 612  
571 TATGATGGCCCGCGGGCAGACATGTGGAGCTGTGGAGTCAATCTCTTTCGCTGCTGCTG 630  
613 TATGATGGCCCGCGGGCAGACATGTGGAGCTGTGGAGTCAATCTTATTTGCGCTGCTG 672  
631 GGGGCTCTGCGCTTTGATGAGCAACAACCTCGCCAGCTGTGGAGAGGTGAACCGGGC 690  
673 GGGGCACTGCGCTTCGATGAGCAACAACCTCGCCAGCTACTGGAGAGGTGAACCGTGG 732  
691 GTCTTCCACATGCGCCACTTCAATCTCCAGATTGCCAGAGCTCTCTGAGGGGAATGATC 750  
733 GTCTTCCACATGCGCTTCAATCTCCAGATTGCCAGAGCTCTCTGAGGGGAATGAT 792  
751 GAATGGAGCGCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATCTTGGTACCTA 810  
793 GAATGGAGCGCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATCTTGGTATCTG 852  
811 GCGGGAAAAACAGAGCCAGACCGTGTCTGGAGCCAGCCCTGCGCGCGGGTAGCCATG 870  
853 GCGGGAAAAACAGAACAGACCTTGTCTGGAGCCAGCCCGCCAGAGTAGCCATG 912  
871 CGGAGCTGCGCTCCCAACCGAGAGCTGGACCCCGACGCTCTTAGAGACATGGCATCTG 930  
913 CGTAGCTGCGCTTCCATGGCGAGCTGAGACCTTCTGAGCTTCTGGAAAGCATGGGCTCTG 972  
931 GCGTCTTCAGGACCGCGAGAGGTGATCGCAGCTGCGCAGTGGAGGAGGAGAACAA 990  
973 GCGTCTTCAGAGACCGCGAGCGGTGCAAGAGAACTGCGAAGCGAGGAGGAGGAAAA 1032  
991 GAAAGATGATATATATCTCTTGGATCGGAAGAGCGGTATCCAGCTGTGGAGGAC 1050  
1033 GAAAGATGATATATATCTCTTGGATCGGAAGAGCGGTATCTAGCTGTGAGAGAC 1092  
1051 CAGGACCTGCGCTCCCGGAATGATGTGACCCCCCGCGGAGCGGTGGATTTCCCATG 1110  
1093 CAGGACCTGCGCTTCTCGAATGATGTGACCCACCTCGTAAGCGTGTGGATTTCCCATG 1152  
1111 CTGAGCGTTCAGGGAAGCGGGACAGAGCGGAGTCCATGGAAGTCTCTGAGCATCAC 1170  
1153 CTGAGCAGACACCGGGAACCGGAGCCAGAGGGAAGTCCATGGAAGTCTCTAGTATACA 1212  
1171 GATGCGGGGTGTGGGTCTCCCTGTACCCAGCGGGCTTTGGAGATGGCCAGCAC 1230  
1213 GATGCTGGAGTGTGGTCTCCAGTCTACCAAGCGGCTTGGAGATGGCCAGCAC 1272  
1231 AGCCAGAGATCCCGTAGCGTCACTGAGGCTCCAGCGGTCTGTCTCCAGCGCTCTAAGC 1290  
1273 AGTCAGAGATCCCGCAGCGTCACTGAGGAGCTTCACTGTGTCTCTCCAGCGCTCTGAGC 1332  
1291 AGCCCAAGAGTCCCGTCTTTTCTTTTCCCGGAGCGGGGCTGGAGATGAGGCTCGA 1350  
1333 AGCCCAAGAGTCCCGTCTTTTCTTTTCTTCCCGGAGCGGCTGGAGATGAGGCTAGA 1392  
1351 GCGCGGGGTCTCCCGACTTCCAAAAACGACAGCTGCTCTCTCTCGGGGCCCCAGAGGGTGG 1410  
1393 GCGGGAGGCTCCCGAATTCCTTCCAAAAACAGACGCTGCTCTCTCTCGGGGCCCCAGAGGGTGG 1452  
1411 GCGCGCGGGAGAGAGCCCGCGCCCGCTCCAGTGTGCGCTCCAGACCGCTGCGCGGCCCCCA 1470

1453 GGCGCTGGAGAGCAGCCACCAACCCCGAGTGCCCGTTCCAGCGCTTGCCTGGAGCAACA 1512  
1471 GGCTCCCGCGCTCTCTGGGGGAGCCCTTGTGACTGCGCTCTGCAACACGCCCGCGGGC 1530  
1513 GGCTCCCGCGCTCTCTCGGGGAAACCCCTTGTGACTCACCTCTGCAACGCTCGAGCC 1572  
1531 AGTCCACACGGGAGCCCGGGGACAAACACCCCGGAGCGGGTGGGGTGGGGGA 1590  
1573 AGCCCTACGGGGAGCCCGAGGAACGAGCGCACCTCCAGCCAGGCGGTGGGGTGGGGGA 1632  
1591 GCGGCTCGGAGAGTGTCTCAATCCGATCCGCAACAGCTTCTCTGGGCTCCCTCGCTTT 1650  
1633 GCGGCTCGGAGAGTGTCTCAATCCGATCCGCAACAGCTTCTCTGGGCTCCCTCGCTTT 1692  
1651 CACCGGCGCAGATGACAGTCCCTACCGCTGAGGAGATGTCCAGCTTGACGCGAGTCC 1710  
1693 CACCGGCGCAGATGACAGTCCCTACCGCTGAGGAGATGTCCAGTTCGACACCGAATCC 1752  
1711 TCCCGGAGCTGGCAAAACGCTCTCTGGTTCGGGAACTTCTCATCTCTCTTGGACAAAGAA 1770  
1753 TCTCTGAGCTGGCAAAACGCTCTCTGGTTCGGGAACTTCTCATCTCTCTTGGACAAAGAA 1812  
1771 CAAATATTCCTGCTGCTAAAGGAGAACTCTCTCAGCAGCATCAAGAGAGACATCTCCAT 1830  
1813 CAAATATTCCTGCTGCTAAAGGAGAACTCTCTCAGCAGCATCAAGAGAGACATCTCCAT 1872  
1831 GCGTTCCTGTCATCCCGAGCCTGAGTCAAGTGTCTGTCTCAGACGAGCTTCAGGGC 1890  
1873 GCGTTCCTGTCATCCCGAGCCTGAGTCAAGTGTCTGTCTCAGACGAGCTTCAGGGC 1932  
1891 GAGTCAAGGCGAGTGGCGGCCCTCTCGTCTTCCAAAGCCGCTCGCTTCAGGCTGGAC 1950  
1933 GAATCAAGGCGAGGCGGGCGGCCCTCTCGTCTTCCAAAGCCCTGTCTCGCTTTTCAAGGTGGAC 1992  
1951 ATCAGCTCTCTGAGGCTCCAGAGCCCTCCCGCAAGGAGCGGAGCGAGAGTGTGTGGC 2010  
1993 ATCAGCTCTCTGAGGCTCCAGAACCTCTCACCCGAGAGATGCGCAGTGTGGTGGC 2052  
2011 ATCTACTCGCTCACTTCTCATCTCTCGGTCGCGCTGCTGCTTCAAGCGAGTGGT 2070  
2053 ATCTACTCAGTCACTTCTCATCTCTCGGTCGCGCTGCTGCTTCAAGCGTGTGGT 2112  
2071 GAGACATTCAGGACAGCTCTCTGAGTCACTGATCAGCAGCCCTCGCTGAGGAGCTTGGCA 2130  
2113 GAGACATTCAGGACAGTGTCTGAGTCACTGAGCAGCCCTCTCTGAGGAGCTTGGCA 2172  
2131 GAGCAGAGAAACGGGGCCAGAGCCCGGCTGTGTGTGCCCCCAGAGCTTCAGAGCC 2190  
2173 GATGAGAGAAACGGAGCCAGAGCCCGGCTGTGTGAGACCCACCCCGAAGCTTCAGAGCC 2232  
2191 CCAACCGGCGCCAGAGCCAGAGCTGTGAGAGTCTCTCCCGGAGGCCCCCGAGGAG 2250  
2233 CCAACGAGCGCTCTGAGCTGATCTGAGTGTCTCTCCCGGAGGAGCCCCCTAAGGAC 2292  
2251 AAGAGCTCTGCGCCAGCAACGAGCCCTCTCTCGCTTCAAG 2289  
2293 AAGAGCTCTGCGCCAGCAATGGAACCCCTCTTACCTTCA 2331

## RESULT 10

LOCUS CQ841950 1902 bp DNA linear PAT 02-AUG-2004  
DEFINITION Sequence 597 from Patent EP1440981.

ACCESSION CQ841950

VERSION CQ841950.1 GI:50893737

KEYWORDS Homo sapiens (human)

SOURCE ORGANISM

Homo sapiens

Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,

Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.

Full-length human cDNA

Patent: JP 1440981-A 597 28-JUL-2004;

Research Association for Biotechnology (JP)

Location/Qualifiers

source

1. .1902

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

## ORIGIN

Query Match 66.0%; Score 1510.4; DB 6; Length 1902;  
Best Local Similarity 99.9%; Pred. No. 2.2e-282;  
Matches 1511, Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 778 CTGAGCAAAATTCAGAAACATCTCTTGGTACCTTAGCGGGGAAACACGAGCGCAGACCCCTGTC 837  
Db 72 CTGAGCAAAATTCAGAAACATCTCTTGGTACCTTAGCGGGGAAACACGAGCGCAGACCCCTGTC 131

Qy 838 CTGAGCGACGCCCTGCGCCGCGGTAGCCATGCGGAGCCTGCCATCCACGGAGAGCTG 897  
Db 132 CTGAGCGACGCCCTGCGCCGCGGTAGCCATGCGGAGCCTGCCATCCACGGAGAGCTG 191

Qy 898 GACCCCGACGCTCTAGAGAGCATGGCATCACTGGGCTGCTTCAGGGACCGCGAGAGCTG 957  
Db 192 GACCCCGACGCTCTAGAGAGCATGGCATCACTGGGCTGCTTCAGGGACCGCGAGAGCTG 251

Qy 958 CATCGAGCTGCGCAGTAGAGAGGAGAAACGAAAGATGATATATATCTGCTTTTG 1017  
Db 252 CATCGAGCTGCGCAGTAGAGAGGAGAAACGAAAGATGATATATATCTGCTTTTG 311

Qy 1018 GATCGGAAGAGCGGTATCCAGCTGTGAGGACAGGACCTGCCCTCCCGGAATGATTT 1077  
Db 312 GATCGGAAGAGCGGTATCCAGCTGTGAGGACAGGACCTGCCCTCCCGGAATGATTT 371

Qy 1078 GACCCCGCGGAGCGTGTGATTTCTCCATGCTGAGCGCTCACGGGAGCGCGACCA 1137  
Db 372 GACCCCGCGGAGCGTGTGATTTCTCCATGCTGAGCGCTCACGGGAGCGCGACCA 431

Qy 1138 GAGCGGAAGTCATGGAAGTCTGAGCATCACGATCCCGGGGTGTGGTCCCTGTGA 1197  
Db 432 GAGCGGAAGTCCATGGAAGTCTGAGCATCACGATCCCGGGGTGTGGTCCCTGTGA 491

Qy 1198 CCGACCGAGCGGGCTTGGAGATGGCCAGCAGCAGCAGATCCCGTAGGTCAGTGA 1257  
Db 492 CCGACCGAGCGGGCTTGGAGATGGCCAGCAGCAGCAGATCCCGTAGGTCAGTGA 551

Qy 1258 GCCTCCACGGTCTGTCTCCAGCCCTTAAGCAGCCCAAGGAGTCCGGTCTTTTCCTTT 1317  
Db 552 GCCTCCACGGTCTGTCTCCAGCCCTTAAGCAGCCCAAGGAGTCCGGTCTTTTCCTTT 611

Qy 1318 TCACCGGAGCGGGGCTGGAGATGAGGCTCGAGCGGGGCTCCCGGACTTCCAAACG 1377  
Db 612 TCACCGGAGCGGGGCTGGAGATGAGGCTCGAGCGGGGCTCCCGGACTTCCAAACG 671

Qy 1378 CAGACGCTGCTTCTCGGGGCCCCAGAGGTTGGGGGCGCGGGAGCAGCCCGCCGCC 1437  
Db 672 CAGACGCTGCTTCTCGGGGCCCCAGAGGTTGGGGGCGCGGGAGCAGCCCGCCGCC 731

Qy 1438 AGTCCCGCTCCACACCCCTGCGCGGCCCGCCAGGCTCCCGCGCTCTCTGGCGGACC 1497  
Db 732 AGTCCCGCTCCACACCCCTGCGCGGCCCGCCAGGCTCCCGCGCTCTCTGGCGGACC 791

Qy 1498 CCTTTGCACTCGCTCTGACACCGCCCGGCGCAGTCCACCGGAGCCCGGGGACAAAC 1557  
Db 792 CCTTTGCACTCGCTCTGACACCGCCCGGCGCAGTCCACCGGAGCCCGGGGACAAAC 851

Qy 1558 CCACCCCGACCGCGCGGTGGCTGCGGGGAGCGCGCTGAGAGTGTGCTCACTCC 1617  
Db 852 CCACCCCGACCGCGCGGTGGCTGCGGGGAGCGCGCTGAGAGTGTGCTCACTCC 911

Qy 1618 ATCCGGACAGCTTCTGGGCTCCCTCGCTTTCACCGGCGCAGATGCGAGTCCCTACC 1677  
Db 1677 ATCCGGACAGCTTCTGGGCTCCCTCGCTTTCACCGGCGCAGATGCGAGTCCCTACC

Db 912 ATCCGCAACAGCTTCTGGGCTCCCTCGCTTTTACCGGCGCAAGATGACAGTCCCTACC 971

Qy 1678 GCTGAGGAGATGTCCAGCTTGACGCGCAGAGTCTCCCGGAGCTGGGCAAAACGCTCTGG 1737

Db 972 GCTGAGGAGATGTCCAGCTTGACGCGCAGAGTCTCCCGGAGCTGGGCAAAACGCTCTGG 1031

Qy 1738 TTCGGAACTTCACTCTCTTGGACAAAGAAACAAATATTCCTCGTCTTAAGGACAAA 1797

Db 1032 TTGGGAACTTCACTCTCTTGGACAAAGAAACAAATATTCCTCGTCTTAAGGACAAA 1091

Qy 1798 CCTCTCAGCAGCATCAAGCAGACATGCTCCATGCTCTTCTGTGATCCCGAGCTGAGT 1857

Db 1092 CCTCTCAGCAGCATCAAGCAGACATGCTCCATGCTCTTCTGTGATCCCGAGCTGAGT 1151

Qy 1858 CACAGTGTGCTGTACAGACAGCTTTCAGGCGCGAGTACAGGCCAGTGGGGCCCTCC 1917

Db 1152 CACAGTGTGCTGTACAGACAGCTTTCAGGCGCGAGTACAGGCCAGTGGGGCCCTCC 1211

Qy 1918 GTCTTCCAAAGCCCGTCCGCTTCCAGGTGGACATCAGCTCTCTGAGGGTCCAGAGCCC 1977

Db 1212 GTCTTCCAAAGCCCGTCCGCTTCCAGGTGGACATCAGCTCTCTGAGGGTCCAGAGCCC 1271

Qy 1978 TCCCGCGCAGCGGACGCGCAGCGAGGTGGTGGCATCTACTCCGTCACTTCACTCTCATC 2037

Db 1272 TCCCGCGCAGCGGACGCGCAGCGAGGTGGTGGCATCTACTCCGTCACTTCACTCTCATC 1331

Qy 2038 TCGGGTCCAGCGCTGGTTCAAGCGAGTGGTGGAGCCATCCAGGACAGCTCTCTGAGC 2097

Db 1332 TCGGGTCCAGCGCTGGTTCAAGCGAGTGGTGGAGCCATCCAGGACAGCTCTCTGAGC 1391

Qy 2098 ACTCATGACCGAGCCCTCCGTGCGAGGCCCTGCGAGAGAGAACCGGGCCACACCCGG 2157

Db 1392 ACTCATGACCGAGCCCTCCGTGCGATGCTCCGTGGAGACGAGAGAACCGGGCCACACCCGG 1451

Qy 2158 CCTGCTGCTGCTCCCGACCCCGGAGCTGCGAGCCCGCCCGCGCGCCAGAGAGCTG 2217

Db 1452 CCTGCTGCTGCTCCCGACCCCGGAGCTGCGAGCCCGCCCGCGCGCCAGAGAGCTG 1511

Qy 2218 AGCAGCTCTCCCGCGAGGCGCCCGCCCAAGGACAGAGCTCTCTGGCCACCAAGCGGACC 2277

Db 1512 AGCAGCTCTCCCGCGAGGCGCCCGCCCAAGGACAGAGCTCTCTGGCCACCAAGCGGACC 1571

Qy 2278 CCTCTGCCCTGA 2289

Db 1572 CCTCTGCCCTGA 1583

## RESULT 11

AK124999

LOCUS

DEFINITION

AK124999 1902 bp mRNA linear PRI 09-SEP-2003  
Homo sapiens cDNA FLJ43009 fis, clone BRTHA2015406, moderately  
similar to Homo sapiens mRNA for putative serine/threonine protein  
kinase.

ACCESSION

AK124999

VERSION

AK124999.1 GI:34530950

KEYWORDS

oligo capping; fis (full insert sequence).

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1

Ninomiya, K., Magatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,

Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, S., Omura, Y., Abe, K.,

Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,

Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,

Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,

Kimura, K., Yamashita, H., Matsuoka, K., Nakamura, Y., Sekine, M.,

Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,

Oshina, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,

Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.

NEDO human cDNA sequencing project

Unpublished

REFERENCE

2 (bases 1 to 1902)

AUTHORS Isogai, T. and Yamamoto, J.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7  
Kazusa-Kamatari, Kisarazu, Chiba 252-0818, Japan  
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
COMMENT NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction: Helix Research Institute (HRI) (supported by Japan  
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
HRI, and Biotechnology Center, National Institute of Technology and  
Evaluation; clone selection for full insert sequencing: HRI and  
RAB; annotation: HRI and RAB.

FEATURES  
source  
1. 1902  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="BRTHA2015406"  
/tissue\_type="thalamus"  
/clone\_lib="BRTHA2"  
/note="Cloning vector: pME18SFL3"

ORIGIN  
Query Match 66.0%; Score 1510.4; DB 9; Length 1902;  
Best Local Similarity 99.9%; Pred. No. 2.2e-282;  
Matches 1511; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 778 CTGAGCAAAATTGAAACATCTTGGTACTTAGGCGGGGAAACACGAGCCAGACCCGTGC 837  
DB 72 CTGAGCAAAATTGAAACATCTTGGTACTTAGGCGGGGAAACACGAGCCAGACCCGTGC 131  
QY 838 GTGAGCAGCCCTGCGCGCGGTAGCATGCGAGCTGCCATCCAAACGAGAGCTG 897  
DB 132 CTGAGCAGCCCTGCGCGCGGTAGCATGCGAGCTGCCATCCAAACGAGAGCTG 191  
QY 898 GACCCGACGCTCTAGAGAGCATGGCATCACTGGGCTGCTTACGGGACCGCGAGAGCTG 957  
DB 192 GACCCGACGCTCTAGAGAGCATGGCATCACTGGGCTGCTTACGGGACCGCGAGAGCTG 251  
QY 958 CATCGAGCTGCCAGTAGGAGGAGAACCAAGAAAGATGATATATATCTGCTTTTG 1017  
DB 252 CATCGAGCTGCCAGTAGGAGGAGAACCAAGAAAGATGATATATATCTGCTTTTG 311  
QY 1018 GATCGGAGGAGCGGTATCCAGCTGTGAGGACGAGACCTGCTCCCGGAATGATGTT 1077  
DB 312 GATCGGAGGAGCGGTATCCAGCTGTGAGGACGAGACCTGCTCCCGGAATGATGTT 371  
QY 1078 GACCCCGCGGAGCGGTGATTTCTCCATGCTGAGCGGTACAGGGAAGCGCGACCA 1137  
DB 372 GACCCCGCGGAGCGGTGATTTCTCCATGCTGAGCGGTACAGGGAAGCGCGACCA 431  
QY 1138 GAGCGGAAGTCCATGGAAGTCTGAGCATCACCATGCGGGGGTGGTGGCTCCCTGTA 1197  
DB 432 GAGCGGAAGTCCATGGAAGTCTGAGCATCACCATGCGGGGGTGGTGGCTCCCTGTA 491  
QY 1198 CCCACCGGAGCGGCTTGGAGATGGCCAGCACAGCCAGATCCCGTAGCGTCAGTGGGA 1257  
DB 492 CCCACCGGAGCGGCTTGGAGATGGCCAGCACAGCCAGATCCCGTAGCGTCAGTGGGA 551  
QY 1258 GCCTCCACGGGTCTGTCTCCAGCCCTTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTT 1317  
DB 552 GCCTCCACGGGTCTGTCTCCAGCCCTTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTT 611  
QY 1318 TCACCGGAGCGGGGCTGGAGTGAAGCTGAGGCTGAGGCGGGGCTCCCGACTTCCAAAACG 1377  
DB 612 TCACCGGAGCGGGGCTGGAGTGAAGCTGAGGCTGAGGCGGGGCTCCCGACTTCCAAAACG 671  
QY 1378 CAGACGCTGCTTCTCGGGGCGCCAGAGGCTGGGGCGCGCGGGGAGCAGCCCGCCCGCCC 1437  
DB 672 CAGACGCTGCTTCTCGGGGCGCCAGAGGCTGGGGCGCGCGGGGAGCAGCCCGCCCGCCC 731  
QY 1438 AGTGCCCGCTCCACACACCCCTGCGCGGCGCCCAAGGCTCCCGCGGCTCTCTGGCGGGAC 1497

DB 732 AGTGCCCGCTCCACACCCCTGCGCGGCGCCCGAGGCTCCCGCGCTCTCTTGGCGGACC 791  
QY 1498 CCCTTGTCACTCCGCTCTGTGCACACGCGCGGGGCGAGTCCACACGCGGACCCCGGGGACAACA 1557  
DB 792 CCCTTGTCACTCCGCTCTGTGCACACGCGCGGGGCGAGTCCACACGCGGACCCCGGGGACAACA 851  
QY 1558 CCACCCCGCAGCCCGCGGGGTGCGTTCGGGGGAGCCGCTGAGGAGTCTCTCACTCC 1617  
DB 852 CCACCCCGCAGCCCGCGGGGTGCGTTCGGGGGAGCCGCTGAGGAGTCTCTCACTCC 911  
QY 1618 ATCCGCAACAGCTTCTTGGGCTCCCTGCTTTTACCGGCGCAAGATGAGGTCCTTACC 1677  
DB 912 ATCCGCAACAGCTTCTTGGGCTCCCTGCTTTTACCGGCGCAAGATGAGGTCCTTACC 971  
QY 1678 GCTGAGGAGATGCTCCAGCTTGAACGCGAGTCTCTCCCGGAGCTGCAAAAACGCTCTGG 1737  
DB 972 GCTGAGGAGATGCTCCAGCTTGAACGCGAGTCTCTCCCGGAGCTGCAAAAACGCTCTGG 1031  
QY 1738 TTCCGGAATCTCATCTCTCTTGGACAAAGAAACAAATATTTCTGTGCTAAAGACAA 1797  
DB 1032 TTCCGGAATCTCATCTCTCTTGGACAAAGAAACAAATATTTCTGTGCTAAAGACAA 1091  
QY 1798 CTTCTCAGCAGCATCAAAAGCAGACATCGTCCATGCTTCTGTCATCCCGAGCTTCTGAGT 1857  
DB 1092 CTTCTCAGCAGCATCAAAAGCAGACATCGTCCATGCTTCTGTCATCCCGAGCTTCTGAGT 1151  
QY 1858 CACAGTGTCTGTTCACAGACCAAGCTTTTCAAGGCGCGAGTACAAGGCCAGTGGCGCCCTCC 1917  
DB 1152 CACAGTGTCTGTTCACAGACCAAGCTTTTCAAGGCGCGAGTACAAGGCCAGTGGCGCCCTCC 1211  
QY 1918 GTCTTCCAAAAGCCGCTCCGCTTCAAGGTGGAATCATGAGTCTCTGAGGGTCCAGAGCCC 1977  
DB 1212 GTCTTCCAAAAGCCGCTCCGCTTCAAGGTGGAATCATGAGTCTCTGAGGGTCCAGAGCCC 1271  
QY 1978 TCCCGCGGAGCGGACGCGAGGAGTGTGGATCTACTCCGTACCTTCACTCTCATC 2037  
DB 1272 TCCCGCGGAGCGGACGCGAGGAGTGTGGATCTACTCCGTACCTTCACTCTCATC 1331  
QY 2038 TCGGGTCCACGCGCTCGGTTCAAGCGAGTGTGGAGACCATCCAGGCAAGTCTCTGAGC 2097  
DB 1332 TCGGGTCCACGCGCTCGGTTCAAGCGAGTGTGGAGACCATCCAGGCAAGTCTCTGAGC 1391  
QY 2098 ACTCATGACAGCCCTTCCGTGAGGCGCTTGGGAGAGAACCGGGGCGGAGAGCCGG 2157  
DB 1392 ACTCATGACAGCCCTTCCGTGAGGCGCTTGGGAGAGAACCGGGGCGGAGAGCCGG 1451  
QY 2158 CTTGCTGGTGGCGCCCGGAGGCTGAGCGCCCGCGCGCGCGAGAGCTCTGAGAGCTG 2217  
DB 1452 CTTGCTGGTGGCGCCCGGAGGCTGAGCGCCCGCGCGCGCGAGAGCTCTGAGAGCTG 1511  
QY 2218 AGCAGCTCTCCCGCGGAGGCGCCCGGAGGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTG 2277  
DB 1512 AGCAGCTCTCCCGCGGAGGCGCCCGGAGGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTG 1571  
QY 2278 CTTGCTGGCTGA 2289  
DB 1572 CTTGCTGGCTGA 1583

RESULT 12  
BC016681  
LOCUS  
DEFINITION Homo sapiens KIAA1811 protein, mRNA (cDNA clone MGC:21870  
IWAG:4341838), complete cds.  
ACCESSION BC016681  
VERSION BC016681.1  
KEYWORDS GI:16741775  
SOURCE MGC.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2128)









QY 1462 GGGCCCCAGAGCTCCCGCGCTCTCTGGCGGGACCCCTTGGACTGGCTCTGACACG 1521  
 Db 1053 -----GGCTCCCGCGCTCTCTGGCGGGACCCCTTGGACTGGCTCTGACACG 1103  
 QY 1522 CCGCGGCGAGTCCACCGGACCCCGGGGACAAACACACCCCGAGCCCGCGCGGTGGC 1581  
 Db 1104 CCGCGGCGAGTCCACCGGACCCCGGGGACAAACACACCCCGAGCCCGCGCGGTGGC 1163  
 QY 1582 GTCGGGGAGCGCGCTGGAGAGTGGTCTCAACTCCATCCGCAACAGCTTCTCGGGTCC 1641  
 Db 1164 GTCGGGGAGCGCGCTGGAGAGTGGTCTCAACTCCATCCGCAACAGCTTCTCGGGTCC 1223  
 QY 1642 CCTCGCTTTCACCGGCGGACAGTGCAGTCCCTACCGCTGAGGAGATGTCAGCTTGACG 1701  
 Db 1224 CCTCGCTTTCACCGGCGGACAGTGCAGTCCCTACCGCTGAGGAGATGTCAGCTTGACG 1283  
 QY 1702 CCAGAGTCTCTCCCGGAGCTGGCAACCGCTCTGGTTCGGGAACTTCATCTCTTGAC 1761  
 Db 1284 CCAGAGTCTCTCCCGGAGTGGCAACCGCTCTGGTTCGGGAACTTCATCTCTTGAC 1343  
 QY 1762 AAAGAAGAACAAATATTCTCGTGTCTAAAGACAAACCTCTCAGCAGCATCAAGCAGAC 1821  
 Db 1344 AAAGAAGAACAAATATTCTCGTGTCTAAAGACAAACCTCTCAGCAGCATCAAGCAGAC 1403  
 QY 1822 ATCGTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTGCTGTGACACAGCAGC 1881  
 Db 1404 ATCGTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTGCTGTGACACAGCAGC 1463  
 QY 1882 TTCAGGCGGAGTACAGCGGACGTGGCGGCGCTCTCGTCTTCCAAAGCCCGTCCGGTTC 1941  
 Db 1464 TTCAGGCGGAGTACAGCGGACGTGGCGGCGCTCTCGTCTTCCAAAGCCCGTCCGGTTC 1523  
 QY 1942 CAGGTGGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCGACGCGGACGGAGCGGA 2001  
 Db 1524 CAGGTGGACATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCGACGCGGACGGAGCGGA 1583  
 QY 2002 GGTGGTGATCTACTCGGTCACTTCACTCTCATCTCGG 2041  
 Db 1584 GGTGGTGATCTACTCGGTCACTTCACTCTCATATCGG 1623

RESULT 14  
 AR541973  
 LOCUS AR541973 1797 bp DNA linear PAT 08-OCT-2004  
 DEFINITION Sequence 221 from patent US 6743619.  
 ACCESSION AR541973  
 VERSION AR541973.1 GI:53934053  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 1797)  
 AUTHORS Tang, Y.T., Zhou, P., Goodrich, R., Liu, C., Asundi, V., Ren, F.,  
 Zhang, J., Zhao, Q.A., Yang, Y., Xue, A.J., Wehrman, T., Wang, J.-R.,  
 Wang, D. and Drmanac, R.T.  
 TITLE Nucleic acids and polypeptides  
 JOURNAL Patent: US 6743619-A 221 01-JUN-2004;  
 FEATURES Location/Qualifiers  
 source 1..1797  
 /organism="unknown"  
 /mol\_type="genomic DNA"  
 ORIGIN  
 Query Match 42.8%; Score 980; DB 6; Length 1797;  
 Best Local Similarity 75.4%; Pred. No. 1.3e-179;  
 Matches 1470; Conservative 0; Mismatches 0; Indels 480; Gaps 1;  
 QY 268 AGGTACCTGGTTCGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAGAG 327  
 Db 87 AGGTACCTGGTTCGGAGCAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAGAG 146  
 QY 328 GGGAGACTGACGCGCCCAAGGAGCGCGAAAGTTCTTCGCGCCAGATTGTGTCTGCGCTGAC 387

147 GGGAGACTGACGCGCCAAAGGAGGCCCGAAAGTTCTTCGCGCAGAGTTGTCTGCGCTGAC 206  
 QY 388 TTCTGCCACAGCTACTCCATCTGCAACAGAGACCTAAAGCCCGAGAAACCTGCTTTGGAT 447  
 Db 207 TTCTGCCACAGCTACTCCATCTGCAACAGAGACCTAAAGCCCGAGAAACCTGCTTTGGAT 266  
 QY 448 GAGAAAAAACAATCCGCATTCGCATTCGGCATTCGGCATTCGGCATTCGGCATTCGGCATTC 507  
 Db 267 GAGAAAAAACAATCCGCATTCGCATTCGGCATTCGGCATTCGGCATTCGGCATTCGGCATTC 326  
 QY 508 CTCTGAGAGACAGCTGCGGCTCCCGCATTTATGCGGTGTCAGAGGTGATTAAAGGGGAA 567  
 Db 327 CTCTGAGAGACAGCTGCGGCTCCCGCATTTATGCGGTGTCAGAGGTGATTAAAGGGGAA 386  
 QY 568 AAATATATGATGCGCGCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTGCTC 627  
 Db 387 AAATATATGATGCGCGCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTGCTC 446  
 QY 628 GTGGGGCTCTGCGCTTTGATGACGACCACTCCCGCAGCTGTGGAGAGAGGTGAACGG 687  
 Db 447 GTGGGGCTCTGCGCTTTGATGACGACCACTCCCGCAGCTGTGGAGAGAGGTGAACGG 506  
 QY 688 GGGTCTTCCACATGCGCGCGCGCATTCATTCCTCCAGATTGCCAGAGCTCTCGAGGGGAATG 747  
 Db 507 GGGTCTTCCACATGCGCGCGCGCATTCATTCCTCCAGATTGCCAGAGCTCTCGAGGGGAATG 566  
 QY 748 ATCGAGTGGAGCGCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATTCCTTGGTAC 807  
 Db 567 ATCGAGTGGAGCGCGGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATTCCTTGGTAC 626  
 QY 808 CTAGCGGGGAAACACAGAGCAGACCCGTGCTGGAGCAGCCCTCGCGCGCGGGTAGCC 867  
 Db 627 CTAGCGGGGAAACACAGAGCAGACCCGTGCTGGAGCAGCCCTCGCGCGCGGGTAGCC 686  
 QY 868 ATCGGAGCTGCTCATCCAGCGGAGCTGAGACCCCGACGCTCTAGAGAGCATGGCATCA 927  
 Db 687 ATCGGAGCTGCTCATCCAGCGGAGCTGAGACCCCGACGCTCTAGAGAGCATGGCATCA 746  
 QY 928 CTGGGCTGCTTCAGGGACCCCGAGAGCTGCATCGCGAGCTGCGAGTGGAGAGGAGAAC 987  
 Db 747 CTGGGCTGCTTCAGGGACCCCGAGAGCTGCATCGCGAGCTGCGAGTGGAGAGGAGAAC 806  
 QY 988 CAAGAAAAAGATATATATATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGTGAG 1047  
 Db 807 CAAGAAAAAGATATATATATCTGCTTTTGGATCGGAAGGAGCGGTATCCAGCTGTGAG 866  
 QY 1048 GACGAGACCTGCTCCCGGAAATGATTTGACCCCGCGGAGCGGTGATTCCTCC 1107  
 Db 867 GACGAGACCTGCTCCCGGAAATGATTTGACCCCGCGGAGCGGTGATTCCTCC 926  
 QY 1108 ATGCTGAGCGCTCAAGGAAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTCTGAGCATC 1167  
 Db 927 ATGCTGAGCGCTCAAGGAAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTCTGAGCATC 986  
 QY 1168 ACCGATCGCGGGGTGGTGGCTCCCTGTATCCACACCGAGCGGCTTTGGAGATGGCCAG 1227  
 Db 987 ACCGATCGCGGGGTGGTGGCTCCCTGTATCCACACCGAGCGGCTTTGGAGATGGCCAG 1046  
 QY 1228 CAGCGCCAGAGATCCCGTAGCGTCAAGTGGAGCTCCACGCGGTCTGTCTCCAGCGCTCTA 1287  
 Db 1047 CAGCGCCAGAG----- 1057  
 QY 1288 AGCAGCCCAAGGAGTCCGCTCTTTTCTTTTACCGGAGCGGGGGCTGGAGATGAGGCT 1347  
 Db 1058 ----- 1057  
 QY 1348 CGAGCGGGGGCTCCCGACTTCCAAAAACGACAGCTGCTCTTCGCGGGCCCCAGGGGT 1407  
 Db 1058 ----- 1057  
 QY 1408 GGGGGCGCGGGGAGCAGCGCCCCCGCGCTCCACACCCCTGCGCGGCC 1467

Db	1058	-----	1057
Qy	1468	CCAGGCTCCCGCGCTCTCTCTGCGGAGCCCTTGTGACTCGCTCTGTGACACGCCCGG	1527
Db	1058	-----	1057
Qy	1528	GCCAGTCCCAACCGGACCCCGGGAACAACACCCGCCAGCCCGCGGTGGGTGGG	1587
Db	1058	-----	1057
Qy	1588	GGAGCCGCTGGAGGATCGTCTCACTCCATCGGAAACAGTTCCTGGGCTCCCTCGC	1647
Db	1058	-----	1057
Qy	1648	TTTCAACCGGCAAGATGACAGTCCCTTACCGCTGAGGAGATGTCAGCTTGACGCCAGAG	1707
Db	1058	-----	1057
Qy	1708	TCCTCCCGGAGTGGCAAAACGCTCTGTGTTGGGAACTTTCATCTCTTGGACAAAGAA	1767
Db	1058	-----GCTGGCAAAACGCTCTGTGTTGGGAACTTTCATCTCTTGGACAAAGAA	1106
Qy	1768	GAACAAATATTCCTGCTGTAAAGGACAAACCTCTCAGCAGCATCAAAGCAGACATCGTC	1827
Db	1107	GAACAAATATTCCTGCTGTAAAGGACAAACCTCTCAGCAGCATCAAAGCAGACATCGTC	1166
Qy	1828	CATGCTTTCTGTGATCCCGAGCTGAGTCACAGTGTGTGTCAACAGCAGCTTCAGG	1887
Db	1167	CATGCTTTCTGTGATCCCGAGCTGAGTCACAGTGTGTGTCAACAGCAGCTTCAGG	1226
Qy	1888	GCCGAGTACAAAGGCAAGTGGCGGCCCTTCCGTCTTCCAAAGCCCGTCCGCTTCAGGTG	1947
Db	1227	GCCGAGTACAAAGGCAAGTGGCGGCCCTTCCGTCTTCCAAAGCCCGTCCGCTTCAGGTG	1286
Qy	1948	GACATCAGCTCCTCTGAGGTCACAGCCCTCCCGCGAGCGGACGCGCGGAGGTGT	2007
Db	1287	GACATCAGCTCCTCTGAGGTCACAGCCCTCCCGCGAGCGGACGCGCGGAGGTGT	1346
Qy	2008	GGCATCTACTCCGTCACCTTCACTCTCATCTCGGTCCTCAGCCGTCGCTTCAAGCAGTG	2067
Db	1347	GGCATCTACTCCGTCACCTTCACTCTCATCTCGGTCCTCAGCCGTCGCTTCAAGCAGTG	1406
Qy	2068	GTGAGACCATTCAGGACAGCTCCTGAGCACTATGACGCGCTCGGTGACGCCCTG	2127
Db	1407	GTGAGACCATTCAGGACAGCTCCTGAGCACTATGACGCGCTCGGTGACGCCCTG	1466
Qy	2128	GCAGCAGAGAACGGGCGCCAGACCCGCGCTCTGTGCTGCCACCCCGAAGCTTCAG	2187
Db	1467	GCAGCAGAGAACGGGCGCCAGACCCGCGCTCTGTGCTGCCACCCCGAAGCTTCAG	1526
Qy	2188	CCCCACCCGCGCCAGACCCAGAGCTG 2217	
Db	1527	CCCCACCCGCGCCAGACCCAGAGCTG 1556	

RESULT 15  
AR232171  
LOCUS AR232171 3364 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 3 from patent US 6455292.  
ACCESSION AR232171  
VERSION AR232171.1 GI:27274062  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3364)  
AUTHORS Shu, Y., Fan, W., Kovacs, K.P., Zidanic, M. and Jay, G.  
TITLE Full-length serine protein kinase in brain and pancreas  
JOURNAL Patent: US 6455292-A 3 24-SEP-2002;  
FEATURES  
1. 3364  
source /organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 34.1%; Score 780.4; DB 6; Length 3364;  
Best Local Similarity 68.0%; Pred. No. 5.6e-141;  
Matches 1279; Conservative 0; Mismatches 406; Indels 195; Gaps 6;  
QY 265 TTTAGGTACTCTGGTCTGAGGACACGCTCTCGGGGGTGTAGCTATTGACCTACCTGGTAAAG 324  
DB 500 TGTAGGTACTCTGGTCTAGAACACGCTGTGAGTGTGAGCTCTTGACTACTCTGGTGAAG 559  
QY 325 AAGGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTTCGCCGACAGTTGTCTGTGCGCTG 384  
DB 560 AAGGGGAGACTGACGCCCAAGGAGGCTCGAAGTTCTTCGCCGACAGTCACTCTGTGCGCTG 619  
QY 385 GACTTCTGCCACAGCTATCTCCATCTGCCACAGACCTAAAGCCCGAGAAACCTGCTTTTG 444  
DB 620 GACTTCTGCCACAGCTACTCCATATGCCACAGGATCTGAAACCTGAAACCTCTGCTG 679  
QY 445 GATGAGAAAAACACTCCGCATTGCGACTTTGGCATGCGCTCCCTGCGAGGTGGGGAC 504  
DB 680 GACGAGAAACAACATCCGCATTCGCAGACTTTGGCATGCGCTCCCTGCGAGGTGGCGAC 739  
QY 505 AGCTTCTCGAGACACAGCTGCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAGGGG 564  
DB 740 AGCTTCTCGAGACACAGCTGTGGTCCCCCCTACCTAGCCCTGCCCGAGGTGATCCGGGG 799  
QY 565 GAAAAATATGATGGCCCGCGGCGAGACATGTGGAGTGTGGAGTGTATCTCTTTCGCCCTG 824  
DB 800 GAGAAATATGACGCGCGGAAAGCGGACGTGTGGAGCTGCGGGGTCTATCTCTGTCGCTTG 859  
QY 625 CTGCTGGGGCTGTCCTTTGATGACGACACACCTCCGCGAGCTGCGAGAGGTGAAG 684  
DB 860 CTGCTGGGGCTGTCCTTTGACGATGACAACTTCGCAAGCTGCTGCGAGAGGTGAAG 919  
QY 685 CGGGGCTCTTCCACATGCGCCCACTTCACTTCTCCAGATTGCGAGAGCTCTCTGAGGGGA 744  
DB 920 CGGGGCTGTTCACATGCGGCACTTTATCCCGCCGACTGCCAGAGTCTGCTACGGGGC 979  
QY 745 ATGATCGAGTGTGAGCGGCAAAAGGCTCAGTCTGAGCAAAATTTCAGAAACATCTCTGG 804  
DB 980 ATGATCGAGTGTGAGCGGCAACCGCCCTCACTAGAGCACATTCAGAAACACATATGG 1039  
QY 805 TACCTAGGGGGGAAACACGAGCCAGACCCGCTGCTGAGGACAGCCCTGCGCCCGGGTA 864  
DB 1040 TATATAGGGGGCAAGATGAGCCCGAACCC-----AGAGCAGCCCATTTCTCGCAAGTG 1093  
QY 865 GCCATGCGGAGCTGCGCATTCACAGGAGCTGTGACCCCGACGCTCTCTAGAGAGCATGGCA 924  
DB 1094 CAGATCGCTCGCTGCCAGCTGTGAGGACATCGACCCGACGCTGTGGACAGCATGCAC 1153  
QY 925 TCACTGGGCTGTTCAGGGACCGGAGAGCTGCTCATCGGAGCTGCGAGTGTGAGGGAG 984  
DB 1154 TCACCTGGGCTGTTCGAGACCCGCAACAGCTGTCTGAGGACCTGTCTCCGAGGAGGAG 1213  
QY 985 AACCAAGAAAGATGATATATTATCTGCTTTTCGATCGGAAGAGCGGTATCCAGCTGT 1044  
DB 1214 AACGAGAGAGATGATTTACTTCTCTCTGGAACGGAAGAGGTATCCCGAGCCAG 1273  
QY 1045 GAGGACGAGGACCTGCTCCCGGAATGATTTGACCCCCCGGAGCGGTGTGATTTCT 1104  
DB 1274 GAGGATGAGGACCTGCTCCCGGAAACGAGATAGACCTCCCGGAGCGGTGTGAGCTCC 1333  
QY 1105 CCATGCTGAGCGCTCAGGGAAACCGGACGAGCGGAGTCCATGGAAGTCTCTGAGC 1164  
DB 1334 CCGATGCTGAACCGGACGCGCAAGCGCGGCGGAGAGCGAAATCCATGGAAGTCTCTCAGC 1393  
QY 1165 ATCAACGATCCCGGGGTGTGCTCCCTGTATCCCAACCGGAGCGCTTTGGAGATGGCC 1224  
DB 1394 GTGACGAGCGG-----GGCTCCCGGTGCTGCGGGCGGCGCACTTGAGATGGCC 1444  
QY 1225 CAGCACGCCAGAGATCCCGTACGTCAGTGTGAGGCTTCCACGGGTCTGTCTCTCAGCCCT 1284  
DB 1445 CAGCACGCCAGAGGCTCTCGGTCTCATCAGCGGTGCTCTCTCAGGCGCTTTCCACGAGCCCA 1504

```
Qy 1285 CTAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACGGAGCCGGGGCTGGAGATGAG 1344
Db |||||
Qy 1505 CTCAGCAGCCCCG----- 1518
Qy 1345 GCTCAGGCGGGGCTCCCGACTTCCAAACGACAGCGTCCCTTCTCGGGGCCCCAGG 1404
Db ----- 1519
Qy 1405 GGTGGGGCGCGGGGAGACCCCGCCCGCCAGTGCOCCTCCACACCCCTGCCCGGC 1464
Db |||||
Qy 1519 -----GGTGACCCCTCACCCCTCACCAAGGGGAGTCCCTCCCC- 1558
Qy 1465 CCCCCAGGCTCCCGCGCTCTCTGGGGGAGCCCTTGCACTCGCCTCTGCACACGCC 1524
Db |||||
Qy 1559 -----ACCCCCAAGGGGACACCTGTCCACACGCCA 1588
Qy 1525 CGGSCCAGTCCACCGGACCCCGGGACACACACCCCGCCAGCCCGGGTGGCGTC 1584
Db |||||
Qy 1589 AAGGAGAGCCGGGTGGACGCCCAACCCACGCCCGCGTCCAGCCC-----AGCGTC 1642
Qy 1585 GGGGAGCGCCTCGGAGAGTCTCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1644
Db |||||
Qy 1643 GGAGGGTGGCTTGAGGGCGCGCTCAACTCCATCAAGAACAGCTTCTGGGCTCACCC 1702
Qy 1645 CGCTTTCACGGCGCAGATGACAGTCCCTACCGCTGAGGAGATGTCAGCTTGACGCCA 1704
Db |||||
Qy 1703 CGCTTTCACCGCCGGAACCTCAAGATTCCGACGCCGGAGGAGATGTCCAACTGACACCA 1762
Qy 1705 GAGTCTCTCCCGGAGCTGGGAAACGCTCTCGGTTCGGGAACTTTCATCTCTCGGCAAA 1764
Db |||||
Qy 1763 GAGTCGTCCCGAGCTGGCGAAGATCTCTGGTTTGGGAACTTTCATCAGCCTGGAGAAG 1822
Qy 1765 GAAGAACAAATATTCCTCGTCTAAAGGACAAACCTCTCAGCAGCATCAAAGCAGACATC 1824
Db |||||
Qy 1823 GAGGAGCAGATCTTCGTGTTCATCAAGACAAACCTCTGAGTCTCATCAAGGCTGACATC 1882
Qy 1825 GTCCATGCTTCTGTGATCCCGAGCCTGAGTCACAGTGTGTGTACAGACAGCTTC 1884
Db |||||
Qy 1883 GTGACGCTTCTGTGATCCAGTTCAGTTCAGTTCAGCCACAGCGTCTATCTCCAAACGAGCTTC 1942
Qy 1885 AGGCGCGAGTACAGGCGAGTGGCGCCCTCTCGTCTTCCAAAGCCGCTCCGCTCCAG 1944
Db |||||
Qy 1943 CGGCGCGAGTACAGGCGACGGGGGGCGAGCCGTGTTCAGAAAGCCGTCAAGTTCAG 2002
Qy 1945 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCAGCGGAGCGGAGGAGT 2004
Db |||||
Qy 2003 GTTGATATCACCTACCGAGGGT-----GGGAGGCGCAGAGGAG 2044
Qy 2005 GGTGGCATCTACTCCGTACCTTCATCTCATCTCGGGTCCAGCCGTTCGGTTCAAGCGA 2064
Db |||||
Qy 2045 AACGGCATCTACTCCGTACCTTCACCTGTCTCTCAGGCGCCAGCCGTTCGCTTCAAGAGG 2104
Qy 2065 GTGGTGAGACCATCCAGGACAGCTCTGAGCACTCATGACAGCCCTCCGTGACGCCC 2124
Db |||||
Qy 2105 GTGGTGAGACCATCCAGGCGCCAGCTGTGAGCACACAGACCCGCTGCGGCCACGAC 2164
Qy 2125 CTGGCAGACGAGAAGACGG 2144
Db |||||
Qy 2165 TTGTCAGACCACTACTG 2184
```

Search completed: February 19, 2005, 12:29:04  
Job time : 9602 secs

This Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 08:07:17 ; Search time 1142 Seconds  
(without alignments)  
11865.401 Million cell updates/sec

Title: US-10-803-277-3  
Perfect score: 2289  
Sequence: 1 atgggacttgagtttggttt.....acgggaccctctgcctga 2289

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002as:\*  
7: Geneseq2002bs:\*  
8: Geneseq2003as:\*  
9: Geneseq2003bs:\*  
10: Geneseq2003cs:\*  
11: Geneseq2003ds:\*  
12: Geneseq2004as:\*  
13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2289	100.0	2289	10	ABV74558 Human kin
2	2020.2	88.3	2112	10	ABV74559 Human kin
3	2020.2	88.3	2337	10	ABV74557 Human kin
4	2020.2	88.3	2337	12	ADL14129 Novel hum
5	2020.2	88.3	2385	4	AAS06717 Polynucle
6	2020.2	88.3	2576	10	ADL14127 Novel hum
7	2020.2	88.3	2576	10	ADF74247 Human nov
8	2020.2	88.3	2897	6	AD26464 Human kin
9	2020.2	88.3	2950	13	ADL14127 Human kin
10	2020.2	88.3	2953	9	AAL55772 Human euk
11	2020.2	88.3	2980	10	ADL14127 Human pro
12	2020.2	88.3	2980	12	ADL14127 Novel hum
13	2020.2	88.3	2980	13	ADQ85869 Human tum
14	2020.2	88.3	2980	13	ADQ85869 Human uro
15	2020.2	88.3	2980	13	ADL14127 Human euk
16	2017.2	88.1	2334	13	ADL14127 Human euk
17	1839	80.3	2799	8	AAL51889 Human cel
18	1510.4	66.0	1902	12	ADQ63436 Novel hum
19	980	42.8	1797	8	ABX70594 Novel hum
20	800.8	35.0	1911	9	AAL60438 Human kin

21	780.4	34.1	3364	8	ABX13584	Abx13584 Human cDN
22	780.4	34.1	3364	10	AD60986	Ad60986 Human ser
23	780.4	34.1	3364	12	ADH59077	Adh59077 Human KSE
24	778.8	34.0	2908	8	ABX13583	Abx13583 Human cDN
25	778.8	34.0	2908	10	AD60985	Ad60985 Human ser
26	778.8	34.0	2908	12	ADH59075	Adh59075 Human KSE
27	777.2	34.0	1827	6	ABQ77626	Abq77626 Human kin
28	777.2	34.0	2007	6	ABQ77625	Abq77625 Human kin
29	777.2	34.0	2647	6	AD34315	Ad34315 Human PKI
30	777.2	34.0	3576	13	ADR50785	Adr50785 Human c-b
31	774.8	33.8	2025	9	AAL60436	Aal60436 Human kin
32	774.8	33.8	3831	12	ADJ96555	Adj96555 Human cal
33	773.2	33.8	2025	6	ABA02995	Aba02995 Human pro
34	773.2	33.8	2025	8	ACC48153	Acc48153 Human ser
35	773.2	33.8	2217	6	ABA02994	Aba02994 Human pro
36	614	26.8	614	4	ABA08924	Aba08924 Human HrP
37	551	24.1	906	4	ABA08296	Aba08296 Human HrP
38	512	22.4	512	6	ABK70216	Abk70216 Human lun
39	408.4	17.8	584	12	ACH73134	Ach73134 Human gen
40	408.4	17.8	19640	11	ACN44570	Acn44570 Human gen
41	365	15.9	700	12	ADQ24923	Adq24923 Human sof
42	337.2	14.7	2720	4	ABL10489	Ab110489 Drosophil
43	296.8	13.0	2173	10	ADL14129	Adl14129 Human cDN
44	296.8	13.0	2333	10	ADL14129	Adl14129 Human cDN
45	216.2	9.4	2011	12	ADQ63225	Adq63225 Novel hum

## ALIGNMENTS

RESULT 1  
ABV74558  
ID ABV74558 standard; cDNA; 2289 BP.  
XX  
AC ABV74558;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human kinase #2 coding sequence.  
XX  
KW Human; kinase; chromosome 19; gene; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 1..2289  
FT /\*tag= a  
FT /product= "Human kinase #2"  
XX  
PN WO200281670-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 04-APR-2002; 2002WO-US010786.  
XX  
PR 06-APR-2001; 2001US-0282036P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Turner CA, Mathur B, Friddle CJ;  
XX  
DR WPI; 2003-058538/05.  
DR P-PSDB; ABB98744.  
XX  
PT New human kinase proteins useful for diagnosis, drug screening, clinical trial monitoring, treatment of disorders and diseases, and cosmetic and nutritional applications.  
XX  
PS Claim 5; Page 41-42; 47pp; English.  
XX  
CC The present sequence is the coding sequence for a novel human kinase. The genomic locus encoding the kinase is thought to be on human chromosome 19. The kinase and its coding sequence are useful for diagnosis, drug

CC	screening, clinical trial monitoring, treatment of disorders and	
CC	diseases, and cosmetic and nutritional applications	
XX		
SQ	Sequence 2289 BP; 457 A; 759 C; 666 G; 407 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 2289; DB 10; Length 2289;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 2289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGGGACTTGAGTTTGGTTTCTCTAGAGGCTGTGTGGAACTGGAGTCACATTCCTCCAGGG 60
Db	1	ATGGGACTTGAGTTTGGTTTCTCTAGAGGCTGTGTGGAACTGGAGTCACATTCCTCCAGGG 60
Qy	61	AGTAGGGAACTGGAACTCTCTCTCCACGGAATTAATGGAACTGGAGTCCTCTCTCC 120
Db	61	AGTAGGGAACTGGAACTCTCTCTCCACGGAATTAATGGAACTGGAGTCCTCTCTCC 120
Qy	121	CCAGGGACCATGGGAATGGAGTCCTCTTTCTCCCAAGGATCATGGGAATGGAGTTCTC 180
Db	121	CCAGGGACCATGGGAATGGAGTCCTCTTTCTCCCAAGGATCATGGGAATGGAGTTCTC 180
Qy	181	TGCCACAGGAGCAGTGGAAATGGAGAGCAGAGCCCTTTGGTCTCTCCACATGCCCTTTC 240
Db	181	TGCCACAGGAGCAGTGGAAATGGAGAGCAGAGCCCTTTGGTCTCTCCACATGCCCTTTC 240
Qy	241	CAGCCCTCTGCCCTCTATATCTCTTTAGGTACTGTCTCTGGAGCAGCTCTCGGGGGT 300
Db	241	CAGCCCTCTGCCCTCTATATCTCTTTAGGTACTGTCTCTGGAGCAGCTCTCGGGGGT 300
Qy	301	GAGCTATTCCGACTACTGTGTAAAGAGGGAGAGCTGACGCCCAAGGAGGCCGGAAGTTC 360
Db	301	GAGCTATTCCGACTACTGTGTAAAGAGGGAGAGCTGACGCCCAAGGAGGCCGGAAGTTC 360
Qy	361	TTCCGCCAGATTGTCTGGCTGGACTTTGCCACAGCTACTTCCATCTGCCACAGAGC 420
Db	361	TTCCGCCAGATTGTCTGGCTGGACTTTGCCACAGCTACTTCCATCTGCCACAGAGC 420
Qy	421	CTAAGCCCGAGAACCTGCTTTTGGATGAGAAAAACAACATCCGCAATTGAGACTTCGGC 480
Db	421	CTAAGCCCGAGAACCTGCTTTTGGATGAGAAAAACAACATCCGCAATTGAGACTTCGGC 480
Qy	481	ATGGCGTCCCTGCAGGTGGGGAAGAGCTCTGGAGACCCAGCTCGGGGTCCGCCATTAT 540
Db	481	ATGGCGTCCCTGCAGGTGGGGAAGAGCTCTGGAGACCCAGCTCGGGGTCCGCCATTAT 540
Qy	541	CGGTGTCCAGAGTGAATTAAGGGGGAATAATGATGCGCCCGGGCAGACATGTGGAGC 600
Db	541	CGGTGTCCAGAGTGAATTAAGGGGGAATAATGATGCGCCCGGGCAGACATGTGGAGC 600
Qy	601	TGTGGAGTCATCTCTTCGCCCTGCTCGTGGGGGCTCTGCCCTTTTGATGACGACAACTC 660
Db	601	TGTGGAGTCATCTCTTCGCCCTGCTCGTGGGGGCTCTGCCCTTTTGATGACGACAACTC 660
Qy	661	CGCCAGCTGTGGAGAGGTGAACCGGGGCTTTCCACATGCCCTTCAATTCCTCCA 720
Db	661	CGCCAGCTGTGGAGAGGTGAACCGGGGCTTTCCACATGCCCTTCAATTCCTCCA 720
Qy	721	GATTCGCGAGCTCTCTGAGGGGAATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTG 780
Db	721	GATTCGCGAGCTCTCTGAGGGGAATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTG 780
Qy	781	GAGCAAAATTCAGAAACATCTTTGGTACTTAGCGGGGAAACAGAGCCAGACCCGTGGCTG 840
Db	781	GAGCAAAATTCAGAAACATCTTTGGTACTTAGCGGGGAAACAGAGCCAGACCCGTGGCTG 840
Qy	841	GAGCCAGCCCTTGGCGCGGTAGCATGCGAGCCCTGCCATCCCAACGAGAGCTGGAC 900
Db	841	GAGCCAGCCCTTGGCGCGGTAGCATGCGAGCCCTGCCATCCCAACGAGAGCTGGAC 900
Qy	901	CCGAGCTCTAGAGAGCATGGCATCATCTGGGCTGCTTCAGGGACCGCGAGAGGCTGCAT 960
Db	901	CCGAGCTCTAGAGAGCATGGCATCATCTGGGCTGCTTCAGGGACCGCGAGAGGCTGCAT 960

Qy	961	CGCGAGCTGCCAGTGTGAGGAGAGAACCAAGAAAGATGATATATATCTGCTTTTGGAT 1020
Db	961	CGCGAGCTGCCAGTGTGAGGAGAGAACCAAGAAAGATGATATATATCTGCTTTTGGAT 1020
Qy	1021	CGGAGGAGCGGTATCCCGAGCTGTGAGGACCAAGGACCTGCTCCCGGGAATGATGTTGAC 1080
Db	1021	CGGAGGAGCGGTATCCCGAGCTGTGAGGACCAAGGACCTGCTCCCGGGAATGATGTTGAC 1080
Qy	1081	CGCCCCCGGAAAGCGTGTGGATTTCTCCATGCTGAGCGCTCACGGGAAGCGGACCAAGAG 1140
Db	1081	CGCCCCCGGAAAGCGTGTGGATTTCTCCATGCTGAGCGCTCACGGGAAGCGGACCAAGAG 1140
Qy	1141	CGGAGTCCATGGAAGTCTCTGAGCATACCGATCCCGGGGTGTGTGCTCCCTGTATACC 1200
Db	1141	CGGAGTCCATGGAAGTCTCTGAGCATACCGATCCCGGGGTGTGTGCTCCCTGTATACC 1200
Qy	1201	ACCCGACGGGCTTTGGAGATGCGCCAGCAGCAGAGATCCCGTAGCGTCAGTGAGGCC 1260
Db	1201	ACCCGACGGGCTTTGGAGATGCGCCAGCAGCAGAGATCCCGTAGCGTCAGTGAGGCC 1260
Qy	1261	TCACAGGCTGTGCTCTCCAGCCCTCTAAGCAGGCCCAAGGAGTCCGGTCTTTTCTCTTTCA 1320
Db	1261	TCACAGGCTGTGCTCTCCAGCCCTCTAAGCAGGCCCAAGGAGTCCGGTCTTTTCTCTTTCA 1320
Qy	1321	CGCGAGCCGGGGCTGGAGATGAGGCTCGAGGCGGGGGCTCCCGCATTTCCAAACCGCAG 1380
Db	1321	CGCGAGCCGGGGCTGGAGATGAGGCTCGAGGCGGGGGCTCCCGCATTTCCAAACCGCAG 1380
Qy	1381	ACGCTGCTCTTCGCGGCCCCAGGGGTGGGGGCGCGGGGAGAGCCCCCGCCCCCAGT 1440
Db	1381	ACGCTGCTCTTCGCGGCCCCAGGGGTGGGGGCGCGGGGAGAGCCCCCGCCCCCAGT 1440
Qy	1441	GCCCGTCCACACCCCTGCGGCCCGCCACAGGCTCCCCCGCTCTCTGTGCGGAGACCCCC 1500
Db	1441	GCCCGTCCACACCCCTGCGGCCCGCCACAGGCTCCCCCGCTCTCTGTGCGGAGACCCCC 1500
Qy	1501	TTGCACTGTGCTCTGACAGCCCGCGGCTGCGGAGAGCGGCTCTCAATCTCCATC 1620
Db	1501	TTGCACTGTGCTCTGACAGCCCGCGGCTGCGGAGAGCGGCTCTCAATCTCCATC 1620
Qy	1561	CCCCCAGCCCGCGGCTGCGGAGAGCGGCTGCGGAGAGTCTCAATCTCCATC 1680
Db	1561	CCCCCAGCCCGCGGCTGCGGAGAGCGGCTGCGGAGAGTCTCAATCTCCATC 1680
Qy	1621	CGCAACAGCTTCTGGGCTCCCTGCTTTTACCGCGGCAAGTGCAGGTCCTTACCGCT 1680
Db	1621	CGCAACAGCTTCTGGGCTCCCTGCTTTTACCGCGGCAAGTGCAGGTCCTTACCGCT 1680
Qy	1681	GAGGAGATGTCAGCTTTGAGCGCCAGAGTCTCTCCCGGAGCTGGCAAAACGCTCTGGTTC 1740
Db	1681	GAGGAGATGTCAGCTTTGAGCGCCAGAGTCTCTCCCGGAGCTGGCAAAACGCTCTGGTTC 1740
Qy	1741	GGGAACCTTCAATCTCTTTGGGAAAGAAACAAATATTTCTGCTGCTAAAGGACAAACCT 1800
Db	1741	GGGAACCTTCAATCTCTTTGGGAAAGAAACAAATATTTCTGCTGCTAAAGGACAAACCT 1800
Qy	1801	CTCAGCAGCATCAAGCAGACATCGCTTCATGCTTTCTGTCATCCCGAGCTCGAGTCAAC 1860
Db	1801	CTCAGCAGCATCAAGCAGACATCGCTTCATGCTTTCTGTCATCCCGAGCTCGAGTCAAC 1860
Qy	1861	AGTGTGCTGTACAGACCAAGCTTTACGGGCGAGTACAGCCAGTGGCGGCCCTCCGTC 1920
Db	1861	AGTGTGCTGTACAGACCAAGCTTTACGGGCGAGTACAGCCAGTGGCGGCCCTCCGTC 1920
Qy	1921	TTCCAAAGCCCGTCCGCTTCCAGTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCC 1980
Db	1921	TTCCAAAGCCCGTCCGCTTCCAGTGGACATCAGCTCTCTGAGGGTCCAGAGCCCTCC 1980
Qy	1981	CCGCGACGGGACGGCAGCGGAGGTGGGCATCTATCTCGTCACTTTCTCATCTCTCG 2040
Db	1981	CCGCGACGGGACGGCAGCGGAGGTGGGCATCTATCTCGTCACTTTCTCATCTCTCG 2040
Qy	2041	GGTCCAGCGCTCGGTTCAAGCGAGTGGTGGAGACATCCAGGCAACAGCTCTCTGAGCACT 2100



```
Db 2041 GGTCCAGCGCTCGGTTCAAGCGAGTGGTGGAGACCATCCAGGCAAGCTCCTGAGCACT 2100
Qy 2101 CATGACGAGCCCTCCGTGCAAGCCCTGGCAGACGAGAAAGAAACGCGGCCCAAGACCCGCCCT 2160
Db 2101 CATGACGAGCCCTCCGTGCAAGCCCTGGCAGACGAGAAAGAAACGCGGCCCAAGACCCGCCCT 2160
Qy 2161 GCTGGTGGCCCAACCCGCAAGCTGACGCCCCCAGCCCGCCGCGCCAGACCCAGAGCTGAGC 2220
Db 2161 GCTGGTGGCCCAACCCGCAAGCTGACGCCCCCAGCCCGCCGCGCCAGACCCAGAGCTGAGC 2220
Qy 2221 AGCTCTCCCGCCGAGGCCCCCAAGAGAGCTCCTGGGCAACAACGGGACCCCT 2280
Db 2221 AGCTCTCCCGCCGAGGCCCCCAAGAGAGCTCCTGGGCAACAACGGGACCCCT 2280
Qy 2281 CTGCCCTGA 2289
Db 2281 CTGCCCTGA 2289

RESULT 2
ABV74559
ID ABV74559 standard; cDNA; 2112 BP.
XX AC ABV74559;
XX AC ABV74559;
Dt 20-JAN-2003 (first entry)
XX DE Human kinase #3 coding sequence.
XX KW Human; kinase; chromosome 19; gene; ss.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..2112
FT /*tag= a
FT /product= "Human kinase #3"
XX W0200281670-A1.
XX PN 17-OCT-2002.
XX PD 04-APR-2002; 2002WO-US010786.
XX PF 06-APR-2001; 2001US-0282036P.
XX PR (LEXI-) LEXICON GENETICS INC.
XX PA Turner CA, Mathur B, Friddle CJ;
XX PI WPI; 2003-058538/05.
XX DR P-PSDB; ABB98745.
XX CC New human kinase proteins useful for diagnosis, drug screening, clinical
XX PT trial monitoring, treatment of disorders and diseases, and cosmetic and
XX PT nutritional applications.
XX PS Claim 5; Page 44; 47pp; English.
XX CC The present sequence is the coding sequence for a novel human kinase. The
XX CC genomic locus encoding the kinase is thought to be on human chromosome
XX CC 19. The kinase and its coding sequence are useful for diagnosis, drug
XX CC screening, clinical trial monitoring, treatment of disorders and
XX CC diseases, and cosmetic and nutritional applications
XX SQ Sequence 2112 BP; 432 A; 711 C; 615 G; 354 T; 0 U; 0 Other;

Query Match 88.3%; Score 2020.2; DB 10; Length 2112;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 265 TTTAGGTACTGGTTCTGGAGCACGTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 324
```

```
Db 88 TATTTGTACCTGGTTCTGGAGCACGTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 147
Qy 325 AAGGGGAGACTGACGCGCAAGAGAGGCCGAAAGTTCTTCCGCCAGATTGTGTCTGCGCTG 384
Db 148 AAGGGGAGACTGACGCGCAAGAGAGGCCGAAAGTTCTTCCGCCAGATTGTGTCTGCGCTG 207
Qy 385 GACTTCTGCCACAGCTACTCTCATCTGCGCACAGAGACCTAAAGCCCGAGAACCTGCTTTG 444
Db 208 GACTTCTGCCACAGCTACTCTCATCTGCGCACAGAGACCTAAAGCCCGAGAACCTGCTTTG 267
Qy 445 GATTGAGAAAAACAACATCCCGCATTTGAGACTTCGGCATGCGCTCCCTGAGGTGGGGAC 504
Db 268 GATTGAGAAAAACAACATCCCGCATTTGAGACTTCGGCATGCGCTCCCTGAGGTGGGGAC 327
Qy 505 AGCCTCTCTGAGACCAAGCTCGGGTCCCCCAATTATGCGTTCAGAGGTGATTAAAGGG 564
Db 328 AGCCTCTCTGAGACCAAGCTCGGGTCCCCCAATTATGCGTTCAGAGGTGATTAAAGGG 387
Qy 565 GAAAAATATGATGCGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 624
Db 388 GAAAAATATGATGCGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTTCGCGCTG 447
Qy 625 CTGTTGGGGCTCTGCGCTTTTGTATGACGACAACCTCCGCGAGCTGTGGAGAGGTGAAA 684
Db 448 CTGTTGGGGCTCTGCGCTTTTGTATGACGACAACCTCCGCGAGCTGTGGAGAGGTGAAA 507
Qy 685 CGGGGGTCTTCCACATGCCCCCACTTCATTCTCTCCAGATTGCCAGAGCCTCTCTGAGGGGA 744
Db 508 CGGGGGTCTTCCACATGCCCCCACTTCATTCTCTCCAGATTGCCAGAGCCTCTCTGAGGGGA 567
Qy 745 ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGTGGAGCAAAATTCAGAAACATCTCTGG 804
Db 568 ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGTGGAGCAAAATTCAGAAACATCTCTGG 627
Qy 805 TACCTAGGGGGGAAACACAGAGCCAGACCCGTGCTGGAGCCAGCCCTGCGCGCCGGGTA 864
Db 628 TACCTAGGGGGGAAACACAGAGCCAGACCCGTGCTGGAGCCAGCCCTGCGCGCCGGGTA 687
Qy 865 GCCATGCGGAGCCTGCGCATCCAAACGGAGAGCTGAGACCCCGACCGTCTTAGAGAGCATGGCA 924
Db 688 GCCATGCGGAGCCTGCGCATCCAAACGGAGAGCTGAGACCCCGACCGTCTTAGAGAGCATGGCA 747
Qy 925 TCACTGGGCTGCTTCAGGGACCGCGAGAGAGCTGATCGCGAGCTGCGCAGTGGAGGAGAG 984
Db 748 TCACTGGGCTGCTTCAGGGACCGCGAGAGAGCTGATCGCGAGCTGCGCAGTGGAGGAGAG 807
Qy 985 AACCAAGAAAGATGATATATTATCTGCTTTTGGATCGGAAGGAGCGGTATCCGAGCTGT 1044
Db 808 AACCAAGAAAGATGATATATTATCTGCTTTTGGATCGGAAGGAGCGGTATCCGAGCTGT 867
Qy 1045 GAGGACCAAGACCTGCGCTCCCGGAAATGATGTTGACCCCCCGGAAAGCGTGTGGATTCT 1104
Db 868 GAGGACCAAGACCTGCGCTCCCGGAAATGATGTTGACCCCCCGGAAAGCGTGTGGATTCT 927
Qy 1105 CCATGCTGAGCCGTACAGGGAAAGCGCGACGAGAGCGGAAGTCCATGGAAGTCTCTGAGC 1164
Db 928 CCATGCTGAGCCGTACAGGGAAAGCGCGACGAGCGGAAGTCCATGGAAGTCTCTGAGC 987
Qy 1165 ATACCCGATCGCGGGGTGCTGCTCCCTGTACCCACCGAGCGGCGCTTGGAGATGCGC 1224
Db 988 ATACCCGATCGCGGGGTGCTGCTCCCTGTACCCACCGAGCGGCGCTTGGAGATGCGC 1047
Qy 1225 CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCCCTCCACGGGTCTGTCTCTCCAGGCCCT 1284
Db 1048 CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCCCTCCACGGGTCTGTCTCTCCAGGCCCT 1107
Qy 1285 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACCGGAGCGGGGGTGGAGATGAG 1344
Db 1108 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTTCACCGGAGCGGGGGTGGAGATGAG 1167
Qy 1345 GCTCGAGCGGGGGCTCCCGACTTCCAAAAACGAGAGCGTCTCTTCGGGGGCCCGAGG 1404
```

Db 1168 GCTCGAGCGGGGCTCCCGACTTCCAAAAACGACAGCGTGCCTTCTCGGGGCCCCAGG 1227  
Qy 1405 GGTGGGGGCGCGGGAGCAGCCCCCGCCCCAGTGGCCGCTCCACACCCCTGCCCCGCGC 1464  
Db 1228 GGTGGGGGCGCGGGAGCAGCCCCCGCCCCAGTGGCCGCTCCACACCCCTGCCCCGCGC 1287  
Qy 1465 CCCCCAGGCTCCCGGGCTCTCTGGGGGAGCCCCCTTGCACTCGGCTCTGACACAGCCCC 1524  
Db 1288 CCCCCAGGCTCCCGGGCTCTCTGGGGGAGCCCCCTTGCACTCGGCTCTGACACAGCCCC 1347  
Qy 1525 CGGGCCAGTCCACCGGGAGCCCCCGGGAGCAACACACCCGCCAGCCCCCGGGCGGTGGCGTC 1584  
Db 1348 CGGGCCAGTCCACCGGGAGCCCCCGGGAGCAACACACCCGCCAGCCCCCGGGCGGTGGCGTC 1407  
Qy 1585 GGGGAGCCGCTGGAGGAGTCTCACTCACTCCATCGGCAACAGCTTCTGGGCTCCCT 1644  
Db 1408 GGGGAGCCGCTGGAGGAGTCTCACTCACTCCATCGGCAACAGCTTCTGGGCTCCCT 1467  
Qy 1645 CGCTTTCACCGGGCAAGATGCAGGTCCCTACCGCTGAGGAGATGCCAGCTTGACGCCA 1704  
Db 1468 CGCTTTCACCGGGCAAGATGCAGGTCCCTACCGCTGAGGAGATGCCAGCTTGACGCCA 1527  
Qy 1705 GAGTCCTCCCGGAGCTGGCAAAACGCTCTGGTTGGGAACTTCATCTCTTGGACAAA 1764  
Db 1528 GAGTCCTCCCGGAGCTGGCAAAACGCTCTGGTTGGGAACTTCATCTCTTGGACAAA 1587  
Qy 1765 GAAGAACAAATATCTCTCGTGAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824  
Db 1588 GAAGAACAAATATCTCTCGTGAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1647  
Qy 1825 GTCCATGCTTCTGTGATGCCAGCTGAGTCACAGTGTGTGTTCACAGACAGCTTC 1884  
Db 1648 GTCCATGCTTCTGTGATGCCAGCTGAGTCACAGTGTGTGTTCACAGACAGCTTC 1707  
Qy 1885 AGGCGGAGTACAGGCGCAGTGGGGGCGCTCCCTCTTCCAAAGCCGCTCCGCTCCAG 1944  
Db 1708 AGGCGGAGTACAGGCGCAGTGGGGGCGCTCCCTCTTCCAAAGCCGCTCCGCTCCAG 1767  
Qy 1945 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGACGGGAGGT 2004  
Db 1768 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGACGGGAGGT 1827  
Qy 2005 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGACGGGAGGT 2064  
Db 1828 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGACGGGAGGT 1887  
Qy 2065 GTGAGGAGACATCCAGGACAGCTCTGAGGACATCATGACAGCCCTCCGTCAGGCC 2124  
Db 1888 GTGAGGAGACATCCAGGACAGCTCTGAGGACATCATGACAGCCCTCCGTCAGGCC 1947  
Qy 2125 CTGGCAGACGAGAAACGGGGCCCGACACCGGGCTGTGTGTGCCCCCAGCCGAGCCTG 2184  
Db 1948 CTGGCAGACGAGAAACGGGGCCCGACACCGGGCTGTGTGTGCCCCCAGCCGAGCCTG 2007  
Qy 2185 CAGCCCCCAGCCGCGCCGACAGCCAGAGTGAAGCTCTCCCGCGAGGCCCCCC 2244  
Db 2008 CAGCCCCCAGCCGCGCCGACAGCCAGAGTGAAGCTCTCCCGCGAGGCCCCCC 2067  
Qy 2245 AAGGACAGAGAGCTCTGCGCCACCAACGGGACCCCTCTGCCCCGTA 2289  
Db 2068 AAGGACAGAGAGCTCTGCGCCACCAACGGGACCCCTCTGCCCCGTA 2112

RESULT 3  
ABV74557  
ID ABV74557 standard; cDNA; 2337 BP.  
XX  
AC ABV74557;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human kinase #1 coding sequence.  
XX

KW Human; kinase; chromosome 19; gene; ss.  
XX Homo sapiens.  
OS Location/Qualifiers  
FH 1..2337  
FT /\*tag= a  
FT /product= "Human kinase #1"  
XX  
XX WO200281670-A1.  
XX  
XX 17-OCT-2002.  
XX  
XX 04-APR-2002; 2002WO-US010786.  
XX  
XX 06-APR-2001; 2001US-0282036P.  
XX  
XX (LEXI-) LEXICON GENETICS INC.  
XX  
XX Turner CA, Mathur B, Friddle CJ;  
XX  
XX WPI; 2003-058538/05.  
XX P-PSDB; ABB98743.  
XX  
XX New human kinase proteins useful for diagnosis, drug screening, clinical  
XX trial monitoring, treatment of disorders and diseases, and cosmetic and  
XX nutritional applications.  
XX  
XX Claim 5; Page 39; 47pp; English.  
XX  
XX The present sequence is the coding sequence for a novel human kinase. The  
XX genomic locus encoding the kinase is thought to be on human chromosome  
XX 19. The kinase and its coding sequence are useful for diagnosis, drug  
XX screening, clinical trial monitoring, treatment of disorders and  
XX diseases, and cosmetic and nutritional applications  
XX  
XX Sequence 2337 BP; 479 A; 786 C; 686 G; 386 T; 0 U; 0 Other;

Query Match 88.3%; Score 2020.2; DB 10; Length 2337;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 265 TTTAGTACTTCTGAGCAGCTCTCGGGGGTGTGAGTATTCGACTACCTGTGTAAG 324  
Db 313 TATTGTACTTCTGAGCAGCTCTCGGGGGTGTGAGTATTCGACTACCTGTGTAAG 372  
Qy 325 AAGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTCCGCCAGATTGTGTGCGCTG 384  
Db 373 AAGGGAGACTGACGCCCAAGGAGGCCGAAAGTTCTCCGCCAGATTGTGTGCGCTG 432  
Qy 385 GACTTCTGACAGCTACTTCCATCTGCCACAGAGCTTAAGCCCGAGAACCTGTCTTTG 444  
Db 433 GACTTCTGACAGCTACTTCCATCTGCCACAGAGCTTAAGCCCGAGAACCTGTCTTTG 492  
Qy 445 GATGAGAAAAACAACTCCGCTTGCAGACTTCCGCTGCGCTCCCTGCAGGTGGGGAC 504  
Db 493 GATGAGAAAAACAACTCCGCTTGCAGACTTCCGCTGCGCTCCCTGCAGGTGGGGAC 552  
Qy 505 AGCTTCTTGAGACAGCTCGGGTCCCCCATTTATGCTGTCCAGAGTGTAGGGG 564  
Db 553 AGCTTCTTGAGACAGCTCGGGTCCCCCATTTATGCTGTCCAGAGTGTAGGGG 612  
Qy 565 GAAAAATGATGCGCGCGGAGACATGTGAGCTGTGGAGTCACTCTTCGCGCTG 624  
Db 613 GAAAAATGATGCGCGCGGAGACATGTGAGCTGTGGAGTCACTCTTCGCGCTG 672  
Qy 625 CTGTTGGGGCTCTGCGCTTTGATACGACAACTCCGCGAGCTGTGTGAGAGAGGTGAAA 684  
Db 673 CTGTTGGGGCTCTGCGCTTTGATACGACAACTCCGCGAGCTGTGTGAGAGAGGTGAAA 732  
Qy 685 CGGGCGCTTTCACATGCCCGCTTTCATCTCCAGATTGCCAGAGCTCTCTGAGGGGA 744  
Db 733 CGGGCGCTTTCACATGCCCGCTTTCATCTCCAGATTGCCAGAGCTCTCTGAGGGGA 792

QY	745	ATGATCGAAGTGGAGCCCGAAAAAAGGCTCAGTCTGGAGCGAAATTCAGAAAAATCCTCTGG	804
DB	793	ATGATCGAAGTGGAGCCCGAAAAAAGGCTCAGTCTGGAGCGAAATTCAGAAAAATCCTCTGG	852
QY	805	TACCTAGGCGGGAACACGAGCCAGACCCGTCCTGGAGCCAGCCCTTGGCCCGCGGTA	864
DB	853	TACCTAGGCGGGAACACGAGCCAGACCCGTCCTGGAGCCAGCCCTTGGCCCGCGGTA	912
QY	865	GCCATGCGGAGCCTGCCATCAACCGGAGAGCTGGACCCCGACGCTCTAGAGAGCATGGCA	924
DB	913	GCCATGCGGAGCCTGCCATCAACCGGAGAGCTGGACCCCGACGCTCTAGAGAGCATGGCA	972
QY	925	TCACTGGGCTGTTAGGGACGGCGAGAGGCTGCATTCGAGAGCTGGCGAGTGAAGAGAG	984
DB	973	TCACTGGGCTGTTAGGGACGGCGAGAGGCTGCATTCGAGAGCTGGCGAGTGAAGAGAG	1032
QY	985	AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAGGAGCGGTATCCAGCTGT	1044
DB	1033	AACCAAGAAAGATGATATATATCTGCTTTTGGATCGGAGGAGCGGTATCCAGCTGT	1092
QY	1045	GAGGACAGGAGCTGCTCCCGGAATGATGTTGACCCCGCCGAAAGCGTGTGATTTCT	1104
DB	1093	GAGGACAGGAGCTGCTCCCGGAATGATGTTGACCCCGCCGGAAGCGTGTGATTTCT	1152
QY	1105	CCCATGCTAGCCGTCAGGGAAAGCGGACACAGAGCGGAAGTCCATGGAACTCTGAGC	1164
DB	1153	CCCATGCTAGCCGTCAGGGAAAGCGGACACAGAGCGGAAGTCCATGGAACTCTGAGC	1212
QY	1165	ATCACCGATGCCGGGGTGGTCCCTCTGTACCCACCCGAGCGGGCTTGGAGATGCC	1224
DB	1213	ATCACCGATGCCGGGGTGGTCCCTCTGTACCCACCCGAGCGGGCTTGGAGATGCC	1272
QY	1225	CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCCTCCACGGGTCTGTCTCCAGCGCT	1284
DB	1273	CAGCACAGCCAGAGATCCCGTAGCGTCAGTGGAGCCTCCACGGGTCTGTCTCCAGCGCT	1332
QY	1285	CTAAGCAGCCCAAGGAGTCGGTCTTTTCTTTTTCACGGAGCCGGGGCTGGAGATGAG	1344
DB	1333	CTAAGCAGCCCAAGGAGTCGGTCTTTTCTTTTTCACGGAGCCGGGGCTGGAGATGAG	1392
QY	1345	GCTCGAGCGGGGCTCCCGACTTCCAAAACGAGAGCTGCTCTTCGGGGCCCGCAGG	1404
DB	1393	GCTCGAGCGGGGCTCCCGACTTCCAAAACGAGAGCTGCTCTTCGGGGCCCGCAGG	1452
QY	1405	GGTGGGGCGCGGGGAGCAGCCCGCCCGCCAGTCCGCTCCACACCCCTGCCGGC	1464
DB	1453	GGTGGGGCGCGGGGAGCAGCCCGCCCGCCAGTCCGCTCCACACCCCTGCCGGC	1512
QY	1465	CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTTGCACTGCTCTGCAACACGCC	1524
DB	1513	CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTTGCACTGCTCTGCAACACGCC	1572
QY	1525	CGGGCAGTCCACCGGGAACCCCGGGACAAACACACCCCGAGCCCGGGTGGGTC	1584
DB	1573	CGGGCAGTCCACCGGGAACCCCGGGACAAACACACCCCGAGCCCGGGTGGGTC	1632
QY	1585	GGGGAGCCGCTGAGAGTGTCTCAATCCATCGCAACAGCTTCTGGGCTCCCT	1644
DB	1633	GGGGAGCCGCTGAGAGTGTCTCAATCCATCGCAACAGCTTCTGGGCTCCCT	1692
QY	1645	CGCTTTTCAACCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCAGCTTGAAGCCCA	1704
DB	1693	CGCTTTTCAACCGCGCAAGATGCAAGTCCCTACCGCTGAGGAGATGTCAGCTTGAAGCCCA	1752
QY	1705	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGTGTTGGGAACTTTCATCTCTTTGGACAAA	1764
DB	1753	GAGTCTCTCCCGGAGCTGGCAAAACGCTCTGTGTTGGGAACTTTCATCTCTTTGGACAAA	1812
QY	1765	GAAGAAACAAATATTTCTGTGCTTAAAGACAAACCTCTCAGCAGCATCAAGCAGCATC	1824
DB	1813	GAAGAAACAAATATTTCTGTGCTTAAAGACAAACCTCTCAGCAGCATCAAGCAGCATC	1872

Qy	1825	GTCAATGCCCTTTCTGTGCGATCCCGAGCGTGAATCAAGTGTGTGTCATCAGAGACCGACTTC	1888
Db	1873	GTCCATGCCCTTTCTGTGCGATCCCGAGCGTGAATCAAGTGTGTGTCATCAGAGACCGACTTC	1932
Qy	1885	AGGGCGAGGTACAAGGCGCAGTGTGCGGCCCTCTCCAAAGCCCGTGTGCGCTTCCAG	1944
Db	1933	AGGGCGAGGTACAAGGCGCAGTGTGCGGCCCTCTCTCAAGCCGCTTCCAG	1992
Qy	1945	GTGGACATCAGCTCTCTGTAGGGTCCAGAGCCCTCCCGCGACGGGACGGCAGCGAGGT	2004
Db	1993	GTGGACATCAGCTCTCTGTAGGGTCCAGAGCCCTCCCGCGACGGGACGGCAGCGAGGT	2052
Qy	2005	GGTGGCATCTACTCCGTACCTTCACTCTCATCTCGGGTCCAGCCGTGCGTTCAAGCGA	2064
Db	2053	GGTGGCATCTACTCCGTACCTTCACTCTCATCTCGGGTCCAGCCGTGCGTTCAAGCGA	2112
Qy	2065	GTGTGGAGACCATCCAGGACAGCTCCTGTAGACATCATGACAGCCCTCCGTGCGAGGCC	2124
Db	2113	GTGTGGAGACCATCCAGGACAGCTCCTGTAGACATCATGACAGCCCTCCGTGCGAGGCC	2172
Qy	2125	CTGGCAGACGAGAAGAAAGGGGCCAGAACCCGGCTGTGTGTCGCCACCCGAAAGCCCTG	2184
Db	2173	CTGGCAGACGAGAAGAAAGGGGCCAGAACCCGGCTGTGTGTCGCCACCCGAAAGCCCTG	2232
Qy	2185	CAGCCCTCCACCCGGCGCCAGACCCAGAGCTGTAGAGCTTCTCCCGCGAGGCCCCCCC	2244
Db	2233	CAGCCCTCCACCCGGCGCCAGACCCAGAGCTGTAGAGCTTCTCCCGCGAGGCCCCCCC	2292
Qy	2245	AAGGACAAAGAGCTCTGTGCCCAACGAGGCCCTCTGCCCTGA	2299
Db	2293	AAGGACAAAGAGCTCTGTGCCCAACGAGGCCCTCTGCCCTGA	2337
RESULT 4			
ADL14129			
ID	ADL14129 standard; cDNA; 2337 BP.		
XX	ADL14129;		
XX	17-JUN-2004 (first entry)		
XX	Novel human gene 55053 coding region.		
KW	cytostatic; cardiant; hypotensive; antiangiinal; osteopathic;		
KW	antiarthritic; antiarheumatic; neuroprotective; antinflflammatory;		
KW	antipapieric; antiasthmatic; cardiovascular; virucide; analgesic; CNS;		
KW	angiogenesis inhibitor; angiogenesis stimulator; cerebroprotective;		
KW	nephrotropic; antithyroid; dermatological; immunomodulator;		
KW	cell proliferation disorder; cell differentiation disorder;		
KW	brain disorder; platelet disorder; breast disorder; colon disorder;		
KW	kidney disorder; renal disorder; lung disorder; ovarian disorder;		
KW	prostate disorder; cervical disorder; spleen disorder; thymus disorder;		
KW	thyroid disorder; testes disorder; haematopoietic disorder;		
KW	pancreatic disorder; skeletal muscle disorder; skin disorder;		
KW	dermal disorder; bone metabolism disorder; immune disorder;		
KW	inflammatory disorder; cardiovascular disorder;		
KW	endothelial cell disorder; liver disorder; viral disease; pain disorder;		
KW	metabolic disorder; neurological disorder;		
KW	central nervous system disorder; erythroid disorder;		
KW	blood vessel disorder; angioinfective disorder; cancer; heart failure;		
KW	hypertension; angina; osteoarthritis; rheumatoid arthritis;		
KW	multiple sclerosis; Crohn's disease; psoriasis; asthma;		
KW	cell proliferation; cell differentiation; cell growth; cell division;		
KW	human; gene; ss.		
XX	Homo sapiens.		
OS	US2004058355-A1.		
XX	25-MAR-2004.		
XX	25-APR-2003; 2003US-00423543.		

30-SEP-1998; 98US-00163821.  
 27-JAN-1999; 99US-0117580P.  
 25-MAR-1999; 99US-00276400.  
 30-JUL-1999; 99US-00365162.  
 09-SEP-1999; 99US-00392189.  
 05-OCT-1999; 99US-00412210.  
 23-NOV-1999; 99US-00448076.  
 29-FEB-2000; 2000US-0186061P.  
 28-APR-2000; 2000US-0200688P.  
 19-MAY-2000; 2000US-0205447P.  
 30-JUN-2000; 2000US-00608921.  
 31-JUL-2000; 2000US-0221925P.  
 25-SEP-2000; 2000US-0234922P.  
 25-SEP-2000; 2000US-0235035P.  
 08-NOV-2000; 2000US-0246669P.  
 03-NOV-2000; 2000US-00711216.  
 14-NOV-2000; 2000US-0248325P.  
 15-NOV-2000; 2000US-0248893P.  
 22-DEC-2000; 2000US-0257511P.  
 05-JAN-2001; 2001US-0260166P.  
 28-FEB-2001; 2001US-00797039.  
 27-APR-2001; 2001US-00845044.  
 20-JUL-2001; 2001US-00909743.  
 31-JUL-2001; 2001US-00920346.  
 13-AUG-2001; 2001US-00928531.  
 14-AUG-2001; 2001US-00929218.  
 15-AUG-2001; 2001US-0312539P.  
 23-SEP-2001; 2001US-00963159.  
 08-NOV-2001; 2001US-00008016.  
 13-NOV-2001; 2001US-00012055.  
 15-NOV-2001; 2001US-00003690.  
 30-JAN-2002; 2002US-00060763.  
 25-MAR-2002; 2002US-00105989.  
 12-APR-2002; 2002US-00121911.  
 12-AUG-2002; 2002US-00217168.  
 22-OCT-2002; 2002US-00278036.  
 02-JAN-2003; 2003US-00336489.  
 03-JAN-2003; 2003US-00336153.  
 (MILL-) MILLENNIUM PHARM INC.  
 Kapeller-Libermann R, Hunter JJ, Meyers RE, Rudolph-Owen LA;  
 Curtis RAJ, Olandt PJ, Tsai F, Galvin KM, Chun M, Williamson MJ;  
 Silos-Santiago I, Bandaru R;  
 WPI; 2004-268788/25.  
 P-PSDB; ADL4128.  
 New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529,  
 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593  
 nucleic acid molecules and proteins, useful for treating, e.g. cancer,  
 heart failure and angina.  
 Claim 1; SEQ ID NO 12; 139pp; English.  
 The invention describes an isolated 21910, 56634, 55053, 2504, 15977,  
 14760, 25501, 17903, 3700, 21529, 26343, 56638, 18610, 33217,  
 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising  
 any one of 40 nucleotide sequences (I). The nucleic acid molecules and  
 polypeptides are useful for diagnosing and treating a subject having a  
 disorder, or a subject at risk of developing a disorder, which is  
 associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,  
 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983,  
 m1983, 38555 or 593 activity, such as cellular proliferative and/or  
 differentiative disorders, brain disorders, platelet disorders, breast  
 disorders, colon disorders, kidney (renal) disorders, lung disorders,  
 ovarian disorders, prostate disorders, cervical disorders, spleen  
 disorders, thymus disorders, thyroid disorders, testes disorders,  
 hematopoietic disorders, pancreatic disorders, skeletal muscle disorders,  
 skin (dermal) disorders, disorders associated with bone metabolism,  
 immune, e.g. inflammatory disorders, cardiovascular disorders,  
 endothelial cell disorders, liver disorders, viral diseases, pain  
 disorders, metabolic disorders, neurological or central nervous system

1105 CCATGCTGAGCCTCAGCGGAAGCGGACGACGAGCGGAGTCCATGGAAGTCTTGAGC 1164  
Db |  
1153 CCCATGCTGAGCCTCAGCGGAAGCGGACGACGAGCGGAGTCCATGGAAGTCTTGAGC 1212  
Qy |  
1165 ATCAACGATGCGGGGCTGCTGCTCCCTGATACCCACCGACGCGGCTTGGAGATGGCC 1224  
Db |  
1213 ATCAACGATGCGGGGCTGCTGCTCCCTGATACCCACCGACGCGGCTTGGAGATGGCC 1272  
Qy |  
1225 CAGCAGCCAGAGATCCCGTAGCGTCAGTGAGAGCTTCCACGCGGTCTGTCTCCAGCCCT 1284  
Db |  
1273 CAGCAGCCAGAGATCCCGTAGCGTCAGTGAGAGCTTCCACGCGGTCTGTCTCCAGCCCT 1332  
Qy |  
1285 CTAGCAGCCCAAGAGTCCGCTCTTTTCTTTTACCGGAGCGGGGCTGAGATGAG 1344  
Db |  
1333 CTAGCAGCCCAAGAGTCCGCTCTTTTCTTTTACCGGAGCGGGGCTGAGATGAG 1392  
Qy |  
1345 GCTCAGCGGGGCTCCCGACTTCCAAAACGAGACGCTGCTTCTCGGGGCCCCAGG 1404  
Db |  
1393 GCTCAGCGGGGCTCCCGACTTCCAAAACGAGACGCTGCTTCTCGGGGCCCCAGG 1452  
Qy |  
1405 GTGGGGGCGCGGGGAGCAGCCCCCGCCCCAGTGCCTCCACACCCCTGCCCGGC 1464  
Db |  
1453 GTGGGGGCGCGGGGAGCAGCCCCCGCCCCAGTGCCTCCACACCCCTGCCCGGC 1512  
Qy |  
1465 CCCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGCACCTCGCTCTGCACAGCCC 1524  
Db |  
1513 CCCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGCACCTCGCTCTGCACAGCCC 1572  
Qy |  
1525 CGGGCAGTCCACCGGAGCCCGGGGACACACACCCCGACCGCCCGGGTGGGGTC 1584  
Db |  
1573 CGGGCAGTCCACCGGAGCCCGGGGACACACACCCCGACCGCCCGGGTGGGGTC 1632  
Qy |  
1585 GGGGAGCCGCTCGGAGAGTCTCTCAATCCATCCGCAACAGCTTCTTGGGCTCCCT 1644  
Db |  
1633 GGGGAGCCGCTCGGAGAGTCTCTCAATCCATCCGCAACAGCTTCTTGGGCTCCCT 1692  
Qy |  
1645 CGCTTTACCGGCGCAGATGAGTCCCTACCGCTGAGGAGTGTCCAGTTGACGCCA 1704  
Db |  
1693 CGCTTTACCGGCGCAGATGAGTCCCTACCGCTGAGGAGTGTCCAGTTGACGCCA 1752  
Qy |  
1705 GAGTCTCCCGGAGTGGCAAAAGCTCTGTGTTTGGGAACTTTCATCTCTTGGCAAA 1764  
Db |  
1753 GAGTCTCCCGGAGTGGCAAAAGCTCTGTGTTTGGGAACTTTCATCTCTTGGCAAA 1812  
Qy |  
1765 GAAGAACAATATTTCTCTGCTGTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1824  
Db |  
1813 GAAGAACAATATTTCTCTGCTGTAAGGACAAACCTCTCAGCAGCATCAAGCAGACATC 1872  
Qy |  
1825 GTCCATGCTTTCTGTGATCCCGAGCTGAGTGCAGTGTGTGTGCAGACAGCTTC 1884  
Db |  
1873 GTCCATGCTTTCTGTGATCCCGAGCTGAGTGCAGTGTGTGTGCAGACAGCTTC 1932  
Qy |  
1885 AGGSCCAGTACAGGCGCAGTGGGGCCCTCCGTCTTCCAAAGCCGCTCCGCTCCAG 1944  
Db |  
1933 AGGSCCAGTACAGGCGCAGTGGGGCCCTCCGTCTTCCAAAGCCGCTCCGCTCCAG 1992  
Qy |  
1945 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGGACGGCAGCGAGGT 2004  
Db |  
1993 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGCGACGGGACGGCAGCGAGGT 2052  
Qy |  
2005 GTTGGATCTACTCCGTCACTTCACTCACTATCTCGGGTCCAGCGCTCGGTTCAAGCGA 2064  
Db |  
2053 GTTGGATCTACTCCGTCACTTCACTCACTATCTCGGGTCCAGCGCTCGGTTCAAGCGA 2112  
Qy |  
2065 GTGTGAGACCATCCAGGACAGCTCTGAGCACTCATGACAGCCCTCGGTGAGGCC 2124  
Db |  
2113 GTGTGAGACCATCCAGGACAGCTCTGAGCACTCATGACAGCCCTCGGTGAGGCC 2172  
Qy |  
2125 CTGCGACAGAGAAAGAGCGGGGCCAGACCCGGGCTGTGTGTGCCCCACCCCGAGGCTG 2184  
Db |  
2173 CTGCGACAGAGAAAGAGCGGGGCCAGACCCGGGCTGTGTGTGCCCCACCCCGAGGCTG 2232  
Qy |  
2185 CAGCCCCACCCGGGCCGCCAGACCCAGAGCTGAGCAGCTTCTCCCGCGGAGGCCCCCC 2244

Db |  
2233 CAGCCCCACCCCGCGCCCGACCCAGAGCTGAGCAGCTTCCCCCGAGGCCCCCC 2292  
Qy |  
2245 AAGGACAAAGAGTCTCTGGCCACCAACGGGACCCCTCTGCCCTGA 2289  
Db |  
2293 AAGGACAAAGAGTCTCTGGCCACCAACGGGACCCCTCTGCCCTGA 2337  
RESULT 5  
AAS06717  
ID AAS06717 standard; cDNA; 2385 BP.  
XX AAS06717;  
AC AAS06717;  
XX 12-SBP-2001 (first entry)  
DT 12-SBP-2001 (first entry)  
XX Polynucleotide sequence encoding human protein kinase #17.  
DE Human; protein kinase; PK; STK; cancer; cardiovascular disease;  
XX metabolic disorder; immune related disease; neurological disorder;  
KW neurodegenerative disorder; inflammatory disorder; infectious disease;  
KW reproductice disorder; gene therapy; ss.  
XX Homo sapiens.  
OS  
XX WO200138503-A2.  
PN 31-MAY-2001.  
XX 22-NOV-2000; 2000WO-US032085.  
XX 24-NOV-1999; 99US-0167482P.  
PR (SUGEN-) SUGEN INC.  
XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
PI Flanagan P, Clary D;  
PI WPI; 2001-343950/36.  
XX P-PSDB; AAU03517.  
XX Nucleic acids encoding human kinase polypeptides, useful for preventing  
diagnosing and/or treating e.g. cancer, immune, cardiovascular and  
neural-associated diseases, and microbial infections.  
XX Example 1; Fig 1; 433pp; English.  
XX AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel  
protein kinases have been identified as members of the tyrosine or  
serine/threonine kinase (PTK and STK) families. The polynucleotides  
encoding protein kinases and the polypeptides may be used in the  
prevention, diagnosis and treatment of diseases associated with  
inappropriate kinase expression. For example, they may be used to treat  
cancers (especially cancers of hematopoietic origin), cardiovascular  
disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
immune related diseases (e.g. rheumatoid arthritis), neurological  
disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
Parkinson's disease), inflammatory disorders (e.g. asthma), infectious  
disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
Additionally, polynucleotides encoding protein kinases may be used for  
gene therapy and as DNA probes in diagnostic assays. The protein kinase  
polypeptides may be used as antigens in the production of antibodies  
against the protein kinases and in assays to identify modulators of  
protein kinase expression and activity  
XX Sequence 2385 BP; 494 A; 768 C; 731 G; 392 T; 0 U; 0 Other;  
SQ  
Query Match 88.3%; Score 2020.2; DB 4; Length 2385;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 265 TTTAGGTACTGTTCTGAGACGCTCTCGGGGGTGAAGCTATTGACTACTGTTAAAG 324  
|

Db 361 TATTTGTACTGTTCTGGAGCAGCTCTCGGGGGTGAGCTATTTGACTTACCTGTGTAAG 420  
Qy 325 AAGGGAGACTGACGGCCCAAGAGGCCCCGAAAGTTCTTCGGCAGATTCTGTCTGCGCTG 384  
Db 421 AAGGGAGACTGACGGCCCAAGAGGCCCCGAAAGTTCTTCGGCAGATTGTGTCTGCGCTG 480  
Qy 385 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACTTAAAGCCCCGAGAACCTGTCTTTTG 444  
Db 481 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACTTAAAGCCCCGAGAACCTGTCTTTTG 540  
Qy 445 GATGAGAAAAACAATCCGCATTGAGAGCTTCGGGATGCGTCCCTCAGAGTGGGGAC 504  
Db 541 GATGAGAAAAACAATCCGCATTGAGAGCTTCGGGATGCGTCCCTCAGAGTGGGGAC 600  
Qy 505 AGCTCTCTGAGACCAAGCTCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG 564  
Db 601 AGCTCTCTGAGACCAAGCTCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG 660  
Qy 565 GAAAAATATGATGGCCCGCCGGGAGAGATGAGAGCTGTGGAGTCAATCCCTTTTCGCCCTG 624  
Db 661 GAAAAATATGATGGCCCGCCGGGAGAGATGAGAGCTGTGGAGTCAATCCCTTTTCGCCCTG 720  
Qy 625 CTGCTGGGGGCTTGCCCTTTTGATGAGCAAACTTCGCCGAGCTGCTGGAGAGGTGAAA 684  
Db 721 CTGCTGGGGGCTTGCCCTTTTGATGAGCAAACTTCGCCGAGCTGCTGGAGAGGTGAAA 780  
Qy 685 CGGGGCTCTTCCACATGCCCACTTCAATTCCTCCAGATTGCCAGAGCTCTCTGAGGGGA 744  
Db 781 CGGGGCTCTTCCACATGCCCACTTCAATTCCTCCAGATTGCCAGAGCTCTCTGAGGGGA 840  
Qy 745 ATGATCGAAGTGGAGCCGAAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAACTCTTTGG 804  
Db 841 ATGATCGAAGTGGAGCCGAAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAACTCTTTGG 900  
Qy 805 TACTAGCCGGGAAACAGAGCCGAGCCGCTGCTGGAGCCAGCCCTGCGCCGCGGGA 864  
Db 901 TACTAGCCGGGAAACAGAGCCGAGCCGCTGCTGGAGCCAGCCCTGCGCCGCGGGA 960  
Qy 865 GCCATGCGGAGCTTCCCATCCAAACGAGAGCTGAGACCCCGACCTCTTAGAGAGCATGGCA 924  
Db 961 GCCATGCGGAGCTTCCCATCCAAACGAGAGCTGAGACCCCGACCTCTTAGAGAGCATGGCA 1020  
Qy 925 TCACTGGGCTGCTTCAGGGAACCGAGAGGTGATCGAGAGCTGCCAGTGGAGGAG 984  
Db 1021 TCACTGGGCTGCTTCAGGGAACCGAGAGGTGATCGAGAGCTGCCAGTGGAGGAG 1080  
Qy 985 AACCAAGAAAGATGATATATATCTGCTTTGGATCGAAGAGCGGTATCCAGCTGT 1044  
Db 1081 AACCAAGAAAGATGATATATATCTGCTTTGGATCGAAGAGCGGTATCCAGCTGT 1140  
Qy 1045 GAGGACCAAGGACCTGCTCTCCCGGAATGATGTGACCCCGGAAAGCGGTGGATCT 1104  
Db 1141 GAGGACCAAGGACCTGCTCTCCCGGAATGATGTGACCCCGGAAAGCGGTGGATCT 1200  
Qy 1105 CCATGCTGAGCGCTCAGGGAGCGGAGACAGAGCGGAGTCCATGGAAGTCTTGAGC 1164  
Db 1201 CCATGCTGAGCGCTCAGGGAGCGGAGACAGAGCGGAGTCCATGGAAGTCTTGAGC 1260  
Qy 1165 ATACCGATGCGGGGGTGTGGCTCCCTGTACCCACCGAGCGGCTTGGAGATGGCC 1224  
Db 1261 ATACCGATGCGGGGGTGTGGCTCCCTGTATACCCACCGAGCGGCTTGGAGATGGCC 1320  
Qy 1225 CAGCACAGCCAGAGATCCCGTATGCTCAGTGGAGCTCAGGGTCTGTCTCCAGCCCT 1284  
Db 1321 CAGCACAGCCAGAGATCCCGTATGCTCAGTGGAGCTCAGGGTCTGTCTCCAGCCCT 1380  
Qy 1285 CTAAGCAGCCAGAGAGTCCGCTTTTCCATCCCGAGCGCGGGCTTGGAGATGAG 1344  
Db 1381 CTAAGCAGCCAGAGAGTCCGCTTTTCCATCCCGAGCGCGGGCTTGGAGATGAG 1440  
Qy 1345 GCTCAGGCGGGGGTCTCCCGACTTCCAAAAACGAGAGCTGCTCTTCGGGGCCCCAGG 1404  
Db 1441 GCTCAGGCGGGGGTCTCCCGACTTCCAAAAACGAGAGCTGCTCTTCGGGGCCCCAGG 1500

Qy 1405 GGTGGGGCGCGCGGGAGCAGCCCCCGCCCCAGTGGCCCCCTCACAACCCCTGCCCCGGC 1464  
Db 1501 GGTGGGGCGCGCGGGAGCAGCCCCCGCCCCAGTGGCCCCCTCACAACCCCTGCCCCGGC 1560  
Qy 1465 CCCCAGAGCTCCCGCGCTCTCTGGGGGAGCCCCCTTGGCACTGCTCTGCTCTGCAACGCGCC 1524  
Db 1561 CCCCAGAGCTCCCGCGCTCTCTGGGGGAGCCCCCTTGGCACTGCTCTGCTCTGCAACGCGCC 1620  
Qy 1525 CGGGCAGTCCACCGGAGCCCCGGGGACAACAACACCCCCAGCCCCCGGGTGGCGTC 1584  
Db 1621 CGGGCAGTCCACCGGAGCCCCGGGGACAACAACACCCCCAGCCCCCGGGTGGCGTC 1680  
Qy 1585 GGGGAGCGCTGAGAGAGTCTCTCAACTCCATCCGACACAGTCTCTGGGCTCCCTC 1644  
Db 1681 GGGGAGCGCTGAGAGAGTCTCTCAACTCCATCCGACACAGTCTCTGGGCTCCCTC 1740  
Qy 1645 CGCTTTCACCGGCGCAAGATGAGAGTCCCTTACCGCTGAGGAGATGTCAGCTTGAAGCA 1704  
Db 1741 CGCTTTCACCGGCGCAAGATGAGAGTCCCTTACCGCTGAGGAGATGTCAGCTTGAAGCA 1800  
Qy 1705 GAGTCTCTCCCGAGCTGGCAAAACGCTCTGGTTTGGGAACTTCACTCTCTTGGACAAA 1764  
Db 1801 GAGTCTCTCCCGAGCTGGCAAAACGCTCTGGTTTGGGAACTTCACTCTCTTGGACAAA 1860  
Qy 1765 GAAGAACAAATATTTCTGTGCTTAAAGGACAAACCTCTCAGCAGCATCAAGACAGCATC 1824  
Db 1861 GAAGAACAAATATTTCTGTGCTTAAAGGACAAACCTCTCAGCAGCATCAAGACAGCATC 1920  
Qy 1825 GTCCATGCTTTCGTGATCCCGAGCTGAGTCAAGTGTCTGTCTCAAGACCAAGCTTC 1884  
Db 1921 GTCCATGCTTTCGTGATCCCGAGCTGAGTCAAGTGTCTGTCTCAAGACCAAGCTTC 1980  
Qy 1885 AGGGCCGAGTACAAGCCAGTGGCGGCCCTCCGCTCTTCCAAAAGCCGCTCCGCTTCCAG 1944  
Db 1981 AGGGCCGAGTACAAGCCAGTGGCGGCCCTCCGCTCTTCCAAAAGCCGCTCCGCTTCCAG 2040  
Qy 1945 GTGGACATCAGCTCTCTCAGAGGCTCCAGAGCCCTCCCGCGACGGGACGGCAGCGAGGT 2004  
Db 2041 GTGGACATCAGCTCTCTCAGAGGCTCCAGAGCCCTCCCGCGACGGGACGGCAGCGAGGT 2100  
Qy 2005 GGTGGCATCTACTCCGTCACTTCACTCTCTCGGGTCCAGCCGCTCGGTTCAGCGA 2064  
Db 2101 GGTGGCATCTACTCCGTCACTTCACTCTCTCGGGTCCAGCCGCTCGGTTCAGCGA 2160  
Qy 2065 GTGGTGGAGACCATCCAGCAGCTCTTGAGCACTCATGACAGCCCTCCGTCAGAGCC 2124  
Db 2161 GTGGTGGAGACCATCCAGCAGCTCTTGAGCACTCATGACAGCCCTCCGTCAGAGCC 2220  
Qy 2125 CTGGCAGACGAGAAAGACGGGGCCAGACCCGGCTTGTGGTGGCCACCCCGAAGCTG 2184  
Db 2221 CTGGCAGACGAGAAAGACGGGGCCAGACCCGGCTTGTGGTGGCCACCCCGAAGCTG 2280  
Qy 2185 CAGCCCCCAGCCCGCGCCGAGACCCAGAGCTGAGAGTCTCTCCCGCGAGGCCCCCCC 2244  
Db 2281 CAGCCCCCAGCCCGCGCCGAGACCCAGAGCTGAGAGTCTCTCCCGCGAGGCCCCCCC 2340  
Qy 2245 AAGGACAGAGAGTCTCTGGCCACCAACGGGACCCCTCTGCCCCCTGA 2289  
Db 2341 AAGGACAGAGAGTCTCTGGCCACCAACGGGACCCCTCTGCCCCCTGA 2385

## RESULT 6

ADE71237  
ID ADE71237 standard; DNA; 2576 BP.

XX ADE71237;

XX AC AC  
XX XX XX  
XX DT 29-JAN-2004 (first entry)

XX DE Novel human protein coding sequence #53.

XX XX human; novel protein; drug; gene; ds.

KW







985 AACCAAGAAAGATGATATATTATCTGCTTTTGGATCGAAGGAGCGGTATCCAGCTGT 1044  
984 AACCAAGAAAGATGATATATTATCTGCTTTTGGATCGAAGGAGCGGTATCCAGCTGT 904  
1045 GAGGACGAGGACCTGCTCCCGGAATGATGTTGACCCCGGAAAGCGTGTGATTCT 1104  
905 GAGGACGAGGACCTGCTCCCGGAATGATGTTGACCCCGGAAAGCGTGTGATTCT 964  
1105 CCATGCTGAGCGCTCAAGGAGCGGAGACGAGGAGGAGTCCATGGAAGTCTGAGC 1164  
965 CCATGCTGAGCGCTCAAGGAGCGGAGACGAGGAGGAGTCCATGGAAGTCTGAGC 1024  
1165 ATCAACGATGCGGGGCTGCTCCCTGATCCACCGAGCGGGCTTGGAGATGGCC 1224  
1025 ATCAACGATGCGGGGCTGCTCCCTGATCCACCGAGCGGGCTTGGAGATGGCC 1084  
1225 CAGCACGAGGAGATCCCGTAGCTCAGTGGAGCTCCACGGTCTGTCTCCAGCCCT 1284  
1085 CAGCACGAGGAGATCCCGTAGCTCAGTGGAGCTCCACGGTCTGTCTCCAGCCCT 1144  
1285 CTAAGACGCCAAGGAGTCCGCTCTTTTCTTTTCAAGGAGCGGGGCTGGAGATGAG 1344  
1145 CTAAGACGCCAAGGAGTCCGCTCTTTTCTTTTCAAGGAGCGGGGCTGGAGATGAG 1204  
1345 GCTCGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTCCGGGCCCCCAGG 1404  
1205 GCTCGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTCCGGGCCCCCAGG 1264  
1405 GGTGGGGGCGGGGAGCAGCCCCCGCCCGAGTCCCGCTCCACACCCCTGCCCCGGC 1464  
1265 GGTGGGGGCGGGGAGCAGCCCCCGCCCGAGTCCCGCTCCACACCCCTGCCCCGGC 1324  
1465 CCCCCAGGCTCCCGGCTCTCTGCGGGGAGCCCCCTTGCACTGCTCTGCAACGCC 1524  
1325 CCCCCAGGCTCCCGGCTCTCTGCGGGGAGCCCCCTTGCACTGCTCTGCAACGCC 1384  
1525 CGGGCAGTCCACCGGAGCCCCGGGAGCAACACACCCCGCCAGCCCCGGGGTGGGTC 1584  
1385 CGGGCAGTCCACCGGAGCCCCGGGAGCAACACACCCCGCCAGCCCCGGGGTGGGTC 1444  
1585 GGGGAGCGCGCTGGAGAGTCTCAATCCATCCGCAACAGCTTCTGGGCTCCCT 1644  
1445 GGGGAGCGCGCTGGAGAGTCTCAATCCATCCGCAACAGCTTCTGGGCTCCCT 1504  
1645 CGCTTTCAACCGGCAAGATGAGTCCCTACCGCTGAGGAGATGTCAGCTTGAGCCCA 1704  
1505 CGCTTTCAACCGGCAAGATGAGTCCCTACCGCTGAGGAGATGTCAGCTTGAGCCCA 1564  
1705 GAGTCTCCCGGAGCTGGGAAACGCTCTGTTGGGAACTTCACTCTCTTGGAGAA 1764  
1565 GAGTCTCCCGGAGCTGGGAAACGCTCTGTTGGGAACTTCACTCTCTTGGAGAA 1624  
1765 GAAGAAACAATATCTCGTGTAAAGAGCAAAACCTCTCAGCAGCATCAAGCAGCATC 1824  
1625 GAAGAAACAATATCTCGTGTAAAGAGCAAAACCTCTCAGCAGCATCAAGCAGCATC 1684  
1825 GTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTGCTGTGTCACAGACAGCTTC 1884  
1685 GTCCATGCTTCTGTGATCCCGAGCTGAGTCAAGTGTGCTGTGTCACAGACAGCTTC 1744  
1885 AGGCGGAGTCAAGGCGAGTGGGCGGCTCTGCTTCCAAAGCCCGTCCGTTCCAG 1944  
1745 AGGCGGAGTCAAGGCGAGTGGGCGGCTCTGCTTCCAAAGCCCGTCCGTTCCAG 1804  
1945 GTGACATCAGTCTCTGAGGTCAGAGCCCTCCCGGAGCGGAGCGGAGGAGT 2004  
1805 GTGACATCAGTCTCTGAGGTCAGAGCCCTCCCGGAGCGGAGCGGAGGAGT 1864  
2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGCTCCAGCCGTCGCTTCAAGCGA 2064  
1865 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGCTCCAGCCGTCGCTTCAAGCGA 1924  
2065 GTGGTGGAGACCATCCAGGCAAGCTCTCTGAGCACTCATGACAGCCCTCCGTCAGGCC 2124

1925 GTGGTGGAGCACTTCCAGGCAAGCTCTCTGAGCACTCATGACGAGCCCTCCGTGAGGCC 1984  
2125 CTGGCAGACGAGAAAGAACCGGGCCAGACCCCGGCTCTGCTGCTCCACCCCGAAGCCTG 2184  
1985 CTGGCAGACGAGAAAGAACCGGGCCAGACCCCGGCTCTGCTGCTCCACCCCGAAGCCTG 2044  
2185 CAGCCCGCCACCCCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCAGGCCCCCCC 2244  
2045 CAGCCCGCCACCCCGGCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCAGGCCCCCCC 2104  
2245 AAGGACAAAGAGCTCTCTGGCCACCAACGGGAGCCCTCTGCCCCTGA 2289  
2105 AAGGACAAAGAGCTCTCTGGCCACCAACGGGAGCCCTCTGCCCCTGA 2149

RESULT 8  
AAD26464  
ID AAD26464 standard; cDNA; 2897 BP.  
XX  
AC AAD26464;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
Human kinase PKIN-17 cDNA.  
XX  
Human; kinase; PKIN-17; cancer; leukaemia; adenocarcinoma; osteoporosis;  
KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;  
KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;  
KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;  
KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;  
KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;  
KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;  
KW hepatitis; hypothyroidism; cerebellar palsy; cataract; angina pectoris;  
KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;  
KW congestive heart failure; ischaemic heart disease; lung tumour; gout;  
KW fatty liver; Niemann-Pick's disease; gene therapy; ss.  
XX  
Homo sapiens.  
XX  
Key Location/Qualifiers  
CDS 1..2385  
FT /tag= a  
FT /product= "Human PKIN-17 protein"  
XX  
XX WO200196547-A2.  
XX  
PD 20-DEC-2001.  
XX  
XX 14-JUN-2001; 2001WO-US019444.  
XX  
XX 15-JUN-2000; 2000US-0212073P.  
PR 23-JUN-2000; 2000US-0213467P.  
PR 30-JUN-2000; 2000US-0215651P.  
PR 07-JUL-2000; 2000US-0216605P.  
PR 13-JUL-2000; 2000US-0218372P.  
PR 25-AUG-2000; 2000US-0228056P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;  
PI Gandhi AR, Tribouley CM, Wallia NK, Yao MG, Lu DAM, Greenwald SR;  
PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang Y;  
PI Baughn MS, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;  
PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;  
PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;  
XX  
XX WPI; 2002-090207/12.  
DR P-PSDB; AAE16271.  
XX  
XX New polypeptides, useful for diagnosing, treating or preventing disorders  
PT of growth and development, cardiovascular and lipid, and diseases such as  
PT cancer, comprise human kinase polypeptides.



Db 2041 GTGACATCAGCTCTCTGAGGTCAGAGCCCTCCCGCGACGGGACGGCGAGGT 2100  
Qy 2005 GGTGGCACTACTCGGTCACTTCACTCTCATCTCGGTCCAGCCGTCGGTTCAAGCGA 2064  
Db 2101 GGTGGCACTACTCGGTCACTTCACTCTCATCTCGGTCCAGCCGTCGGTTCAAGCGA 2160  
Qy 2065 GTGTGGAGACATCCAGGACAGCTCTGAGCACTCATGACAGCCCTCGTGCAGGCC 2124  
Db 2161 GTGTGGAGACATCCAGGACAGCTCTGAGCACTCATGACAGCCCTCGTGCAGGCC 2220  
Qy 2125 CTGGCAGACGAGAGAACGGGCGCCAGACCCGGCTGTGTGTGCCCCACCCGGAAGCTG 2184  
Db 2221 CTGGCAGACGAGAGAACGGGCGCCAGACCCGGCTGTGTGTGCCCCACCCGGAAGCTG 2280  
Qy 2185 CAGCCCCACCGCGCGCCAGACCCAGAGCTGAGCACTCTCCCGCGGAGGCCCCCC 2244  
Db 2281 CAGCCCCACCGCGCGCCAGACCCAGAGCTGAGCACTCTCCCGCGGAGGCCCCCC 2340  
Qy 2245 AAGGACAGAGCTCTGCGCCACCAACCGGACCCCTCTGCCCTGA 2289  
Db 2341 AAGGACAGAGCTCTGCGCCACCAACCGGACCCCTCTGCCCTGA 2385

RESULT 9

ADSL6433 ID ADSL6433 standard; cDNA; 2950 BP.

XX AC ADSL6433;  
XX 18-NOV-2004 (first entry)  
XX Human eukaryotic protein kinase-55053 (EPK-55053) cDNA #2.  
KW Eukaryotic protein kinase-55053; EPK-55053; CNS disorder;  
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;  
KW amyotrophic lateral sclerosis; epilepsy; autonomic function disorder;  
KW sleep disorder; depression; mania; anxiety disorder; phobic disorder;  
KW learning disorder; memory disorder; amnesia; attention deficit disorder;  
KW cardiovascular system disorder; arteriosclerosis; ischaemia;  
KW reperfusion injury; restenosis; vascular heart disease;  
KW hormonal disorder; diabetes; thyroid disorder; reproductive disorder;  
KW fertility disorder; neuroprotective; nootropic; antiparkinsonian;  
KW anticonvulsant; hypnotic; antidepressant; antimanic; tranquiliser;  
KW cardiovascular; antiarteriosclerotic; vasotrophic; antidiabetic;  
KW antithyroid; gynaecological; human; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH 86..2422  
CDS /\*tag= a  
FT /product= "Eukaryotic protein kinase-55053 (EPK-55053)"  
XX

US6787345-B1.

XX 07-SEP-2004.

XX 15-NOV-2001; 2001US-00003690.

XX 15-NOV-2000; 2000US-0248893P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtis RAJ;

XX WPI; 2004-632931/61.

XX P-PSDB; ADSL6426.

XX New isolated eukaryotic kinase (EPK-55053) nucleic acid and protein,  
XX useful for diagnosing or treating EPK-55053 mediated or related  
XX disorders, e.g. Alzheimer's disease, multiple sclerosis, depression,  
XX ischemia, restenosis, or diabetes.

XX Example 1; Fig 1; 55pp; English.  
XX

CC The invention relates to an eukaryotic protein kinase-55053 (EPK-55053)  
CC and its corresponding nucleic acid sequence. The EPK-55053 nucleic acid  
CC molecules, proteins and antibodies are useful in screening assays,  
CC diagnostic assays, prognostic assays, in monitoring clinical trials,  
CC pharmacogenetics or for treating EPK-55053 mediated or related disorders.  
CC EPK-55053 mediated or related disorders include CNS disorders  
CC (Alzheimer's disease, Parkinson's disease, multiple sclerosis,  
CC amyotrophic lateral sclerosis or epilepsy), autonomic function disorders  
CC (sleep disorders, depression, mania, anxiety disorders or phobic  
CC disorders), learning or memory disorders (amnesia or attention deficit  
CC disorder), cardiovascular system disorders (arteriosclerosis, ischaemia,  
CC reperfusion injury, restenosis or vascular heart disease), hormonal  
CC disorders (diabetes or thyroid disorders) and reproductive or fertility  
CC disorders. The present sequence is human EPK-55053 cDNA. Note: This  
CC sequence is stated to be similar to the sequence shown as SEQ ID NO:1 in  
CC the sequence listing of the specification. However this does not appear  
CC to be the case.

XX SQ Sequence 2950 BP; 606 A; 955 C; 880 G; 509 T; 0 U; 0 Other;

Query Match 88.3%; Score 2020.2; DB 13; Length 2950;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 265 TTTAGGTACCTGGTTCTGGAGCACGCTCTCGGGGGGTGAGCTATTTCGACTACCTCGTAAAG 324  
Db 398 TATTTGTACCTGGTTCTGGAGCACGCTCTCGGGGGGTGAGCTATTTCGACTACCTCGTAAAG 457  
Qy 325 AAGGGGAGACTGACCGCCCAAGGAGGCCGAAAGTTCTTCCGCCAGATGTGTTCGCGCTG 384  
Db 458 AAGGGGAGACTGACCGCCCAAGGAGGCCGAAAGTTCTTCCGCCAGATGTGTTCGCGCTG 517  
Qy 385 GACTTCTGCCACAGCTACTCCATCTGCGACAGACCTTAAGCCCGAGACCTGCTTTTG 444  
Db 518 GACTTCTGCCACAGCTACTCCATCTGCGACAGACCTTAAGCCCGAGACCTGCTTTTG 577  
Qy 445 GATGAGAAAAACAACATCCCATTCGACAGCTTCGGCATGGCTCCCTCGAGGTGGGGAC 504  
Db 578 GATGAGAAAAACAACATCCCATTCGACAGCTTCGGCATGGCTCCCTCGAGGTGGGGAC 637  
Qy 505 AGCTCTCTGAGACAGCTCGGGTCCCGCATATGCGTGTCCAGAGGTGATTAAAGGG 564  
Db 638 AGCTCTCTGAGACAGCTCGGGTCCCGCATATGCGTGTCCAGAGGTGATTAAAGGG 697  
Qy 565 GAAAAATATGATGGCGCGCGGCGAGACATGTGAGCTGTGAGTCATCTTTCGCCCTG 624  
Db 698 GAAAAATATGATGGCGCGCGGCGAGACATGTGAGCTGTGAGTCATCTTTCGCCCTG 757  
Qy 625 CTGCTGGGGGCTCTGCCCTTTTGATGACGACAACTCCCGCAGCTGTGAGAGGTGAAA 684  
Db 758 CTGCTGGGGGCTCTGCCCTTTTGATGACGACAACTCCCGCAGCTGTGAGAGGTGAAA 817  
Qy 685 CGGGGGGTCTTCCACATGCCCACTTTCATTTCTCCAGATTGCCAGAGCTCTCTGAGGGGA 744  
Db 818 CGGGGGGTCTTCCACATGCCCACTTTCATTTCTCCAGATTGCCAGAGCTCTCTGAGGGGA 877  
Qy 745 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGAGCAAAATTGAGAAACATCTTGG 804  
Db 878 ATGATCGAAGTGGAGCCCGGAAAAAGGCTCAGTCTGAGCAAAATTGAGAAACATCTTGG 937  
Qy 805 TACCTAGCGGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGGCCCGCGGTA 864  
Db 938 TACCTAGCGGGGAAACACGAGCCAGACCCGCTGCTGGAGCCAGCCCTGGCCCGCGGTA 997  
Qy 865 GCCATCGGAGCTTGCATCCAAACGAGAGCTGAGACCCCGAGCTCTTAGAGAGCATGGCA 924  
Db 998 GCCATCGGAGCTTGCATCCAAACGAGAGCTGAGACCCCGAGCTCTTAGAGAGCATGGCA 1057  
Qy 925 TCACTGGGCTGTCTTAGGGAACCGGAGAGGCTGATCGCGAGCTGCCAGTGGAGGAGAG 984



Db 1058 TCACTGGGCTGCTTCAGGACCCGAGAGAGGCTGCATCGGAGCTGCGCAGTGAGGAGAG 1117  
Qy 985 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCAGCTGT 1044  
Db 1118 AACCAAGAAAGATGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCAGCTGT 1177  
Qy 1045 GAGGACAGGACCTGCTCCCGGATGATGTTGACCCCGGAGAGCGTGTGGATTCT 1104  
Db 1178 GAGGACAGGACCTGCTCCCGGATGATGTTGACCCCGGAGAGCGTGTGGATTCT 1237  
Qy 1105 CCAATGCTGAGCCGTCAACGGGAGCGGACGAGCGGAAGTCCATGGAAGTCTTGAGC 1164  
Db 1238 CCAATGCTGAGCCGTCAACGGGAGCGGACGAGCGGAAGTCCATGGAAGTCTTGAGC 1297  
Qy 1165 ATCAACGATGCGGGGTGTGGTCCCTGTTACCCACGAGCGGCTTGGAGTGGCC 1224  
Db 1298 ATCAACGATGCGGGGTGTGGTCCCTGTTACCCACGAGCGGCTTGGAGTGGCC 1357  
Qy 1225 CAGCACAGCCAGAGATCCCGTAGGCTCAGTGGAGCTTCCAGGGTCTGTCTCCAGCCCT 1284  
Db 1358 CAGCACAGCCAGAGATCCCGTAGGCTCAGTGGAGCTTCCAGGGTCTGTCTCCAGCCCT 1417  
Qy 1285 CTAAAGCAGCCCAAGGAGTCCGGTCTTTTCCCTTTACCGGAGCGGGGCTGGAGATGAG 1344  
Db 1418 CTAAAGCAGCCCAAGGAGTCCGGTCTTTTCCCTTTTACCGGAGCGGGGCTGGAGATGAG 1477  
Qy 1345 GCTGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTCCGGGCCCCAGG 1404  
Db 1478 GCTGAGCGGGGCTCCCGACTTCCAAACGAGAGCTGCTCTCCGGGCCCCAGG 1537  
Qy 1405 GGTGGGCGCGGGGAGCAGCCCCCGCCAGTGCCTCCACACCCCTGCCCCG 1464  
Db 1538 GGTGGGCGCGGGGAGCAGCCCCCGCCAGTGCCTCCACACCCCTGCCCCG 1597  
Qy 1465 CCCCAGGCTCCCCGCTCTCTGCGGGAGACCCCTTGCATCGCTCTGCAACGCC 1524  
Db 1598 CCCCAGGCTCCCCGCTCTCTGCGGGAGACCCCTTGCATCGCTCTGCAACGCC 1657  
Qy 1525 CGGGCAGTCCACCGGACCCCGGGGACACACACCCCGCCAGCCCGGGGTGGCGTC 1584  
Db 1658 CGGGCAGTCCACCGGACCCCGGGGACACACACCCCGCCAGCCCGGGGTGGCGTC 1717  
Qy 1585 GGGGAGCGCGCTGAGGAGTCTGCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1644  
Db 1718 GGGGAGCGCGCTGAGGAGTCTGCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1777  
Qy 1645 CGCTTTCACCGCGCAAGATGAGTCCCTACCGTGGAGAGTGTCCAGCTTGACGCCA 1704  
Db 1778 CGCTTTCACCGCGCAAGATGAGTCCCTACCGTGGAGAGTGTCCAGCTTGACGCCA 1837  
Qy 1705 GAGTCTCCCGGAGCTGGCAAAACGCTCCTGGTTTCGGGAACTTCATCTCTTGGACAAA 1764  
Db 1838 GAGTCTCTCCCGGAGCTGGCAAAACGCTCCTGGTTTCGGGAACTTCATCTCTTGGACAAA 1897  
Qy 1765 GAAGAACAAATATCTCGTGTAAAGACAAAACCTCTCAGCAGCATCAAGCAGACATC 1824  
Db 1898 GAAGAACAAATATCTCGTGTAAAGACAAAACCTCTCAGCAGCATCAAGCAGACATC 1957  
Qy 1825 GTCCATGCTTCTGTCGATCCCGAGCTGAGTGCAGTGTGCTGTACAGACAGCTTC 1884  
Db 1958 GTCCATGCTTCTGTCGATCCCGAGCTGAGTGCAGTGTGCTGTACAGACAGCTTC 2017  
Qy 1885 AGGGCCGAGTACAAGGCGAGTGGCGGCCCTCCGCTCTTCCAAAGCCCGTCCGCTTCAG 1944  
Db 2018 AGGGCCGAGTACAAGGCGAGTGGCGGCCCTCCGCTCTTCCAAAGCCCGTCCGCTTCAG 2077  
Qy 1945 GTGGAATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCAGCGGAGCGGAGCGGAGGT 2004  
Db 2078 GTGGAATCAGTCTCTGAGGGTCCAGAGCCCTCCCGCAGCGGAGCGGAGCGGAGGT 2137  
Qy 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCACTCGGGTCCCGAGCGCTGGTTCAGGCA 2064  
Db 2138 GGTGGCATCTACTCCGTCACCTTCACTCTCACTCGGGTCCCGAGCGCTGGTTCAGGCA 2197

Qy 2065 GTGGTGAGACCATCCAGGCACAGCTCTGAGCACTCATGACAGCCCTCGTCAAGGCC 2124  
Db 2198 GTGGTGAGACCATCCAGGCACAGCTCTGAGCACTCATGACAGCCCTCGTCAAGGCC 2257  
Qy 2125 TTGGCAGACGAGAGAACCGGGCCAGACCCGGCTGCTGGTGCCTCCACCCCGAAGCTG 2184  
Db 2258 TTGGCAGACGAGAGAACCGGGCCAGACCCGGCTGCTGGTGCCTCCACCCCGAAGCTG 2317  
Qy 2185 CAGCCCCCAGCCCGCCGAGACCCAGAGCTGAGAGCTCTCCCGCCGAGGCCCCCCCC 2244  
Db 2318 CAGCCCCCAGCCCGCCGAGACCCAGAGCTGAGAGCTCTCCCGCCGAGGCCCCCCCC 2377  
Qy 2245 AAGGACAAAGAGCTCTGCGCCACCAACCGGAGCCCTCTGCCCCGTA 2289  
Db 2378 AAGGACAAAGAGCTCTGCGCCACCAACCGGAGCCCTCTGCCCCGTA 2422

RESULT 10  
AAL55772  
ID AAL55772 standard; cDNA; 2953 BP.  
XX  
AC AAL55772;  
XX  
DT 17-SEP-2003 (first entry)  
XX  
Human eukaryotic protein kinase 55053 cDNA.  
XX  
Cardiac; antianginal; antiarteriosclerotic; antidiabetic; thyromimetic;  
XX  
antiarrhythmic; cytosolic; nootropic; neuroprotective; antiparkinsonian;  
XX  
anticongulant; antidepressant; tranquiliser; antimigraine; EPK 55053;  
XX  
eukaryotic protein kinase; cellular growth disorder; angina; cancer;  
XX  
cognitive; neurodegenerative; Alzheimer's disease; learning; hormone;  
XX  
autonomic function; memory; neuropsychiatric; depression; reproductive;  
XX  
musculoskeletal; immune system; human; ss; gene.  
XX  
Homo sapiens.  
XX  
Key Location/Qualifiers  
5'UTR 1..85  
/tag= a  
/note= "5, untranslated region"  
CDS 85..2422  
/tag= b  
/product= "Human eukaryotic protein kinase 55053 protein"  
2423..2953  
3'UTR /tag= c  
/note= "3, untranslated region"  
WO2003042371-A2.  
XX  
22-MAY-2003.  
XX  
15-NOV-2002; 2002WO-US036967.  
XX  
15-NOV-2001; 2001US-00003690.  
XX  
(MILL-) MILLENNIUM PHARM INC..  
XX  
Curtis RAJ;  
XX  
WPI; 2003-449574/42.  
XX  
P-PSDB; AAO3053.  
XX  
New isolated EPK-55053 nucleic acid and polypeptide, useful for  
XX  
diagnosing and treating EPK-55053-related disorders, such as  
XX  
hypertension, arteriosclerosis, myocardial infarction, diabetes mellitus,  
XX  
cancer and/or epilepsy.  
XX  
Claim 1; Fig 1A-1B; 86pp; English.  
XX  
The invention relates to a novel isolated nucleic acid molecule  
XX  
comprising a sequence which encodes a eukaryotic protein kinase (EPK) -  
CC





QY 2185 CAGCCCCCACCAGCCCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCGCCCCC 2244  
DB 2318 CAGCCCCCACCAGCCCGCCAGACCCAGAGCTGAGCAGCTCTCCCGCCGAGGCCGCCCCC 2377  
QY 2245 AAGGACAAAGCTCTCTGGCCACCAAGGAGACCCCTCTGCGCTGA 2289  
DB 2378 AAGGACAAAGCTCTCTGGCCACCAAGGAGACCCCTCTGCGCTGA 2422

RESULT 11

ID ADE38430 standard; DNA; 2980 BP.

AC ADE38430;

XX 29-JAN-2004 (first entry)

XX Human protein 68862 gene sequence.

XX tumorigenic disorder; angiogenic disorder; aberrant gene expression;  
XX aberrant protein activity; cytostatic; antithyroid; antidiabetic;  
XX ophthalmological; cancer; breast cancer; colon cancer; lung cancer;  
XX prostatic cancer; Grave's disease; diabetic retinopathy; gene; ds;  
XX protein 68862.

XX Homo sapiens.

XX Location/Qualifiers

FT Key 86..2422

FT CDS /\*tag= a

FT /product= "Human protein 68862"

XX WO2003065006-A2.

XX 07-AUG-2003.

XX 30-JAN-2003; 2003WO-US002598.

XX 31-JAN-2002; 2002US-0353600P.

XX 15-MAR-2002; 2002US-0364517P.

XX 09-APR-2002; 2002US-0371075P.

XX 10-APR-2002; 2002US-0371507P.

XX 16-APR-2002; 2002US-0372984P.

XX 19-APR-2002; 2002US-0374194P.

XX 24-MAY-2002; 2002US-0382995P.

XX 31-MAY-2002; 2002US-0385023P.

XX 14-JUN-2002; 2002US-0388853P.

XX 17-JUN-2002; 2002US-0389395P.

XX 25-JUN-2002; 2002US-0391324P.

XX 15-JUL-2002; 2002US-0395944P.

XX 22-JUL-2002; 2002US-0397726P.

XX 13-AUG-2002; 2002US-0403046P.

XX 22-AUG-2002; 2002US-0405155P.

XX 27-AUG-2002; 2002US-0406361P.

XX 25-OCT-2002; 2002US-0421195P.

XX 12-NOV-2002; 2002US-0425456P.

XX 19-NOV-2002; 2002US-0427626P.

XX 10-DEC-2002; 2002US-0432122P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hunter JJ, Macbeth KJ, Tsai F, Lesoon A, Lightcap ES;

PI Williamson MW, Rudolph-Owen LA;

XX WPI; 2003-646176/61.

DR P-PSDB; ADE38431.

XX Treating subject having tumorigenic disorder or angiogenic disorder  
PT created by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic  
PT acid, by administering a modulator.

XX Disclosure; SEQ ID NO 91; 454pp; English.

XX

CC This invention relates to a novel method of treating a human subject  
CC having a tumorigenic disorder or angiogenic disorder, caused by aberrant  
CC gene expression or activity of an isolated protein, by administering a  
CC modulator. The modulator may have cytostatic, antithyroid, antidiabetic  
CC or ophthalmological activity. The method is useful for treating a subject  
CC having a tumorigenic or angiogenic disorder, in particular for treating  
CC cancer (for example breast cancer, colon cancer, lung cancer or prostatic  
CC cancer) and, for example, Grave's disease and diabetic retinopathy. The  
CC present sequence is a DNA sequence which encodes the novel isolated human  
CC protein 68862 of the invention.

SQ Sequence 2980 BP; 625 A; 959 C; 886 G; 510 T; 0 U; 0 Other;

Query Match 88.3%; Score 2020.2; DB 10; Length 2980;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 265 TTTAGGTACTGGTTCTGGAGCACGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG 324

DB 398 TATTTGTACTGGTTCTGGAGCACGCTCTCGGGGGTGAGCTATTGCACTACCTGGTAAAG 457

QY 325 AAGGGGAGACTGACGCGCCCAAGGAGGCCGAAAGTTCTTCGGCCAGATTGTCTGCGCTG 384

DB 458 AAGGGGAGACTGACGCGCCCAAGGAGGCCGAAAGTTCTTCGGCCAGATTGTCTGCGCTG 517

QY 385 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACTAAAGCCCGAGAACCTGCTTTTG 444

DB 518 GACTTCTGCCACAGCTACTCCATCTGCCACAGAGACTAAAGCCCGAGAACCTGCTTTTG 577

QY 445 GATGAGAAAAACAATCCGATTCGAGACTTCGGCATGCGCTCCCTGAGGTTGGGGGAC 504

DB 578 GATGAGAAAAACAATCCGATTCGAGACTTCGGCATGCGCTCCCTGAGGTTGGGGGAC 637

QY 505 AGCTCTCTGGAGACCAAGCTGCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAGGGG 564

DB 638 AGCTCTCTGGAGACCAAGCTGCGGGTCCCCCATTTATGCGTGTCCAGAGGTGATTAAGGGG 697

QY 565 GAAAAATATGATGCGCGCGGGCAGACATGTGAGCTGTGGAGTCACTCTTCGCGCTG 624

DB 698 GAAAAATATGATGCGCGCGGGCAGACATGTGAGCTGTGGAGTCACTCTTCGCGCTG 757

QY 625 CTGCTGGGGCTCTGCGCTTTGATGACGACCACTCCGCCAGCTGTGGAGAGGTGAAA 684

DB 758 CTGCTGGGGCTCTGCGCTTTGATGACGACCACTCCGCCAGCTGTGGAGAGGTGAAA 817

QY 685 CGGGGGCTCTTCCACATGCCCCCACTTCATTCCTCCAGATTGCCAGAGCCTCTTGAGGGGA 744

DB 818 CGGGGGCTCTTCCACATGCCCCCACTTCATTCCTCCAGATTGCCAGAGCCTCTTGAGGGGA 877

QY 745 ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAATTCAGAAACATCCTTGG 804

DB 878 ATGATCGAAGTGGAGCCGAAAAAGGCTCAGTCTGGAGCAATTCAGAAACATCCTTGG 937

QY 805 TACCTAGGGGGGAAACACGAGCCAGACCCGCTGCTGGAGCAGCCCTGCGCCCGGGTA 864

DB 938 TACCTAGGGGGGAAACACGAGCCAGACCCGCTGCTGGAGCAGCCCTGCGCCCGGGTA 997

QY 865 GCCATGCGGAGCCTGCGCATCCAAACGGAGAGCTGGACCCCGACCTCTTAGAGAGCATGGCA 924

DB 998 GCCATGCGGAGCCTGCGCATCCAAACGGAGAGCTGGACCCCGACCTCTTAGAGAGCATGGCA 1057

QY 925 TCCTGGGGCTGCTTCAGGGACCGGAGAGGCTGATCGGAGCTGCGCAGCTGAGGAGGAG 984

DB 1058 TCCTGGGGCTGCTTCAGGGACCGGAGAGGCTGATCGGAGCTGCGCAGCTGAGGAGGAG 1117

QY 985 AACCAAGAAAAAGATGATATATTCTCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044

DB 1118 AACCAAGAAAAAGATGATATATTCTCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1177

QY 1045 GAGGACCAAGGACCTGCTCCCGGAATGATGTTGACCCCCCGGAAACGCTGTGGATTCT 1104

DB 1178 GAGGACCAAGGACCTGCTCCCGGAATGATGTTGACCCCCCGGAAACGCTGTGGATTCT 1237

QY 1105 CCCATGCTGAGCGCTCAGGGAAAGGGGACGAGCGGAGTCCATGGAAGTCTCTAGC 1164  
Db |||||  
QY 1238 CCCATGCTGAGCGCTCAGGGAAAGGGGACGAGCGGAGTCCATGGAAGTCTCTAGC 1297  
Db |||||  
QY 1165 ATCAACGATGCGGGGGTGGTGGTCTCCCTGTACCCACCGAGCGGCTTGGAGATGGCC 1224  
Db |||||  
QY 1298 ATCAACGATGCGGGGGTGGTGGTCTCCCTGTACCCACCGAGCGGCTTGGAGATGGCC 1357  
Db |||||  
QY 1225 CAGCACGACGAGATCCCGTAGCGTCACTGAGGAGCCCTCCAGCGGTCTGTCTCCAGCCCT 1284  
Db |||||  
QY 1358 CAGCACGACGAGATCCCGTAGCGTCACTGAGGAGCCCTCCAGCGGTCTGTCTCCAGCCCT 1417  
Db |||||  
QY 1285 CTAGACGACGAGGAGTCCCGTCTTTCTTTTCA CGGAGCGGCGGCTTGGAGATGAG 1344  
Db |||||  
QY 1418 CTAGACGACGAGGAGTCCCGTCTTTCTTTTCA CGGAGCGGCGGCTTGGAGATGAG 1477  
Db |||||  
QY 1345 GCTCAGGCGGGGCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGCCCCAGG 1404  
Db |||||  
QY 1478 GCTCAGGCGGGGCTCCCGACTTCCAAAACGAGAGCTGCTTCTCGGGGCCCCAGG 1537  
Db |||||  
QY 1405 GGTGGGGCGCGGGGAGACCCCGCCCGCCAGTGCCTCCACACCCCTGCGCGGC 1464  
Db |||||  
QY 1538 GGTGGGGCGCGGGGAGACCCCGCCCGCCAGTGCCTCCACACCCCTGCGCGGC 1597  
Db |||||  
QY 1465 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGCATCGCTCTGCACACGCC 1524  
Db |||||  
QY 1598 CCCCAGGCTCCCGCGCTCTCTGGGGGACCCCTTGCATCGCTCTGCACACGCC 1657  
Db |||||  
QY 1525 CGGGCAGTCCACCGGGACCCCGGGGACACACCCCGCCAGCGCGGGGGGTC 1584  
Db |||||  
QY 1658 CGGGCAGTCCACCGGGACCCCGGGGACACACCCCGCCAGCGCGGGGGTC 1717  
Db |||||  
QY 1585 GGGGAGCGCTCGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1644  
Db |||||  
QY 1718 GGGGAGCGCTCGGAGAGTGTCTCAACTCCATCCGCAACAGCTTCTGGGCTCCCT 1777  
Db |||||  
QY 1645 CGCTTTCAGCGCGCAAGATGAGGTCTTACCGCTGAGGAGATGTCACTTGAACCCA 1704  
Db |||||  
QY 1778 CGCTTTCAGCGCGCAAGATGAGGTCTTACCGCTGAGGAGATGTCACTTGAACCCA 1837  
Db |||||  
QY 1705 GAGTCCTCCCGGAGTGGCAAAAGCTCTCGTTCGGGAGCTTCACTCTCTGGGAGAA 1764  
Db |||||  
QY 1838 GAGTCCTCCCGGAGTGGCAAAAGCTCTCGTTCGGGAGCTTCACTCTCTGGGAGAA 1897  
Db |||||  
QY 1765 GAGCAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGATC 1824  
Db |||||  
QY 1898 GAGCAACAAATATTCCTCGTGTAAAGGACAAACCTCTCAGCAGCATCAAGCAGATC 1957  
Db |||||  
QY 1825 GTCCATGCTTCTGTGCTGATCCCGAGCTGAGTCACTGAGTGTGTGTCACAGACAGGTT 1884  
Db |||||  
QY 1958 GTCCATGCTTCTGTGCTGATCCCGAGCTGAGTCACTGAGTGTGTGTCACAGACAGGTT 2017  
Db |||||  
QY 1885 AGGGCCAGTACAGGCGAGTGGGGCCCTCCCTGCTTCCAAAGCCGCTCCGCTTCCAG 1944  
Db |||||  
QY 2018 AGGGCCAGTACAGGCGAGTGGGGCCCTCCCTGCTTCCAAAGCCGCTCCGCTTCCAG 2077  
Db |||||  
QY 1945 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGACGGCAGCGAGGT 2004  
Db |||||  
QY 2078 GTGACATCAGCTCTCTGAGGGTCCAGAGCCCTCCCGGACGGGACGGCAGCGAGGT 2137  
Db |||||  
QY 2005 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCCGAGCGGTTCAAGCGA 2064  
Db |||||  
QY 2138 GGTGGCATCTACTCCGTCACCTTCACTCTCATCTCGGGTCCCGAGCGGTTCAAGCGA 2197  
Db |||||  
QY 2065 GTGTGAGACCATCCAGGACAGCTCTGAGGACCTCATGACAGCCCTCGGTGACGCC 2124  
Db |||||  
QY 2198 GTGTGAGACCATCCAGGACAGCTCTGAGGACCTCATGACAGCCCTCGGTGACGCC 2257  
Db |||||  
QY 2125 CTGCGACAGGAGAAAGCGGGGCCAGACCGGGCTCTGTGTGCTGCCACCCGAGGCTG 2184  
Db |||||  
QY 2258 CTGCGACAGGAGAAAGCGGGGCCAGACCGGGCTCTGTGTGCTGCCACCCGAGGCTG 2317  
Db |||||

QY 2185 CAGCCCCACCGCGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGAGGCCCCCCC 2244  
Db |||||  
QY 2318 CAGCCCCACCGCGCGCCAGACCCAGAGCTGAGAGCTCTCCCGCGAGGCCCCCCC 2377  
Db |||||  
QY 2245 AAGGACAAAGAGTCTCTGGCCACCAACGAGACCCCTCTGCGCTGA 2289  
Db |||||  
QY 2378 AAGGACAAAGAGTCTCTGGCCACCAACGAGACCCCTCTGCGCTGA 2422  
Db |||||  
RESULT 12  
ADL14127  
ID ADL14127 standard; cDNA; 2980 BP.  
XX  
AC ADL14127;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Novel human gene 55053 cDNA.  
XX  
KW cytostatic; cardiant; hypotensive; antiangiinal; osteopathic;  
KW antiarthritic; antirheumatic; neuroprotective; antiinflammatory;  
KW antipsoriatic; antihistamic; cardiovascular; virucide; analgesic; CNS;  
KW angiogenesis inhibitor; angiogenesis stimulator; cerebroprotective;  
KW nephrotropic; antithyroid; dermatological; immunomodulator;  
KW cell proliferation disorder; cell differentiation disorder;  
KW brain disorder; platelet disorder; breast disorder; colon disorder;  
KW kidney disorder; renal disorder; lung disorder; ovarian disorder;  
KW prostate disorder; cervical disorder; spleen disorder; thymus disorder;  
KW thyroid disorder; testes disorder; haematopoietic disorder;  
KW pancreatic disorder; skeletal muscle disorder; skin disorder;  
KW dermal disorder; bone metabolism disorder; immune disorder;  
KW inflammatory disorder; cardiovascular disorder;  
KW endothelial cell disorder; liver disorder; viral disease; pain disorder;  
KW metabolic disorder; neurological disorder;  
KW central nervous system disorder; erythroid disorder;  
KW blood vessel disorder; angiogenic disorder; cancer; heart failure;  
KW hypertension; angina; osteoarthritis; rheumatoid arthritis;  
KW multiple sclerosis; Crohn's disease; psoriasis; asthma;  
KW cell proliferation; cell differentiation; cell growth; cell division;  
KW human; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2004058355-A1.  
XX  
PD 25-MAR-2004.  
XX  
PF 25-APR-2003; 2003US-00423543.  
XX  
PR 30-SEP-1998; 98US-00163821.  
PR 27-JAN-1999; 99US-0117580P.  
PR 25-MAR-1999; 99US-00276400.  
PR 30-JUL-1999; 99US-00365162.  
PR 09-SEP-1999; 99US-00392189.  
PR 05-OCT-1999; 99US-00412210.  
PR 23-NOV-1999; 99US-00448076.  
PR 29-FEB-2000; 2000US-0186061P.  
PR 28-APR-2000; 2000US-0200688P.  
PR 19-MAY-2000; 2000US-0205447P.  
PR 30-JUN-2000; 2000US-00608921.  
PR 31-JUL-2000; 2000US-0221925P.  
PR 25-SEP-2000; 2000US-0234922P.  
PR 25-SEP-2000; 2000US-0235035P.  
PR 08-NOV-2000; 2000US-0246669P.  
PR 09-NOV-2000; 2000US-00711216.  
PR 14-NOV-2000; 2000US-0248325P.  
PR 15-NOV-2000; 2000US-0248893P.  
PR 22-DEC-2000; 2000US-0257511P.  
PR 05-JAN-2001; 2001US-0260166P.  
PR 28-FEB-2001; 2001US-00797039.  
PR 27-APR-2001; 2001US-00845044.  
PR 20-JUL-2001; 2001US-00909743.  
PR 31-JUL-2001; 2001US-00920346.

PR	13-AUG-2001;	2001US-00928531.	
PR	14-AUG-2001;	2001US-00929218.	
PR	15-AUG-2001;	2001US-0312539P.	
PR	25-SEP-2001;	2001US-00963159.	
PR	08-NOV-2001;	2001US-00008016.	
PR	13-NOV-2001;	2001US-00012055.	
PR	15-NOV-2001;	2001US-00003690.	
PR	30-JAN-2002;	2002US-00060763.	
PR	25-MAR-2002;	2002US-00105989.	
PR	12-APR-2002;	2002US-00121911.	
PR	12-AUG-2002;	2002US-00217168.	
PR	22-OCT-2002;	2002US-00278036.	
PR	02-JAN-2003;	2003US-00336489.	
PR	03-JAN-2003;	2003US-00336153.	
XX	(MILL-) MILLENNIUM PHARM INC.		
XX			
XX	Kapeller-Libermann R, Hunter JU, Meyers RE, Rudolph-Owen LA;		
PI	Curtis RAJ, Olandt PJ, Tsai F, Galvin KM, Chun M, Williamson MJ;		
PI	Silos-Santiago I, Bandaru R;		
XX			
DR	WPI; 2004-268788/25.		
DR	P-PSDB; ADL14128.		
XX			
PT	New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529,		
PT	26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593		
PT	nucleic acid molecules and proteins, useful for treating, e.g. cancer,		
PT	heart failure and angina.		
XX			
PS	Claim 1; SEQ ID NO 10; 139pp; English.		
XX			
CC	The invention describes an isolated 21910, 56634, 55053, 2504, 15977,		
CC	14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217,		
CC	21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising		
CC	any one of 40 nucleotide sequences (I). The nucleic acid molecules and		
CC	polypeptides are useful for diagnosing and treating a subject having a		
CC	disorder, or a subject at risk of developing a disorder, which is		
CC	associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,		
CC	17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983,		
CC	m1983, 38555 or 593 activity, such as cellular proliferative and/or		
CC	differentiative disorders, brain disorders, platelet disorders, breast		
CC	disorders, colon disorders, kidney (renal) disorders, lung disorders,		
CC	ovarian disorders, prostate disorders, cervical disorders, spleen		
CC	disorders, thymus disorders, thyroid disorders, testes disorders,		
CC	hematopoietic disorders, pancreatic disorders, skeletal muscle disorders,		
CC	skin (dermal) disorders, disorders associated with bone metabolism,		
CC	immune, e.g. inflammatory disorders, cardiovascular disorders,		
CC	endothelial cell disorders, liver disorders, viral diseases, pain		
CC	disorders, metabolic disorders, neurological or central nervous system		
CC	disorders, erythroid disorders, blood vessel disorders or angiogenic		
CC	disorders (all claimed), e.g. cancer, heart failure, hypertension,		
CC	angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's		
CC	disease, psoriasis, or asthma. The nucleic acid molecules and		
CC	polypeptides are also useful as modulating agents in regulating a variety		
CC	of cellular processes, e.g. cell proliferation, differentiation, growth and		
CC	division. This sequence encodes a novel human protein of the invention.		
CC	Note: The sequences given in the specification are also available in		
CC	electronic format from		
CC	ftp.seqdata.uspto.gov/sequence.html?DocID=20040058355.		
XX			
SQ	Sequence 2980 BP; 625 A; 959 C; 886 G; 510 T; 0 U; 0 Other;		
	Query Match 88.3%; Score 2020.2; DB 12; Length 2980;		
	Best Local Similarity 99.9%; Pred. No. 0;		
	Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	265 TTTAGGTACCTGGTCTCGAGACAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 324		
Db	398 TATTGTGTTACCTGGTCTCGAGACAGCTCTCGGGGGGTGAGCTATTTCGACTACCTGGTAAAG 457		
QY	325 AAGGGAGACTGACGCCCAAGAGAGGCCGGAAGTTCTTCGCCAGATTGTGTCTGGCTG 384		
Db	458 AAGGGGAGACTGACGCCCAAGAGAGGCCGGAAGTTCTTCGCCAGATTGTGTCTGGCTG 517		

QY	385 GACTTCTGCCACAGCTATTCTCAATCTGTGCCACAGAGACCTTAAAGCCCGAGAACCTGCTTTTG 444	
Db	518 GACTTCTGCCACAGCTATTCTCAATCTGTGCCACAGAGACCTTAAAGCCCGAGAACCTGCTTTTG 577	
QY	445 GATGAGAAAAACAATCCGCAATTCGAGACTTCGGCATCGCTCCCTGAGGTGGGGGAC 504	
Db	578 GATGAGAAAAACAATCCGCAATTCGAGACTTCGGCATCGCTCCCTGAGGTGGGGGAC 637	
QY	505 AGCCTCTCGAGACACAGCTCGGGTCCCGCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG 564	
Db	638 AGCCTCTCGAGACACAGCTCGGGTCCCGCCCATTTATGCGTGTCCAGAGGTGATTAAAGGG 697	
QY	565 GAAAAATATGATGGCCCGCCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG 624	
Db	698 GAAAAATATGATGGCCCGCCGCGGAGACATGTGGAGCTGTGGAGTCACTCTTTCGCCCTG 757	
QY	625 CTCGTGGGGGCTCTGCGCTTTTGTATGAGACAACCTCCGCGAGCTGTGGAGAGGTGAAA 684	
Db	758 CTCGTGGGGGCTCTGCGCTTTTGTATGAGACAACCTCCGCGAGCTGTGGAGAGGTGAAA 817	
QY	685 CGGGGGCTCTCCACATGCCCACTTTCTTCCAGATTTCGCCAGAGCTCTGCGCGCGGTA 744	
Db	818 CGGGGGCTCTCTCCACATGCCCACTTTCTTCCAGATTTCGCCAGAGCTCTGCGCGCGGTA 877	
QY	745 ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATCTCTGG 804	
Db	878 ATGATCGAAGTGGAGCCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAAAATCTCTGG 937	
QY	805 TACCTAGGCGGGAAAAACAAGAGCAGACCCGCTGCTGGAGCAGCCCTGCGCGCGGGTA 864	
Db	938 TACCTAGGCGGGAAAAACAAGAGCAGACCCGCTGCTGGAGCAGCCCTGCGCGCGGGTA 997	
QY	865 GCATCGCGAGCTGCTCATTCACAGAGAGCTGAGCCCGAGCTCTAGAGAGCATGGCA 924	
Db	998 GCATCGCGAGCTGCTCATTCACAGAGAGCTGAGCCCGAGCTCTAGAGAGCATGGCA 1057	
QY	925 TCATCGGGTGTCTTACGAGACCCGCGAGAGGCTGCATCGCGAGCTGCGCAGTGAAGGAG 984	
Db	1058 TCATCGGGTGTCTTACGAGACCCGCGAGAGGCTGCATCGCGAGCTGCGCAGTGAAGGAG 1117	
QY	985 AACCAAGAAAAAGATGATATATTATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1044	
Db	1118 AACCAAGAAAAAGATGATATATTATCTGCTTTTGGATCGGAAGAGCGGTATCCAGCTGT 1177	
QY	1045 GAGGACACGACCTGCTCCCGGAATGATTTGACCCCGGAGCGTGTGGATTCT 1104	
Db	1178 GAGGACACGACCTGCTCCCGGAATGATTTGACCCCGGAGCGTGTGGATTCT 1237	
QY	1105 CCATGCTGAGCCGCTCACGGGAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1164	
Db	1238 CCATGCTGAGCCGCTCACGGGAAGCGCGACACAGAGCGGAAGTCCATGGAAGTCTTGAGC 1297	
QY	1165 ATCACCAGTCCCGGGGTGTGCTCCCTGTATCCACCGAGCGGCTTGGAGATGGCC 1224	
Db	1298 ATCACCAGTCCCGGGGTGTGCTCCCTGTATCCACCGAGCGGCTTGGAGATGGCC 1357	
QY	1225 CAGCAGACACAGATCCCGTAGCGTCAGTGGAGCTCCACGGGTCTGTCTCCAGCCCT 1284	
Db	1358 CAGCAGACACAGATCCCGTAGCGTCAGTGGAGCTCCACGGGTCTGTCTCCAGCCCT 1417	
QY	1285 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTCAACCGAGCCGGGGGTGGAGATGAG 1344	
Db	1418 CTAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTCAACCGAGCCGGGGGTGGAGATGAG 1477	
QY	1345 GCTCGAGGGGGGCTCCCGACTTCCAAAAACGACAGCGTGCCTTCTCGGGGGCCCCAGG 1404	
Db	1478 GCTCGAGGGGGGCTCCCGACTTCCAAAAACGACAGCGTGCCTTCTCGGGGGCCCCAGG 1537	
QY	1405 GGTGGGGGGCGCGGGGAGAGAGCCCGCGCCCGCAGTCCCGCTCCACACCCCTGCCCGC 1464	
Db	1538 GGTGGGGGGCGCGGGGAGAGAGCCCGCGCCCGCAGTCCCGCTCCACACCCCTGCCCGC 1597	

```
QY 1465 CCCCAGGCTCCCGCGCTCTCTGGGGGAGACCCCTTGCACTCGCCTCTGCACAGCCC 1524
Db 1598 CCCCAGGCTCCCGCGCTCTCTGGGGGAGACCCCTTGCACTCGCCTCTGCACAGCCC 1657
QY 1525 CGGCCAGTCCACCGGAGCCCGGGGACAAACACACACCCCGGCGGGTGGGGTC 1584
Db 1658 CGGCCAGTCCACCGGAGCCCGGGGACAAACACACACCCCGGCGGGTGGGGTC 1717
QY 1585 GGGGAGCGGCTGGAGAGTGTCTCAATCCATCCGCAACAGCTTCTGGGTCGCCCT 1644
Db 1718 GGGGAGCGGCTGGAGAGTGTCTCAATCCATCCGCAACAGCTTCTGGGTCGCCCT 1777
QY 1645 CGCTTTTCCAGCGGCGCAAGATGACGTCCCTACCGCTGAGGAGATGTCAGCTTACGCCA 1704
Db 1778 CGCTTTTCCAGCGGCGCAAGATGACGTCCCTACCGCTGAGGAGATGTCAGCTTACGCCA 1837
QY 1705 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTCGGGAATTCATCTCTTGGCAAA 1764
Db 1838 GAGTCTCTCCCGGAGCTGGCAAAACGCTCTCTGGTTCGGGAATTCATCTCTTGGCAAA 1897
QY 1765 GAAGAAATAATTTCTGTGCTTAAAGGACAAACCTTCTAGCAGCATCAAGCAGACATC 1824
Db 1898 GAAGAAATAATTTCTGTGCTTAAAGGACAAACCTTCTAGCAGCATCAAGCAGACATC 1957
QY 1825 GTCCATGCTTCTGTGATCCCGAGCTGAGTCACAGTGTGCTGTCACAGCAGCTTC 1884
Db 1958 GTCCATGCTTCTGTGATCCCGAGCTGAGTCACAGTGTGCTGTCACAGCAGCTTC 2017
QY 1885 AGGCCGAGTACAAAGGCGAGTGGGGCCCTCTCTTCAAAAGCCGCTCCGCTTCCAG 1944
Db 2018 AGGCCGAGTACAAAGGCGAGTGGGGCCCTCTCTTCAAAAGCCGCTCCGCTTCCAG 2077
QY 1945 GTGACATCAGTCTCTGTAGGGTCCAGAGCCCTTCCCGGACGCGGACGCGAGGT 2004
Db 2078 GTGACATCAGTCTCTGTAGGGTCCAGAGCCCTTCCCGGACGCGGACGCGAGGT 2137
QY 2005 GGTGGCATCTACTCGGTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 2064
Db 2138 GGTGGCATCTACTCGGTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 2197
QY 2065 GTGTGGAGACATTCAGGACAGCTCTGAGCACTCATGACACGCTCCGTCGACGCC 2124
Db 2198 GTGTGGAGACATTCAGGACAGCTCTGAGCACTCATGACACGCTCCGTCGACGCC 2257
QY 2125 CTGCGACAGGAGAAACGGGGCCCGAGACCGGCTCTGCTGCTGCTGCTGCTGCTG 2184
Db 2258 CTGCGACAGGAGAAACGGGGCCCGAGACCGGCTCTGCTGCTGCTGCTGCTGCTG 2317
QY 2185 CAGCCCCCAGCGGCGCCGAGCCAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2244
Db 2318 CAGCCCCCAGCGGCGCCGAGCCAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2377
QY 2245 AAGGACAAGAGCTCTCTGGCCCAACAGCGGACCCCTCTGCGCTGA 2289
Db 2378 AAGGACAAGAGCTCTCTGGCCCAACAGCGGACCCCTCTGCGCTGA 2422
```

## RESULT 13

ADQ85869 standard; cDNA; 2980 BP.

```
XX ADQ85869;
AC AC
XX 07-OCT-2004 (first entry)
XX Human tumour-associated antigenic target (TAT) cDNA sequence #2741.
XX human; tumour-associated antigenic target; TAT; cytosolic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
XX Homo sapiens.
XX W02004060270-A2.
```

```
XX 22-JUL-2004.
XX 15-OCT-2003; 2003WO-US029126.
XX 18-OCT-2002; 2002US-0418988P.
XX (GETH ) GENENTECH INC.
XX (WUTD/) WU T D.
XX (ZHOU/) ZHOU Y.
XX Wu TD, Zhou Y;
XX WPI; 2004-534300/51.
```

New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.

Claim 1; SEQ ID NO 2741; 5504pp; English.

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also useful for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

Sequence 2980 BP; 607 A; 939 C; 909 G; 525 T; 0 U; 0 Other;

Query Match 88.3%; Score 2020.2; DB 13; Length 2980;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 265 TTAGGTACTGTTCTGGAGCAGCTCTCGGGGGTGGAGTATTCGACTACTGTTAAG 324
Db 491 TATTGTACTGTTCTGGAGCAGCTCTCGGGGGTGGAGTATTCGACTACTGTTAAG 550
QY 325 AAGGGAGACTGACGCCCAAGGAGGCCCGAAAGTTCTTCCGCCAGATTGTGTGCGCTG 384
Db 551 AAGGGAGACTGACGCCCAAGGAGGCCCGAAAGTTCTTCCGCCAGATTGTGTGCGCTG 610
```



```
QY 385 GACTTCTGCACAGCTACTCCATCTGCCACAGAGCTTAAAGCCCGAGAACCTGCTTTTG 444
D 386 |||||
D 387 |||||
D 388 |||||
D 389 |||||
D 390 |||||
D 391 |||||
D 392 |||||
D 393 |||||
D 394 |||||
D 395 |||||
D 396 |||||
D 397 |||||
D 398 |||||
D 399 |||||
D 400 |||||
D 401 |||||
D 402 |||||
D 403 |||||
D 404 |||||
D 405 |||||
D 406 |||||
D 407 |||||
D 408 |||||
D 409 |||||
D 410 |||||
D 411 |||||
D 412 |||||
D 413 |||||
D 414 |||||
D 415 |||||
D 416 |||||
D 417 |||||
D 418 |||||
D 419 |||||
D 420 |||||
D 421 |||||
D 422 |||||
D 423 |||||
D 424 |||||
D 425 |||||
D 426 |||||
D 427 |||||
D 428 |||||
D 429 |||||
D 430 |||||
D 431 |||||
D 432 |||||
D 433 |||||
D 434 |||||
D 435 |||||
D 436 |||||
D 437 |||||
D 438 |||||
D 439 |||||
D 440 |||||
D 441 |||||
D 442 |||||
D 443 |||||
D 444 |||||
D 445 |||||
D 446 |||||
D 447 |||||
D 448 |||||
D 449 |||||
D 450 |||||
D 451 |||||
D 452 |||||
D 453 |||||
D 454 |||||
D 455 |||||
D 456 |||||
D 457 |||||
D 458 |||||
D 459 |||||
D 460 |||||
D 461 |||||
D 462 |||||
D 463 |||||
D 464 |||||
D 465 |||||
D 466 |||||
D 467 |||||
D 468 |||||
D 469 |||||
D 470 |||||
D 471 |||||
D 472 |||||
D 473 |||||
D 474 |||||
D 475 |||||
D 476 |||||
D 477 |||||
D 478 |||||
D 479 |||||
D 480 |||||
D 481 |||||
D 482 |||||
D 483 |||||
D 484 |||||
D 485 |||||
D 486 |||||
D 487 |||||
D 488 |||||
D 489 |||||
D 490 |||||
D 491 |||||
D 492 |||||
D 493 |||||
D 494 |||||
D 495 |||||
D 496 |||||
D 497 |||||
D 498 |||||
D 499 |||||
D 500 |||||
D 501 |||||
D 502 |||||
D 503 |||||
D 504 |||||
D 505 |||||
D 506 |||||
D 507 |||||
D 508 |||||
D 509 |||||
D 510 |||||
D 511 |||||
D 512 |||||
D 513 |||||
D 514 |||||
D 515 |||||
D 516 |||||
D 517 |||||
D 518 |||||
D 519 |||||
D 520 |||||
D 521 |||||
D 522 |||||
D 523 |||||
D 524 |||||
D 525 |||||
D 526 |||||
D 527 |||||
D 528 |||||
D 529 |||||
D 530 |||||
D 531 |||||
D 532 |||||
D 533 |||||
D 534 |||||
D 535 |||||
D 536 |||||
D 537 |||||
D 538 |||||
D 539 |||||
D 540 |||||
D 541 |||||
D 542 |||||
D 543 |||||
D 544 |||||
D 545 |||||
D 546 |||||
D 547 |||||
D 548 |||||
D 549 |||||
D 550 |||||
D 551 |||||
D 552 |||||
D 553 |||||
D 554 |||||
D 555 |||||
D 556 |||||
D 557 |||||
D 558 |||||
D 559 |||||
D 560 |||||
D 561 |||||
D 562 |||||
D 563 |||||
D 564 |||||
D 565 |||||
D 566 |||||
D 567 |||||
D 568 |||||
D 569 |||||
D 570 |||||
D 571 |||||
D 572 |||||
D 573 |||||
D 574 |||||
D 575 |||||
D 576 |||||
D 577 |||||
D 578 |||||
D 579 |||||
D 580 |||||
D 581 |||||
D 582 |||||
D 583 |||||
D 584 |||||
D 585 |||||
D 586 |||||
D 587 |||||
D 588 |||||
D 589 |||||
D 590 |||||
D 591 |||||
D 592 |||||
D 593 |||||
D 594 |||||
D 595 |||||
D 596 |||||
D 597 |||||
D 598 |||||
D 599 |||||
D 600 |||||
D 601 |||||
D 602 |||||
D 603 |||||
D 604 |||||
D 605 |||||
D 606 |||||
D 607 |||||
D 608 |||||
D 609 |||||
D 610 |||||
D 611 |||||
D 612 |||||
D 613 |||||
D 614 |||||
D 615 |||||
D 616 |||||
D 617 |||||
D 618 |||||
D 619 |||||
D 620 |||||
D 621 |||||
D 622 |||||
D 623 |||||
D 624 |||||
D 625 |||||
D 626 |||||
D 627 |||||
D 628 |||||
D 629 |||||
D 630 |||||
D 631 |||||
D 632 |||||
D 633 |||||
D 634 |||||
D 635 |||||
D 636 |||||
D 637 |||||
D 638 |||||
D 639 |||||
D 640 |||||
D 641 |||||
D 642 |||||
D 643 |||||
D 644 |||||
D 645 |||||
D 646 |||||
D 647 |||||
D 648 |||||
D 649 |||||
D 650 |||||
D 651 |||||
D 652 |||||
D 653 |||||
D 654 |||||
D 655 |||||
D 656 |||||
D 657 |||||
D 658 |||||
D 659 |||||
D 660 |||||
D 661 |||||
D 662 |||||
D 663 |||||
D 664 |||||
D 665 |||||
D 666 |||||
D 667 |||||
D 668 |||||
D 669 |||||
D 670 |||||
D 671 |||||
D 672 |||||
D 673 |||||
D 674 |||||
D 675 |||||
D 676 |||||
D 677 |||||
D 678 |||||
D 679 |||||
D 680 |||||
D 681 |||||
D 682 |||||
D 683 |||||
D 684 |||||
D 685 |||||
D 686 |||||
D 687 |||||
D 688 |||||
D 689 |||||
D 690 |||||
D 691 |||||
D 692 |||||
D 693 |||||
D 694 |||||
D 695 |||||
D 696 |||||
D 697 |||||
D 698 |||||
D 699 |||||
D 700 |||||
D 701 |||||
D 702 |||||
D 703 |||||
D 704 |||||
D 705 |||||
D 706 |||||
D 707 |||||
D 708 |||||
D 709 |||||
D 710 |||||
D 711 |||||
D 712 |||||
D 713 |||||
D 714 |||||
D 715 |||||
D 716 |||||
D 717 |||||
D 718 |||||
D 719 |||||
D 720 |||||
D 721 |||||
D 722 |||||
D 723 |||||
D 724 |||||
D 725 |||||
D 726 |||||
D 727 |||||
D 728 |||||
D 729 |||||
D 730 |||||
D 731 |||||
D 732 |||||
D 733 |||||
D 734 |||||
D 735 |||||
D 736 |||||
D 737 |||||
D 738 |||||
D 739 |||||
D 740 |||||
D 741 |||||
D 742 |||||
D 743 |||||
D 744 |||||
D 745 |||||
D 746 |||||
D 747 |||||
D 748 |||||
D 749 |||||
D 750 |||||
D 751 |||||
D 752 |||||
D 753 |||||
D 754 |||||
D 755 |||||
D 756 |||||
D 757 |||||
D 758 |||||
D 759 |||||
D 760 |||||
D 761 |||||
D 762 |||||
D 763 |||||
D 764 |||||
D 765 |||||
D 766 |||||
D 767 |||||
D 768 |||||
D 769 |||||
D 770 |||||
D 771 |||||
D 772 |||||
D 773 |||||
D 774 |||||
D 775 |||||
D 776 |||||
D 777 |||||
D 778 |||||
D 779 |||||
D 780 |||||
D 781 |||||
D 782 |||||
D 783 |||||
D 784 |||||
D 785 |||||
D 786 |||||
D 787 |||||
D 788 |||||
D 789 |||||
D 790 |||||
D 791 |||||
D 792 |||||
D 793 |||||
D 794 |||||
D 795 |||||
D 796 |||||
D 797 |||||
D 798 |||||
D 799 |||||
D 800 |||||
D 801 |||||
D 802 |||||
D 803 |||||
D 804 |||||
D 805 |||||
D 806 |||||
D 807 |||||
D 808 |||||
D 809 |||||
D 810 |||||
D 811 |||||
D 812 |||||
D 813 |||||
D 814 |||||
D 815 |||||
D 816 |||||
D 817 |||||
D 818 |||||
D 819 |||||
D 820 |||||
D 821 |||||
D 822 |||||
D 823 |||||
D 824 |||||
D 825 |||||
D 826 |||||
D 827 |||||
D 828 |||||
D 829 |||||
D 830 |||||
D 831 |||||
D 832 |||||
D 833 |||||
D 834 |||||
D 835 |||||
D 836 |||||
D 837 |||||
D 838 |||||
D 839 |||||
D 840 |||||
D 841 |||||
D 842 |||||
D 843 |||||
D 844 |||||
D 845 |||||
D 846 |||||
D 847 |||||
D 848 |||||
D 849 |||||
D 850 |||||
D 851 |||||
D 852 |||||
D 853 |||||
D 854 |||||
D 855 |||||
D 856 |||||
D 857 |||||
D 858 |||||
D 859 |||||
D 860 |||||
D 861 |||||
D 862 |||||
D 863 |||||
D 864 |||||
D 865 |||||
D 866 |||||
D 867 |||||
D 868 |||||
D 869 |||||
D 870 |||||
D 871 |||||
D 872 |||||
D 873 |||||
D 874 |||||
D 875 |||||
D 876 |||||
D 877 |||||
D 878 |||||
D 879 |||||
D 880 |||||
D 881 |||||
D 882 |||||
D 883 |||||
D 884 |||||
D 885 |||||
D 886 |||||
D 887 |||||
D 888 |||||
D 889 |||||
D 890 |||||
D 891 |||||
D 892 |||||
D 893 |||||
D 894 |||||
D 895 |||||
D 896 |||||
D 897 |||||
D 898 |||||
D 899 |||||
D 900 |||||
D 901 |||||
D 902 |||||
D 903 |||||
D 904 |||||
D 905 |||||
D 906 |||||
D 907 |||||
D 908 |||||
D 909 |||||
D 910 |||||
D 911 |||||
D 912 |||||
D 913 |||||
D 914 |||||
D 915 |||||
D 916 |||||
D 917 |||||
D 918 |||||
D 919 |||||
D 920 |||||
D 921 |||||
D 922 |||||
D 923 |||||
D 924 |||||
D 925 |||||
D 926 |||||
D 927 |||||
D 928 |||||
D 929 |||||
D 930 |||||
D 931 |||||
D 932 |||||
D 933 |||||
D 934 |||||
D 935 |||||
D 936 |||||
D 937 |||||
D 938 |||||
D 939 |||||
D 940 |||||
D 941 |||||
D 942 |||||
D 943 |||||
D 944 |||||
D 945 |||||
D 946 |||||
D 947 |||||
D 948 |||||
D 949 |||||
D 950 |||||
D 951 |||||
D 952 |||||
D 953 |||||
D 954 |||||
D 955 |||||
D 956 |||||
D 957 |||||
D 958 |||||
D 959 |||||
D 960 |||||
D 961 |||||
D 962 |||||
D 963 |||||
D 964 |||||
D 965 |||||
D 966 |||||
D 967 |||||
D 968 |||||
D 969 |||||
D 970 |||||
D 971 |||||
D 972 |||||
D 973 |||||
D 974 |||||
D 975 |||||
D 976 |||||
D 977 |||||
D 978 |||||
D 979 |||||
D 980 |||||
D 981 |||||
D 982 |||||
D 983 |||||
D 984 |||||
D 985 |||||
D 986 |||||
D 987 |||||
D 988 |||||
D 989 |||||
D 990 |||||
D 991 |||||
D 992 |||||
D 993 |||||
D 994 |||||
D 995 |||||
D 996 |||||
D 997 |||||
D 998 |||||
D 999 |||||
D 1000 |||||
```

```
1691 CCCCCAGGCTCCCGCGCTCCTCTGCGGGGACCCCTTTGCACTCGCCTCTGCACAGCCC 1750
1525 CGGGCAGTCCACCGGACCCCGGGGACAAACACACCCCGGAGCCCGGGGGTGGCGTC 1584
1751 CGGGCAGTCCACCGGACCCCGGGGACAAACACACCCCGGAGCCCGGGGGTGGCGTC 1810
1585 GGGGAGCGCGCTGAGGAGTCTCAACTCCATCCGCAACAGCTTCTGCGGCTCCCT 1644
1811 GGGGAGCGCGCTGAGGAGTCTCAACTCCATCCGCAACAGCTTCTGCGGCTCCCT 1870
1645 CGCTTTCACCGGCGAAGATGCGAGTCCGTACCGCTGAGGAGATCTCCAGCTTGAAGCCA 1704
1871 CGCTTTCACCGGCGAAGATGCGAGTCCGTACCGCTGAGGAGATCTCCAGCTTGAAGCCA 1930
1705 GAGTCTCCCGCGAGCTGGCAAAACGCTCTGCTGGTTCGGGAACTTCACTCTCTTGAACAA 1764
1931 GAGTCTCCCGCGAGCTGGCAAAACGCTCTGCTGGTTCGGGAACTTCACTCTCTTGAACAA 1990
1765 GAAGAACAAATATCTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGCATC 1824
1991 GAAGAACAAATATCTCTGCTGCTAAAGGACAAACCTCTCAGCAGCATCAAGCAGCATC 2050
1825 GTCCATGCTTCTGCTGATCCCGAGCTGAGTCAAGTGTCTGTCAAGCAGCATCAGCTTC 1884
2051 GTCCATGCTTCTGCTGATCCCGAGCTGAGTCAAGTGTCTGTCAAGCAGCATCAGCTTC 2110
1885 AGGGCGAGTACAAAGGCGAGTGGCGGCCCTCTGCTTCCAAAGCCGCTCGCTTCCAG 1944
2111 AGGGCGAGTACAAAGGCGAGTGGCGGCCCTCTGCTTCCAAAGCCGCTCGCTTCCAG 2170
1945 GTGGAATCAGCTCTCTGAGGCTCAGAGCCCTCCCGGAGCGGAGCGGAGCT 2004
2171 GTGGAATCAGCTCTCTGAGGCTCAGAGCCCTCCCGGAGCGGAGCGGAGCT 2230
2005 GTGGAATCAGCTCTCTGAGGCTCAGAGCCCTCCCGGAGCGGAGCGGAGCT 2064
2231 GTGGAATCAGCTCTCTGAGGCTCAGAGCCCTCCCGGAGCGGAGCGGAGCT 2290
2065 GTGGAATCAGCTCTCTGAGGCTCAGAGCCCTCCCGGAGCGGAGCGGAGCT 2124
2291 GTGGAATCAGCTCTCTGAGGCTCAGAGCCCTCCCGGAGCGGAGCGGAGCT 2350
2125 CTGCGAGCAGAGAAACCGGGGCGGAGCCCGGCTGCTGGTCCCGGAGCGGAGCT 2184
2351 CTGCGAGCAGAGAAACCGGGGCGGAGCCCGGCTGCTGGTCCCGGAGCGGAGCT 2410
2185 CAGCCCCCAGCGGGCGGCGGAGCCCGGAGCTGAGCAGCTCTCCCGGAGCGGAGCT 2244
2411 CAGCCCCCAGCGGGCGGCGGAGCCCGGAGCTGAGCAGCTCTCCCGGAGCGGAGCT 2470
2245 AAGGACAAAGAGTCTCTGCGGCGGAGCCCTCTGCGGCTGA 2289
2471 AAGGACAAAGAGTCTCTGCGGCGGAGCCCTCTGCGGCTGA 2515
```

## RESULT 14

ADQ89183  
ID ADQ89183 standard; cDNA; 2980 BP.

AC ADQ89183;

DT 21-OCT-2004 (first entry)

Human urological disorder related protein 55053 encoding cDNA SEQ.135.

urological disorder; uropathic; cytostatic; urinary incontinence;  
benign prostatic hyperplasia; human; gene; ss.

OS Homo sapiens.

Key Location/Qualifiers  
FH 86. .2422  
CDS



```
FT      /*tag= a
PN      /product= "urological disorder related protein 55053"
XX      WO2004065576-A2.
XX      05-AUG-2004.
XX      14-JAN-2004; 2004WO-US000750.
XX      15-JAN-2003; 2003US-0440318P.
XX      04-FEB-2003; 2003US-0444783P.
XX      27-MAR-2003; 2003US-0457901P.
XX      08-MAY-2003; 2003US-0468775P.
XX      19-MAY-2003; 2003US-0471614P.
XX      16-JUN-2003; 2003US-0478742P.
XX      18-JUL-2003; 2003US-0488529P.
XX      30-JUL-2003; 2003US-0491156P.
XX      02-SEP-2003; 2003US-0499594P.
XX      26-SEP-2003; 2003US-0506332P.
XX      (MILL-) MILLENNIUM PHARM INC.
XX      Karicheti V, Silos-Santiago I, Eliasof SD;
XX      WPI; 2004-562167/54.
XX      P-PSDB; ADQ89184.
XX      Use of polypeptides related to urological disorders, e.g. 44390, 54181,
XX      211 or for identifying a compound capable of treating a urological
XX      disorder or identifying and treating a subject having a urological
XX      disorder.
XX      Claim 1; SEQ ID NO 135; 542pp; English.
XX      The present invention describes the use of polypeptides related to
XX      urological disorders for identifying a compound capable of treating a
XX      urological disorder, identifying a subject having a urological disorder,
XX      or treating a subject having a urological disorder. Also described: (1) a
XX      method for identifying a compound capable of treating a urological
XX      disorder; (2) a method for identifying a subject having a urological
XX      disorder. The compound has uteropathic and cytostatic activities. The
XX      polypeptides related to urological disorders are useful for identifying a
XX      compound capable of treating a urological disorder, identifying a subject
XX      having a urological disorder, or treating a subject having a urological
XX      disorder. Disorders include urinary incontinence and benign prostatic
XX      hyperplasia. The present sequence encodes a human urological disorder
XX      related protein, which is used in the exemplification of the present
XX      invention.
XX      SQ      Sequence 2980 BP; 625 A; 959 C; 886 G; 510 T; 0 U; 0 Other;
Query Match      88.3%; Score 2020.2; DB 13; Length 2980;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      265 TTTAGGTACCTGGTTCTGGAGACAGTCTCGGGGGGTGAGCTATTGCACTACCTGGTAAAG 324
DB      398 TATTGTACCTGGTTCTGGAGACAGTCTCGGGGGGTGAGCTATTGCACTACCTGGTAAAG 457
QY      325 AAGGGAGACTGACGCCCAAGAGAGCCGAAAGTTCTTCGCCAGATGTGTCTGCGCTG 384
DB      458 AAGGGAGACTGACGCCCAAGAGAGCCGAAAGTTCTTCGCCAGATGTGTCTGCGCTG 517
QY      385 GACTTCTGCCACAGCTACTCCATCTGCCACAGACACTTAAGCCCGAGAACCTGCTTTTG 444
DB      518 GACTTCTGCCACAGCTACTCCATCTGCCACAGACACTTAAGCCCGAGAACCTGCTTTTG 577
QY      445 GATGAGAAAAACAACATCCGATTCGAGACTTCGGCATGGCGTCCCTGCAAGGTGGGGAC 504
DB      578 GATGAGAAAAACAACATCCGATTCGAGACTTCGGCATGGCGTCCCTGCAAGGTGGGGAC 637
QY      505 AGCCTCTGGAGACCAAGTGGGGTCCCCCATTTATCGGTGTCCAGAGGTGATTAAGGGG 564
638 AGCCTCTGGAGACCAAGTGGGGTCCCCCATTTATCGGTGTCCAGAGGTGATTAAGGGG 697
565 GAAAAATATGATGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTCTTCGCCCTG 624
698 GAAAAATATGATGCGCGCGGCGAGACATGTGGAGCTGTGGAGTCACTCTCTTCGCCCTG 757
625 CTGCTGGGGGCTCTGCCCTTTTGATGACGACAACTCCGCCAGCTGTGGAGAAAGTGA 684
758 CTGCTGGGGGCTCTGCCCTTTTGATGACGACAACTCCGCCAGCTGTGGAGAAAGTGA 817
685 CGGGGCGTCTTTCACATGCGCCCACTTCACTCTCCAGATTGCCAGAGCTCTCTCAGGGGA 744
818 CGGGGCGTCTTTCACATGCGCCCACTTCACTCTCCAGATTGCCAGAGCTCTCTCAGGGGA 877
745 ATGATCGAAGTGGAGCGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTTGG 804
878 ATGATCGAAGTGGAGCGCCGAAAAAGGCTCAGTCTGGAGCAAAATTCAGAAACATCTTTGG 937
805 TACCTAGCGGGGAAAACAGAGCCAGACCCGCTGCTCTGGAGCAGCCCTTGGCCGCGGGTA 864
938 TACCTAGCGGGGAAAACAGAGCCAGACCCGCTGCTGGAGCAGCCCTTGGCCGCGGGTA 997
865 GCCATGCGGAGCCTGCGCATCCAGCGAGAGCTGACCCCGACGCTCTAGAGAGCATGCA 924
998 GCCATGCGGAGCCTGCGCATCCAGCGAGAGCTGACCCCGACGCTCTAGAGAGCATGCA 1057
925 TCACTGGGCTGCTTCAGGGACCGGAGAGCTGCGATCGCGAGCTGCGCAGTGGAGAGAG 984
1058 TCACTGGGCTGCTTCAGGGACCGGAGAGCTGCGATCGCGAGCTGCGCAGTGGAGAGAG 1117
985 AACCAAGAAAAGATGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCCAAGTGT 1044
1118 AACCAAGAAAAGATGATATATATCTGCTTTTGGATCGAAGAGCGGTATCCCAAGTGT 1177
1045 GAGGACCAAGACCTGCTCCCGGAATGATGTTGACCCCGGAGAGCGGTGCGATCTCT 1104
1178 GAGGACCAAGACCTGCTCCCGGAATGATGTTGACCCCGGAGAGCGGTGCGATCTCT 1237
1105 CCATGCTGAGCCGTCAACGGGAAAGCGGACGAGCGGAAAGTCCATGGAAGTCTCTGAGC 1164
1238 CCATGCTGAGCCGTCAACGGGAAAGCGGACGAGCGGAAAGTCCATGGAAGTCTCTGAGC 1297
1165 ATCAACGATCGGGGGTGTGCTCCCTGTATCCACCGAGCGGGCTTTGGAGATGCGC 1224
1298 ATCAACGATCGGGGGTGTGCTCCCTGTATCCACCGAGCGGGCTTTGGAGATGCGC 1357
1225 CAGCAGACCAAGATCCCGTAGGCTCAGTGGAGCTTCCAGGGTCTGTCTCTCAGGCCT 1284
1358 CAGCAGACCAAGATCCCGTAGGCTCAGTGGAGCTTCCAGGGTCTGTCTCTCAGGCCT 1417
1285 CTAAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTACCGGAGCGGGGCTGGAGATGAG 1344
1418 CTAAAGCAGCCCAAGAGTCCGGTCTTTTCTTTTACCGGAGCGGGGCTGGAGATGAG 1477
1345 GCTCGAGCGGGGGCTCTCCCGACTTCCAAACCGAGACGCTGCTTCTCGGGGCCCCCAGG 1404
1478 GCTCGAGCGGGGGCTCTCCCGACTTCCAAACCGAGACGCTGCTTCTCGGGGCCCCCAGG 1537
1405 GGTGGGGGCGCGGGGAGAGCCCCCGCCCCCGAGTCCCGCTCCACACCCCTGCCCCGC 1464
1538 GGTGGGGGCGCGGGGAGAGCCCCCGCCCCCGAGTCCCGCTCCACACCCCTGCCCCGC 1597
1465 CCCCAGGCTCCCGGCTCTCTTGGGGGACCCCTTTCGACTCGCTCTGCAACACGCC 1524
1598 CCCCAGGCTCCCGGCTCTCTTGGGGGACCCCTTTCGACTCGCTCTGCAACACGCC 1657
1525 CGGGCCAGTCCACCGGGACCCCGGGGACAAACCAACCCCGGCGGGGGTGGGGTC 1584
1658 CGGGCCAGTCCACCGGGACCCCGGGGACAAACCAACCCCGGCGGGGGTGGGGTC 1717
1585 GGGGAGCGCCCTGGAGAGTCTGCTCAACTCCATCCATCCGGAACAGCTTCTTGGGCTCCCT 1644
```





This Page Blank (uspto)